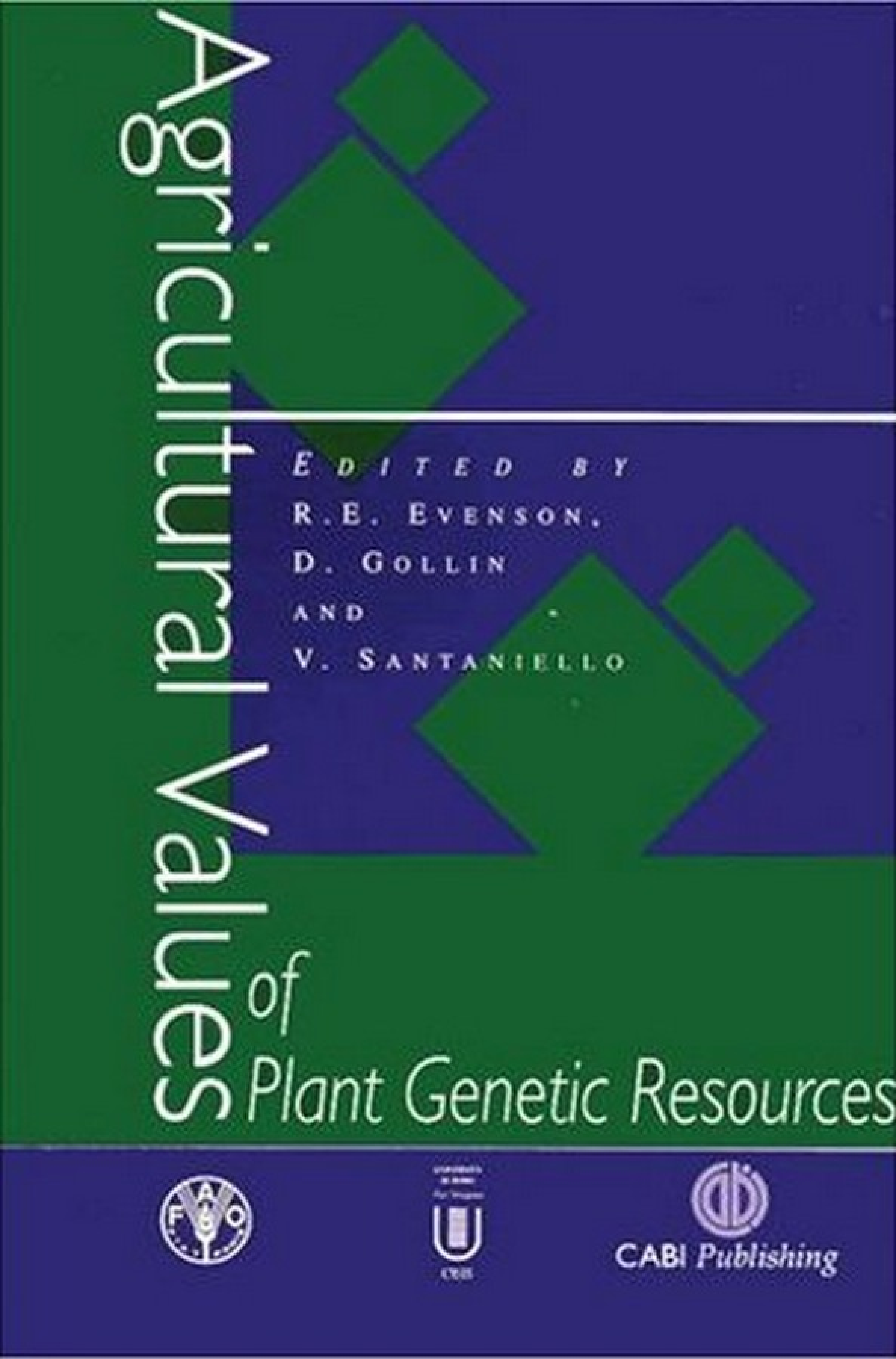

Agricultural Values of Plant Genetic Resources

Edited by

R.E. Evenson,
D. Gollin
and
V. Santaniello

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Foreword

There is growing international consensus on the urgency of slowing the human-induced deterioration of biodiversity, a deterioration that may be coming at high costs to present and future generations. Indeed, within the United Nations system, the adoption of the International Undertaking on Plant Genetic Resources in 1983, at the Food and Agriculture Organization (FAO), and of the Convention on Biological Diversity (CDB) in 1992, at the Rio Earth Summit, were motivated by the universal goal of achieving a better sustainability and diversity of species and ecosystems. As this Convention also recognized the particular relevance of biodiversity for food and agriculture, the FAO adopted a resolution in 1993 requesting member countries to negotiate (through the FAO Inter-governmental Commission on Genetic Resources for Food and Agriculture) the revision of the International Undertaking in harmony with the CBD. The Third Conference of the Parties to the Convention also decided to establish a multi-year programme of activities on agricultural biological diversity with the goals of: (i) promoting the positive effects and mitigating the negative impacts of agricultural practices on biological diversity in agro-ecosystems and their interface with other ecosystems; (ii) promoting the conservation and sustainable use of genetic resources of actual or potential value for food and agriculture; and (iii) promoting the fair and equitable sharing of benefits arising from the utilization of genetic resources. Benefit sharing is also called for under the International Undertaking's endorsement of the concept of Farmers' Rights, which aims, *inter alia*, to 'allow farmers, their communities, and countries in all regions, to participate fully in the benefits derived, at present and in the future, from the improved use of plant genetic resources'. The CBD Secretariat has agreed to work jointly with the FAO in the implementation of this programme of activities.

In considering the sharing of benefits between providers and users of genetic material, at national and global levels, questions of economic efficiency arise. Unfortunately, the economic benefits associated with the conservation and sustainable use of genetic resources for food and agriculture are poorly understood. In fact, FAO's desire to address this topic area was the impetus for the Economic and Social Department of FAO, in conjunction with the University of Rome 'Tor Vergata', to co-sponsor the Symposium on the Economics of Valuation and Conservation of Genetic Resources for Agriculture in May 1996. The chapters presented in this book were derived from this symposium. The purpose of the symposium was to bring to focus the key issues and to discuss economic instruments that could encourage the implementation of both socially acceptable strategies for the conservation and sustainable use of genetic resources for food and a fair and equitable sharing of the related benefits and costs. I believe that the symposium was particularly timely in addressing these issues only a few weeks before a Global Plan of Action for the Conservation and Sustainable Use of Plant Genetic Resources for Food and Agriculture was adopted in Leipzig, Germany, at the International Technical Conference on Plant Genetic Diversity.

Determining the value (private and public) of genetic resources, and hence the benefit of having more or less of them is by no means a trivial task. The market price of germplasm is not an appropriate indicator of the value, because it does not normally reflect in full all of the actual or potential kinds of benefits derivable from a genetic material: specifically, benefit from current use, benefit from future use options, and benefit from existence *per se*. Under the prevailing market conditions, the price of germplasm captures mainly the so-called *use value* of genetic resources (i.e. the value associated with the direct and indirect benefits resulting from the use of germplasm by farmers and plant breeders). For them, seeds are inputs to more productive or disease-resistant varieties. To a large extent, this use value is a function of the breeding technology and of the income achievable from the productive use of the improved seed. Improvements in breeding technology, for example through biotechnology, will increase breeders' demand for germplasm and thus raise its value and market price. One share of the economic benefits of more successful breeding goes ultimately to consumers in the form of lower food prices and another to farmers in the form of greater revenues due to higher yields.

The second value component, the so-called *option value*, is much less well captured in the market price of germplasm. It reflects the future benefit to the society associated with a reduced disappearance and a better preservation of genetic resources for future needs of breeders. In other words, the option value reflects the economic benefit of avoiding irreversible decisions which would limit the options for breeders in the future. The market price of seeds and germplasm is not a good indicator of this value component because, for a number of reasons, there is only a limited current market demand for such future use options. Unless appropriate institutions are established, those who would have to bear the consequences of reduced future agro-biodiversity are not well represented in today's markets for germplasm exchange.

Theoretically, there could be a third component of the value of genetic resources, the *existence value* (i.e. the value of ensuring the survival of a species, variety or breed just for its own sake or for some moral reason). While this may be the case for some rare animal breeds which people wish to keep just for their beauty, such existence values are likely to be of little practical relevance for the plant genetic resources of interest to food and agriculture. But reference to this value category is made mainly to illustrate the complexity of the valuation problem.

From an economic standpoint, one of the key issues is how to factor uncertainty into the estimation of benefits and costs of programmes for maintaining agro-biodiversity. Uncertainty in this case regards the possibility of acquiring better information about future consequences of erosion of agro-biodiversity over time. If such information is forthcoming, there is a value on those initial actions that preserve future flexibility and a cost on those which reduce flexibility, because the latter precludes the exploitation of the additional information at a later date. If a society takes measures to halt the erosion of agro-biodiversity now, and, subsequently, future generations place a low value on the greater agro-biodiversity, it will still be possible to revert to the old practices that were more harmful for biodiversity. But if no measures are taken now and the genetic resource base is allowed to deteriorate, it will be too late to act if it is subsequently discovered that future generations depend and place a higher value on agro-biodiversity. In other words, there is a premium associated with actions that preserve flexibility.

This flexibility premium is another term for option value or quasi-option value of maintaining a sufficiently large biodiversity. Ultimately this premium will manifest itself through greater stability and/or more rapid growth of agriculture and through the ability of breeders to respond to yet unknown human needs for food quality and safety. To avoid undervaluation of genetic resources for food and agriculture, this flexibility premium must be part of the total economic valuation.

Examples abound of other issues for which economic analysis may aid the decision maker. For instance, considering that some genetic resources are more in need of conservation than others, and, certainly, some geographic regions are more important sources of germplasm than others, what are the criteria for decision making? If numerous communities have basically the same genetic resources, is conservation advisable in all of them or just in a few, and what are the appropriate actions to be taken? Can existing, or new *sui generis* systems of intellectual properties' rights, including farmers' rights, be formulated in such a way that these questions are answered through some sort of a market mechanism?

I have attempted to raise only few of the many questions that need to be answered if action on the conservation and more sustainable use of agro-biodiversity is to be taken seriously. In a more comprehensive fashion, *Agricultural Values of Plant Genetic Resources* should help the reader to become informed about some of the key issues involved in the economics of the valuation and conservation of genetic resources of interest to food and agriculture. These chapters demonstrate that, while research on the economics of this subject is in its infancy and measures of the economic benefits are uncertain, economics can provide insights on this subject that can be useful to the policymaker.

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Abbreviations

ARBN	Asian Rice Biotechnology Network
ARS	Agricultural Research Service
BPH	brown plant hopper
BSE	bovine spongiform encephalitis
CBD	Convention on Biological Diversity
CGIAR	Consultative Group on International Agricultural Research
CGR	crop genetic resources
CIAT	Centro Internacional de Agricultura Tropical
CIMMYT	International Maize and Wheat Improvement Centre
CIRAD	Centre de Cooperation Internationale en Research Agronomique pour le Developpement
COP	Conference of the Parties to the CBD
EMBRAPA	Empresa Brasiliera de Pesquisa Agropecuaria
ENEA	National Agency for Alternative Energy
FAO	Food and Agriculture Organization
GATT	General Agreement on Tariffs and Trades
GEM Project	Germplasm Enhancement Maize Project
GEU	genetic evaluation and utilization
HPR	host plant resistance
HPT	host plant tolerance
HYV	high-yielding variety
i.i.d.	independent and identical distribution
IARC	international agricultural research centre
IBPGR	International Board for Plant Genetic Research
ICRISAT	International Crops Research Institute for the Semi-arid Tropics

IITA	International Institute of Tropical Agriculture
INGER	International Network for the Genetic Evaluation of Rice
IPF	invention possibilities frontier
IPGRI	International Plant Genetic Resources Institute
IPP	international plant protection
IPRs	intellectual property rights
IRG	International Rice Genebank
IRGC	International Rice Germplasm Collection
IRPB	IRRI plant breeding programme
IRRI	International Rice Research Institute
IUCN	International Union for the Conservation of Nature
LAMP	Latin American Maize Project
MV	modern varieties
NARS	national agricultural research system
NGO	non-governmental organization
NMS	nuclear male sterility
NPV	net present value
ORSTOM	Office de la Recherche Scientifique et Technique Outre-Mer
PGR	plant genetic research
PGS	Plant Genetic Systems
PVP	plant variety protection
R&D	research and development
RPA	research problem area
RT	research technique
SFN	search field narrowing
2SLS	two-stage least squares
SPD	subjective probability distribution
SPE	subjective probability estimate
SSR	simple sequence repeat
TD	technological determination
TFP	total factor productivity index
TRIPS	trade-related aspects of international property rights
UNCED	United Nations Conference on the Environment and Development
UPON	Union for the Protection of New Varieties of Plants
USDA	United States Department of Agriculture
WARDA	West Africa Rice Development Authority

Introduction and Overview: Agricultural Values of Plant Genetic Resources

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Plant genetic resources (PGRs) can be classified into two broad groups. The first group is made up of the genetic resources within the cultivated species. These include the 'landraces' or 'farmer varieties' selected by farmers over many generations and 'tailored' to different producing environments. Also included in this group are the wild species and wild relatives of the cultivated species. The value of this first group of PGRs for plant breeding is well recognized and reflected in the investments made to collect, evaluate and conserve these PGRs in *ex situ* gene bank collections.[1]

The second group of PGRs encompasses the genetic resources from other plant species (and, in practice, even from species outside the Plant Kingdom). Until the development of modern 'biotechnology' techniques, this group of PGRs was not valued for plant breeding use. With the development of methods for transforming DNA (and gene-controlled traits) from 'alien' species into economically valuable plants, this second group takes on potential plant-breeding value.

Interested parties have supported the collection and preservation of both groups of PGRs. Until recently, these interests have not been closely allied. Agricultural research programmes and plant-breeding programmes, as noted above, have supported the collection, preservation and evaluation of PGRs of the first group for many years. For most major crop species, a high proportion of potentially valuable landrace and their wild-weeding relatives are in gene bank collections (see Table I.1). The parties interested in preserving the second group (i.e. the non-cultivated species) of PGRs are motivated by broader concerns associated with maintaining the 'biodiversity' of all species. They support *in situ* collections, and the maintenance of natural preserves and natural habitats.

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Table I.1. Genetic diversity collection and utilization by commodity.

							Ex situ						
	Area (Mha)	Landraces (× 1000)	% in collections	Wild species	% in collections	*In situ* collections	Major collections (× 1000)	Accessions (× 1000)	% CGIAR	% Dup.	% I.R	% WS	Utilization distribution
Commodity													
Bread wheat			95	24	60	Few	24	784	16	50	17	2	
Durum wheat		150	95	24	60	Few	7	20	14	32	53		High
Triticele			40				5	40	38	66			
Rice	149	140	90	20	10	Few	20	420	26	75	25	1	High
Maize	130	65	90		15	Few	22	277	5	80	16	0	High in LDCA
Sorghum	43	45	80	20	0	Few	19	169	21	42	18	0	Low
Millets	38	30	80		10	None	18	90	21		33	2	Low
Barley		30					16	484	5	23	9	1	
Oats							20	222	0		1	4	
Rye							8	287	0		8	0	
Food legumes													
Beans			50		70	Few	15	268	15	76	21	1	Low–medium
Soybeans	66	30	60			None	23	174	0	?	2	1	Low–medium
Chick peas					75		13	67	41	75	29	1	
Lentils					95		5	26	30	95	30	3	
Fava beans					25		10	29	33	35	42	0	
Peas					0		18	72	0		4	0	
Groundnuts		15			28		16	81	18	28	15	1	
Cowpeas					30		12	86	19	30	19	2	
Pigeon peas					22		4	25	52	22	50	2	
Lupin							10	28	0		12	16	
Root crops													
Potato	19	30	95		30	Few	16	31	20	100	13	5	High
Sweet potato	10	5	50			Few	7	32	21	93	16	6	Medium
Cassava	16		35		29		5	28	30	90	23	2	Low–medium
Yam		3					2	12	25	20	24	0	
Sugar cane		20	70										

The two interest groups are finding more common interests in recent years (and are resolving conflicting interests as well). This is in part due to improved awareness by the biodiversity interests in the history of conservation of PGRs by agriculturalists. It is also in part due to a recognition by both interest groups that valuing PGRs is important to conservation–preservation policy. The biodiversity interests have traditionally stressed 'existence' values and 'biophilia' values in support of policies. They are increasingly recognizing that the 'hard' economic values associated with plant improvement provide important additions to their policy arsenals. Agriculturalists, by the same token, are also stressing their own broader conservation interests and are beginning to expand their perception of usable PGRs as new biotechnology techniques come into use.

This volume is addressed to the assessment of economic value for PGRs. The focus of attention for chapters attempting actual value estimates is on the first group of PGRs (i.e. the cultivated species), but two chapters do deal with the implications of biotechnology (and both argue that the new biotechnology methods endow non-cultivated PGRs and other PGRs with plant breeding value, but not at the expense of value for the cultivated PGRs). The estimation of PGR values is a relatively new field of inquiry for economists and this immaturity is no doubt reflected in the papers in the volume.

The volume is organized in five parts and includes 19 chapters. Part I (Chapters 1–4) covers models of value of PGRs. Part II (Chapters 5 and 6) covers empirical studies of PGRs, field diversity and yield vulnerability. Part III is the core of the volume. It includes seven empirical studies of PGR values. Most of these studies associated PGR values with 'genetic trait' values associated with PGRs. One chapter (13) reports a 'breeding production function' study. Part IV addresses the issue of property rights in PGRs. These are important because they provide incentives for collection and preservation of PGRs and because they endow PGRs with value. The final part includes two chapters addressing the implications of modern biotechnology methods for PGR values.

In this introduction we discuss three topics that pervade the volume. These are valuation concepts, plant breeding institutions and valuation methods. We then provide a brief overview of the chapters in the volume.

Activities (Investments) and Values

Economists make a distinction between *use* and *non-use,* or existence, value. Table I.2 depicts relationships among activities or investments and four types of use values and non-use values. The activities associated with PGRs require real economic resources or investments and each of these activities is designed to add economic value to them. It is important to note that the 'natural' value of PGRs (e.g. the value of farmers' rights) is the value of the final product (e.g. a new variety of rice) minus the valued added by each activity.

Our main concern in this volume will be with the direct use value of PGRs for breeding. We will also be concerned with the indirect use option value

Table I.2. Plant genetic resource activities and values.

	Direct use value		Indirect use value		Non-use existence value
Activities	Breeding	Recreation	Option	Diversity	
Genetic resource in nature		×	×		×
Inventorying	×	×	×		×
Collection					
Ex situ	×		×		
In situ	×	×	×		×
On-farm	×	×	×		×
Evaluation					
Agronomic	×	×	×	×	
Genetic	×		×	×	
Exchange					
Information system	×		×		
Restriction	×		×		
Pre-breeding					
Landrace combination	×			×	
Advanced lines	×			×	
Breeding					
IARCs	×			×	
NARs	×			×	
Private	×			×	

associated with possible future breeding use. Indirect use diversity values will also be considered (Part II). It is important, however, to note that PGRs have recreational values in specialized parks, nature preserves, etc, and that these are significant. Existence values are also important, although they are probably confined to PGRs in *in situ* collections.

Proponents of existence value argue that genetic resources are priceless in an economic sense and support the preservation of biodiversity as a moral and ethical issue and as a matter of the long-term sustainability of human life. Proponents of use value argue from a more utilitarian claim: biodiversity should be preserved, it is argued, because it can confer benefits on humans. This can be characterized as the utilitarian view of genetic resources.

The utilitarian approach in turn generates several further strands of argument. Many biological scientists advocate the viewpoint that all – or almost all – genetic resources are potentially valuable and hence should be conserved. Wilson (1988) is a notable proponent of this view; McNeeley *et al.* (1990) also speak from this perspective in calling for 'a global strategy for conserving the greatest possible biological diversity'. This viewpoint rests on the assumption that all genetic material has potential value; without knowing what technologies will be available in the future, and without knowing what environmental conditions the world may face in the future, it is argued, we have little basis for distinguishing ‘useful’ genetic resources from any others. As a result, the only sensible strategy is to seek the greatest possible preservation of diversity.

An alternative viewpoint, drawn largely from economics, suggests that the costs of preserving genetic resources should be viewed seriously, and that the benefits should be quantified to the greatest possible extent (see, for example, Brown, 1990; Evenson, 1993; and Wright, 1995). This literature takes seriously the tradeoffs between the current and future well-being of society and tends to focus on diversity in the economically important cultivated species. Economists in general are more sceptical than biologists concerning the need to protect all forms of genetic diversity. As Brown (1990) notes, ‘if we can’t save all species, we need a ranking based on one or more criteria, from which we select the highest ranked for preservation’.

Plant Genetic Resources: Sources of Value

Before it is possible to assign a value to any collection of genetic resources, it is necessary to agree on the source of value. Some have argued for a non-utilitarian approach to valuing genetic resources. For example, Oldfield (1989), Busch *et al*. (1989) and Shiva *et al*. (1991) are among those arguing that the value of genetic resources lies fundamentally in an environmental ethic.

As Shiva writes, ‘the conservation of biodiversity ... is based primarily on the ethical ground that all life forms have value in themselves, independent of the value that man puts on them’. This viewpoint received special note in the 1982 World Charter for Nature of the United Nations, and from the International Union for the Conservation of Nature (IUCN) which affirmed support for an ethical foundation to biodiversity conservation (McNeeley *et al*. 1990).

There is undoubtedly merit to this argument. Nonetheless, as Brown (1990) points out, this is an unsatisfying framework to bring to policy decisions. Given that human actions *do* affect the environment, and given that human actions *can* bring about the extinction of other species, on what basis should people guide their actions? Preserving biodiversity entails choices: about which species or habitats to preserve, and about how much current consumption to forego in order to realize future benefits. These choices should be made explicit. To ignore such tradeoffs is to ignore the fact that humans will inevitably make choices that affect biological systems. As Swaney and Olson (1992) write, ‘We *are* valuing biodiversity. We can choose to continue to undervalue [biodiversity], or we can change our valuations, but we cannot choose to not value it’.

What then are the sources of economic value? Evenson (1993) distinguishes between ‘consumer good’ (existence) values and ‘producer good’ (use) values of genetic resources. In this taxonomy, most genetic resources are directly valued by consumers only to the extent that people derive pleasure or satisfaction from knowing that genetic resources exist. Thus, people may derive value simply from knowing that elephants exist or that rainforests are being preserved. This contrasts with the ‘producer good’ value that people gain when producers use genetic resources to produce consumer goods: for example, for the use of genetic materials to produce cheaper grain or better-tasting tomatoes.

Other researchers develop more complicated taxonomies for understanding the value of genetic resources. For example, Brown (1990) allows for the ‘indirect production value’ that species can add from their services to the ecosystem; for example, earthworms help to aerate soil, and certain birds and bugs control pests. Likewise, Brown explicitly considers the ‘future non-consumption use value’ that is derived from preserving genetic resources as a form of insurance against an uncertain future.

Thus, although the categorizations differ slightly, economists agree on a utilitarian approach to valuing genetic resources. The value of genetic resources and biodiversity reflects the increased well-being that people derive from them – whether directly or through their use in production. In this volume we relate the breeding value of genetic resources to the activities shown in Table I.2.

The Cost of Extinction

Biologists argue that the extinction of a species imposes losses on humans. Two distinct effects are noted. First, an extinct species is ‘lost’ for future use, in the sense that its genetic materials cannot be put to utilitarian purposes. If a species is extinct, we can never know whether it might have offered a cure for cancer or – more prosaically – a gene that could be used in crop improvement. Second, the loss of any species can perturb the delicate ecological balance of a natural system. This in turn can cause damaging effects for humans.

In both cases, however, the costs of extinction can be overestimated if we do not recognize the opportunities for people to find substitutes. As Simpson *et al.* (1996 and Chapter 3) point out, people can often find alternative sources of naturally occurring pharmaceutical products. There are arguably very few cases where a particular pharmaceutical product can be found only in a single species. More commonly, the compound occurs in several closely related species; or perhaps various related compounds are found in (related or unrelated) species occupying similar ecological niches. People can develop synthetic compounds with the same attributes as the natural material, and so forth. The scope for humans to substitute and adapt to the extinction of species is remarkable and should not be underestimated. From the woolly mammoth to the passenger pigeon, humans have survived the loss of economically important species without irreparable material losses.

The case of the passenger pigeon is instructive. It has been argued (e.g. Oldfield, 1989) that as populations of passenger pigeons were decimated by commercial hunters, markets did not adequately respond to the population shifts by driving up the price of passenger pigeons. A primary reason for this was the widespread availability of consumption substitutes: North American consumers were not greatly distressed to switch their consumption of fowl from passenger pigeons to chickens. Since chickens could be raised at a relatively modest cost, the market price of passenger pigeons remained comparably low. The principle of substitution operates more generally. The extinction of a species for which many close substitutes exist matters much less than the extinction of a species with no close substitutes. Thus, for most people (though perhaps not for entomologists), the loss of one species of ant probably causes less loss of utility than the loss of a species with fewer close substitutes, such as African elephants.[2]

Even if a major crop species were to become extinct, humans could partially adapt to the loss by cultivating and consuming other crop and animal species. Much harm might result, and many people could potentially face catastrophe, but losses would be neither universal nor immeasurable.

The Cost of Genetic Uniformity in Commonly Used Species

Within the agricultural sciences, a common justification for preserving germplasm is the need to be prepared for potential outbreaks of diseases or pests. Large collections of germplasm – often at the intra-species level – give scientists the resources with which to respond to emerging disease and pest problems. Anecdotal evidence supports the idea that disease and pest resistance are often distributed sparsely across a population. Thus, small collections may not offer adequate protection against potential problems.

A related issue is the role of genetic uniformity in the susceptibility of crops to massive failures. Where cultivated varieties of a crop are closely related, it is suggested, new pests and diseases can spread rapidly and with enormous destructive potential. Several historical episodes are cited as evidence: the Irish potato famine, the Southern corn leaf blight epidemic in the United States, and a handful of other well-documented cases (e.g. Hargrove *et al.*, 1990; Ryan, 1992).

As Wright (1995) points out, however, such episodes are indeed rare. The Irish potato famine did lead to disaster, but the Southern corn leaf blight epidemic barely caused a ripple. Where reasonable substitutes are available, the failure of a single crop is not necessarily a grave disaster. Even in developing countries with no formal futures markets, producers can rely on a variety of *ex post* consumption smoothing techniques to make up for the income losses associated with crop failures. (See, for example, Rosenzweig and Stark, 1989; Alderman and Paxson, 1992; Rosenzweig, 1992; Rosenzweig and Wolpin, 1993; Townsend, 1995; and Udry, 1990.) Similarly, consumers can readily switch to available substitutes and take advantage of various consumption smoothing mechanisms to deal with any related price rises. As Sen has shown in his seminal study of famines (1981), crop failure does not correspond to famine. Famine instead depends on a variety of other institutional and market failures – often involving war, violence or deliberate exploitation.

Taken together, these findings suggest that preservation of germplasm collections offers only one of a number of forms of production and consumption insurance. There is no particular reason to think it is economically efficient to insure future consumption with gene banks. Certainly it is a mistake to assign a value to gene banks on the basis that they are the sole source of insurance against crop losses.[3]

Part II of this volume includes two studies of field diversity and the role of modern varieties. Also, see Chapter 4 for a discussion of land conversion.

Choices Across Species and Individuals

Most economists agree with biological scientists that genetic resources have value. Most economists could be convinced, given supporting evidence, that there is a case for the collection and preservation of many 'useful' species, such as rice, wheat and their wild relatives. A question on which economists might differ with biologists is how many species to conserve or how far to extend conservation efforts.

Wilson (1988), for example, argues that the potential value of genetic materials, combined with inherent uncertainty about the future, justifies preserving essentially all known species, including insects and presumably microorganisms. Myers (1988) suggests that the loss of species today could not only decrease human welfare in the near future (due to emergent pests and diseases) but could also lead to cataclysmic effects on the future course and pace of evolution.

Many scientists also view with scepticism the prospect of preserving biodiversity in *ex situ* collections. Oldfield (1989) summarizes some of the arguments against exclusive reliance on *ex situ* conservation. While acknowledging the usefulness of *ex situ* storage for plant breeders and researchers, biologists point out that known species constitute only a small proportion of the species that exist. By definition, it is not possible to develop *ex situ* collections of unknown species. Thus, the logical alternative, as Wilson (1988) argues, is to preserve habitat – and particularly those habitats, such as tropical rainforests, that support large numbers of species.[4]

A problem with this viewpoint, however, is that it is costly to preserve genetic materials, whether *in situ* or *ex situ*. Although *ex situ* collections may have relatively low operating costs, there is an enormous number of species that could potentially be preserved. Within species, there is additional variation that may merit protection. For example, many of the world's most prominent gene banks focus on protecting intraspecies diversity (in wheat, rice, maize and other agricultural commodities). Perhaps *in situ* collections could be more cost-effective under some circumstances, but nonetheless, the cost of protecting all of the world's genetic resources would be prohibitive.

The costs of conserving germplasm thus necessitate some implicit ranking of the value of different species, and even of the value of individuals within plant and animal species. This value must be based on current and future consumption and production values, as described above.

Even if we accept the argument that many species may eventually find economic uses, some will not be used for years or decades. But as Brown (1990) notes, ‘the positive interest (discount) rate signifies that a good event has more value today than the same good event in the future’. This suggests to most economists that it would be sensible to place a higher value on conserving the genetic resources of currently useful species than on protecting species that have no immediate use. At the very least, there is a reason to think hard about which species merit conservation.

Inter-species Diversity vs. Intra-species Diversity

A related issue is the tradeoff between conservation of different species and the conservation of individuals within species. Many of the world’s largest gene banks are dedicated to preservation of very small numbers of species. For example, the International Rice Germplasm Collection (IRGC) at the International Rice Research Institute (IRRI) in the Philippines contains a collection of over 80,000 types of landraces of rice. But almost all of these types belong to two species, *Oryza sativa* and *Oryza glaberrima*. Relatively small numbers are specimens of approximately 20 wild species of rice (Hodgkin, 1991). Similarly large gene banks for wheat, maize and other major food crops are found in major producing countries and international agricultural research centres.

Such large resources are devoted to major crop plants because intra-species genetic variation has proved extremely valuable in the past (see, for example, Chapters 9–13). Plant breeders have traditionally drawn on intra-species diversity to improve crop yields, protect cultivars from diseases and pests, and otherwise raise productivity.

Efforts to preserve intra-species genetic diversity inevitably compete, however, with efforts to preserve inter-species diversity. Should scarce funds for conservation of genetic resources be used to safeguard intra-species diversity in a few widely used plants and animals, or should it be used to expand the number of species whose genetic material is saved for posterity?

Most of the non-agricultural literature on biodiversity implicitly assumes that protecting inter-species diversity is the most urgent priority. For example, Schücking and Anderson (1991) refer to the ‘biodiversity crisis’ in terms of rapid loss of species. Similarly, McNeely *et al*. (1990) acknowledge the importance of genetic diversity at the individual level but focus on species diversity and ecosystem diversity.

To date, however, relatively small numbers of species have been used for economic purposes. Oldfield (1989) cites figures showing that only 150 species of plants have been commercially cultivated in the history of agriculture, out of some 250,000 plant species known to exist. Oldfield uses these figures to argue that humans have grown to rely on a dangerously small base of genetic material and should take steps to preserve the remaining species. Alternatively, however, it can be argued that over several millennia humans have discovered the subset of species of most value to human welfare.

Values and Breeding Activities

Referring again to Table I.2, note that several activities are entailed in plant breeding. First, some type of inventorying activity is required before PGRs can be systematically collected. Collections are vital to breeders. They must be maintained and must have some basic information systems to be used by breeders. *Ex situ* collections are the dominant form of collection for plant breeders. Many advocates of preserving biodiversity favour *in situ* or on-farm collections on the grounds that they are 'dynamic'. They are often thought to be natural, but farmer-created PGRs are not natural and *in situ* collections of them cannot be natural. Breeders are increasingly designing on-farm or *in situ* collections to actually force dynamic change in diversity. Animal breeders are increasingly using *ex situ* cryopreservation for sperm and ovum, but they continue to rely on *in situ* and on-farm breeding herds.

Next we note that collections are more valuable to breeders when they are evaluated. Evaluations range from basic 'passport' evaluations to agronomic and genetic evaluations. For most crops, important 'traits' such as host plant resistance to plant diseases and insects or host plant tolerance to abiotic stress (cold, drought) are controlled by single (or few) genes. Agronomic (phenotypic) evaluation of collection accessions to identify these traits is valuable to breeders. As biotechnology techniques are increasingly used, genetic evaluations become more important.

PGRs must be exchanged between collection organizations and breeding programmes. This requires resources, and in some cases it may be subject to restrictions. Some of this exchange is direct, as when international agricultural research centres (IARCs) send landraces to national agricultural research system (NARS) breeders. Some is indirect as when NARS breeders identify promising parental breeding materials in international nurseries (see the rice study below). Many PGRs are proprietary (i.e. held privately) and may or may not be exchanged for a price.

Pre-breeding is increasingly becoming important in breeding programmes.[5] This is illustrated in rice breeding where the breeding programmes at the International Rice Research Institute produce pre-bred advanced lines, selected combinations of landraces that are then used in NARS breeding programmes, thus saving extensive efforts by NARS breeders. (See Chapter 7 for pre-breeding in maize.) Pre-breeding is subject to serious market failure (see below).

Breeding activities may take place in IARCs, NARS or in private sector programmes. All breeding programmes benefit from the antecedent activities. Under conditions of perfect markets, each of these activities (or products thereof) would be priced, and we could determine the value of PGRs by determining the value of new plant cultivars or of superior livestock and subtracting the value added by each activity to reach a residual natural PGR value.

But perfect markets do not exist for all of these activities (though imperfect markets exist for some and improved markets could be created through stronger intellectual property rights (IPRs)). The most fundamental reason for this is that the PGRs embodied in a plant or animal can be replicated or reproduced at low cost in other plants and animals. This gives them a 'non-rival good' quality similar to an invention. An invention may be embodied in a second machine or good without altering its performance in the first machine or good in which it is embodied. The same is effectively true for PGRs although a reproduction process is entailed.

If the 'owner' of an invention or PGR can control the use of the invention or PGR, a market for the invention or PGR will exist. For crops a natural form of control exists for hybrid crops where farmers do not save seed from their harvest and thus purchase new seeds each season. Private sector firms can earn a return to plant breeding activities through seed sales. In fact, markets for prebred inbred lines exist and proprietary PGR collections have value (as reflected in the sales values of companies). When farmers can save seed from harvest, the new seed market is typically not large enough to justify private breeding investments. IPRs, patents or breeders' rights, are designed to create seed markets by giving the IPR holder a (limited) 'right to exclude' others from using the protected seed without permission. IPRs are being strengthened, and private sector breeding and pre-breeding activities are growing. But many countries do not have and could not enforce IPRs for plants. (See Chapters 14–17 for discussions of farmers' rights.)

Option values, as noted in Table I.2, are largely associated with breeding values because this is the potential use value from PGRs. Naturally occurring unknown PGRs have options value, as do incompletely known PGRs.

Diversity values refer to the public goods nature of diversity in farmers' fields. Note that this is not due to the risk-averse behaviour of farmers. Farmers will directly value crop varieties with 'stability' under changing weather conditions, etc., in their planting decisions. But stability and diversity may have public-good value as well because of reduced danger of pest outbreaks, etc. Plant and animal breeders can incorporate these features into breeding programmes, but some regulation (or subsidy) may be required to achieve the desired effects in farmers' fields.

Plant Genetic Resources and Their Utilization

Table I.1 reports data compiled by the Food and Agriculture Organization (FAO) of the United Nations on estimates of the number of landraces within the major cultivated species for each crop.[6] Estimates of the proportion in collections are also presented. In general, landrace diversity is roughly proportional to planted area. For cereals, 80–90% of the original landraces are held in collections. For food legumes and root crops the proportions collected are lower.

Table I.1 also reports the number of relevant (i.e. related) wild species and estimates of collection for these. Wild species materials tend to be unrelated to area planted. The collection of wild species materials depends on sampling. These wild species have less diversity than reflected in the landrace diversity in the cultivated species.

Table I.1 also summarizes the very limited data for *in situ* collections for crops. For some important crops no *in situ* collections exist. No breeding programmes in any crop report significant utilization of *in situ* collections for breeding purposes.

In contrast, all important crops have *ex situ* collections. There are hundreds of such collections, with roughly 6 million accessions for all crops. Accessions are roughly proportional to the landraces in each crop. (There are roughly 1 million distinct crop landraces.)

The Consultative Group on International Agricultural Research (CGIAR) research centres (the IARCs) hold substantial proportions of the accessions for most crops. The CGIAR accessions are not fully duplicated in NARS collections. The proportions of accessions that are landraces are surprisingly low, as are the proportions of wild species (relative) accessions. Thus while the quantitative magnitude of *ex situ* accessions is high, there are quality problems in the management of these *ex situ* collections.

In Table I.1 rough indicators of genetic resource utilization are reported. These are based on very sketchy reports; the most detailed evidence on genetic resource utilization is for rice.

Gollin and Evenson (Chapter 13) studied rice varietal releases of *indica*- and *javanica*-type rice over the 1962–1991 period. A total of 1709 varietal releases were classified according to releasing country and release date. The genealogies (parentage) of each release were analysed and this enabled further characterization of breeding strategies and of the landrace complexities of these releases (see Hargrove *et. al.*, 1990).

Table I.3 summarizes these releases. IRRI made a number of the crosses from which these varieties were selected, but officially released only a few varieties. India, with 26 different rice breeding programmes, led all countries in releases, with 643 over the period. Releases were made from more than 100 breeding programmes. Annual releases were approximately 20 per year in the early green revolution period, rose to nearly 80 per year in 1976–1980, and have been around 75 per year since 1980.

Panel I of Table I.3 reports international exchange of varieties by comparing the location of the breeding programme where the cross was made with the location of the releasing programme. IRRI was an important producer of the crosses from which releases were made. In the early green revolution period, 1966–1970, IRRI made 25% of all crosses leading to varieties. This percentage has declined somewhat (to 12% in the most recent period) but IRRI's plant breeding programme remains a potent contributor to varietal development.

Panel II of Table I.3 summarizes parental data. Here we see that IRRI produced the crosses from which 24% of varietal parents were selected. Other NARS produced the crosses from which an additional 18% of varietal parents were selected.

Panel III of Table I.3 provides further data on breeding strategies. It shows that the most frequent (successful) breeding strategy over this period has been the 'one parent from IRRI, one from the NARS' strategy. The international

Table I.3. Flows of international genetic resources, by time period.

	Pre-1965	1966–1970	1971–1975	1976–1980	1981–1985	1986–1991	Total
I. Released varieties, percentage based on:							
IRRI cross (through INGER)	3 (0)	25 (0)	19 (2)	22 (13)	18 (14)	12 (11)	17 (8)
Other NARS cross (through INGER)	16 (0)	7 (0)	6 (0)	6 (2)	6 (4)	5 (3)	6 (3)
Own NARS cross	81	68	75	72	76	83	77
II. Parents of released varieties, percentage with one or more parents:							
IRRI cross (through INGER)	0 (0)	24 (0)	29 (0)	33 (9)	23 (20)	19 (15)	24 (10)
Other NARS cross (through INGER)	27 (7)	25 (2)	21 (5)	15 (9)	18 (15)	20 (15)	18 (10)
Own NARS cross	73	51	50	52	59	6	58
III. Frequency of parental/cross, percentage with no foreign genetic resource:							
All NARS parents	24	11	8	6	7	10	8
IV. Landrace content of released varieties, parent greater than:							
4	10	31	47	67	62	56	55
9	0	3	13	39	34	32	27
15	8	0	3	21	18	18	14
Average number of landraces	2.55	4.01	5.29	8.15	7.49	7.23	…
Percentage from IRRI	3	3	59	79	74	71	68
V. Landrace introduction:							
Number from IRRI	0	16	14	21	11	13	80
Number of NARS	21	87	126	146	171	180	758

IRRI, International Rice Research Institute; INGER, International Network for the Genetic Evaluation of Rice; NARS, national agricultural research system.

exchange dimension of rice breeding is shown by the relatively low percentage of varietal releases where all parental material is from national sources (most of these releases were made in India).

Panel IV of Table I.3 shows the increase in landrace content of released varieties. The average number of landraces has risen from less than three to around eight, with some recently released varieties having more than 25 landraces in their genealogies. More than 70% of these landraces were brought into the genealogies through an IRRI ancestor.

Panel V shows another dimension of IRRI's role in breeding. It shows the number of new landraces introduced into the landrace pool by period and by originating source. Here we note first that an impressive number of new landraces and one or two wild species have been introduced into the pool of released varieties. The fact that the 1709 releases included 838 landraces that were not in the pre-1965 varietal landrace pool shows that genetic resource collections have been valuable. Second, the data in Panel V show that IRRI has actually introduced very few landraces into the pool. Only 80 of the 838 new landraces were introduced via IRRI crosses. By contrast we note that of all of the landraces in released varieties, roughly 70%, were introduced via an IRRI cross. This is the result of two factors. First, IRRI's powerful breeding lines incorporate many landraces first incorporated in a NARS cross. Secondly, the widespread use of IRRI crosses as breeding lines multiplies the usage of the landrace content in them.

Gollin and Evenson (1997; and Chapter 13) have noted that a small set of landraces have been built into the IRRI breeding lines based on the original semi-dwarf plant design which has, to date, served as the basis for much of the varietal development described here. IRRI, with excellent access to genetic resources, did not invest heavily in efforts to exploit more landrace materials and was not highly successful in doing so. This was in part because the 'narrowness' of the original green revolution plant design limited the combinability and usefulness of new landrace materials. NARS, even though they had poorer access to genetic resource collections, had somewhat broader plant design bases and NARS were more diligent in searching for landrace-based traits.

Empirical Approaches to Assessing Value

Given that plant genetic materials have an economic value, what are effective ways of measuring this value? Among economists, the predominant viewpoint is that genetic resources can be viewed like any other public or non-market good (Brown, 1990). The fundamental problem in placing values on such goods is that they are seldom sold on markets. When they are, there are serious problems in interpreting the market prices as indicators of true (social) value.

Several recent surveys of empirical approaches have been undertaken. Swanson *et al.* (1994) provide an excellent summary of theoretical and empirical approaches; a previous survey was conducted by Brown (1990).

Measures of Willingness to Pay

To place values on non-market goods, economists often turn to a variety of techniques for eliciting the private values that individuals would be 'willing to pay' in a market situation. In some cases, these values are collected through direct surveys (Hannemann, 1994). In other cases, individuals' behaviour may give some indication of the value that they place on a public good: for example, time and money spent on travelling to a park may reveal the value people place on the park. Likewise, the money spent on certain private goods that are complementary to public goods may give an indication of value: expenditure on binoculars and bird books may reveal the value that people place on the diversity of bird life.

Several researchers have used innovative approaches to measuring the value of genetic resources by estimating the willingness of different individuals to pay for the preservation of plant genetic resources. Pearce and Cervigni (1994) offer a good survey of the alternative methodologies and single out a few empirical studies that have been undertaken using different techniques.

Willingness to Pay for On-farm Diversity

One approach to valuing plant genetic resources – at least for crop plants – is to study the actual tradeoffs that farmers are willing to make in order to maintain genetic diversity in their fields. Particularly in poor countries, farmers may elect to plant a number of different varieties of a crop in order to insure themselves against variety-specific production shocks. Varietal diversification is one of many ways in which poor households may seek to reduce their exposure to risk. (See Rosenzweig and Stark, 1989; Alderman and Paxson, 1992; Rosenzweig and Wolpin, 1993; Townsend, 1995; etc.) Thus, if one particular variety proves susceptible to a pest or disease, other varieties in the farmer's fields may be resistant. Varietal diversification is achieved at a price, however. Typically, this price is measured in terms of lost yield potential. Suppose that one variety has the highest expected yield across possible agroclimatic states of the world. A risk-averse farmer might rationally plant some land in this variety while allocating other land to varieties or crops that have lower yields but little covariance in production with the high-yielding cultivar. This provides some insurance across agroclimatic states. However, the tradeoff for the insurance is the loss of expected yield. This lost yield can be thought of as a measure of the farmer's willingness to pay for genetic diversity.[7] (See Chapter 6 for an application.)

Heisey *et al.* (1997) considered the case of wheat cultivation in the Pakistani Punjab, where wheat rusts are an important source of yield losses. The rusts are a family of pathogens noted for evolving rapidly in response to selection pressures. In particular, planting of large contiguous areas with cultivars carrying the same genetic base of resistance is believed to speed the evolution of new rust biotypes. In turn, the emergence of new rust biotypes can cause substantial losses to farms and high social costs if epidemics occur. From a social standpoint, then, it is desirable to maintain some degree of diversity in the rust resistance genes incorporated in farmers' portfolio of varieties.

In practice, however, farmers do not choose to grow wheat cultivars with the level of rust resistance that would be socially desirable. First, farmers choose to grow high-yielding cultivars, whether or not they are known to be susceptible to rust. Second, farmers choose to grow high-yielding cultivars, whether or not they have the same basis of genetic resistance as those grown by other farmers. When many farmers choose to grow the same, higher-yielding cultivars, or when they grow different, higher-yielding cultivars with similar resistance genes, there is a lower level of genetic diversity in farmers' fields than the level that would most effectively protect against the emergence and spread of new strains of rust.

Heisey *et al.* (1997) compared the portfolio of wheat varieties actually cultivated by Pakistani farmers with an alternative portfolio and area distribution of cultivars that maximized diversity, as measured by genealogical indicators. Switching from the cultivars and areas actually planted to a more genetically diverse portfolio would have generated yield losses worth tens of millions of dollars annually, even without considering the costs of the policy interventions required to achieve it.

If the yield differential across varieties is sufficiently high, farmers may be better off growing only a single variety, even if they are highly risk averse. If the mean yield of a modern variety is high enough, farmers might not grow traditional varieties even if the traditional varieties have lower yield variance (or have yields that negatively co-vary with the yields of the modern variety). In fact, Meng and Taylor (1996) found that in Turkey modern varieties had both higher yields and lower variance than traditional varieties, at least at the regional level.[8] This suggests that, under some circumstances, this approach to measuring farmers' willingness to pay for genetic diversity could generate negative estimates.

In spite of the difficulties in interpretation, this approach offers an innovative and intriguing framework for measuring the value of genetic resources. Continued research along these lines may prove fruitful. (Part II of this volume offers empirical evidence on this issue.)

Contingent Valuation Measures

An extensive theoretical and empirical literature exists on other measures of willingness to pay, often referred to as contingent valuation; surveys include Hanemann (1994). Contingent valuation techniques have often been used to assign values to public goods and environmental resources. Some authors have attempted to apply these techniques to assess public willingness to pay for biodiversity preservation.

Evenson (1993) points out, however, that contingent valuation approaches are ill-suited to measuring the value of genetic resources. An average individual knows little about the International Rice Germplasm Collection (IRGC) and has little basis for gauging its value. Still less can this average individual compare the values of IRGC with the value of the sorghum collection maintained by the International Crops Research Institute for the Semi-arid Tropics (ICRISAT) or the wheat collection maintained by the International Maize and Wheat Improvement Centre (CIMMYT). The responses elicited from surveys may thus be inconsistent or even meaningless.

Brown (1990) reported some examples of contingent valuation methods used to place values on wildlife and sport fisheries. These methods work reasonably well on goods that are directly valued by consumers, but they are less applicable to goods such as PGRs that are primarily producer goods.

Hedonic Pricing

Evenson (1993) and Gollin and Evenson (1997) suggest that hedonic valuation techniques may be useful in valuing genetic resources as a producer good. Previous studies have considered the use of hedonics to value the benefits that consumers receive from environmental amenities (see Pearce and Cervigni, 1994).

Hedonic valuation uses statistical techniques to assign value to the characteristics of goods; it is the same approach, in effect, used by appraisers to place a value on a house. The underlying principle is to observe how the value of the final good changes depending on its characteristics. For example, appraisers might observe how the sale price of a house depends on the roofing material; this implicitly assigns a value to different types of roofing.

Similarly, it is possible to look at the productivity of rice in different localities and to associate productivity levels with the characteristics of the breeding stock used by plant breeders in that locality. Gollin and Evenson used this approach to analyse the productivity of alternative categories of rice germplasm in India (see Chapter 9).

In this research, gains in rice output were first divided into gains from yield and gains from expansion of the area under cultivation. Next, rice yield gains were disaggregated into gains from varietal improvement, other technological advances, and other sources of change. Finally, varietal improvement was assumed to depend on the stocks of advanced crossing material from different sources, on research activity, and on other research resources. The stocks of advanced crossing material were in turn assumed to depend on previously available stocks of landraces and wild species.

This theoretical framework allows direct estimation of the contribution of germplasm to rice productivity. In this model, the value of rice germplasm is based directly on its contribution to plant breeding and hence to varietal improvement.

Gollin and Evenson found that the contribution of certain types of germplasm to rice productivity gains in India was very high. In particular, germplasm that can be thought of as part of an 'old' core collection proved to have continuing value in the 1970s and 1980s. This reflects the fact that semi-dwarf genes and important disease resistance traits remain valuable. Moreover, Gollin and Evenson found (not surprisingly) a high value for the small set of genetic materials incorporated into breeding stocks through deliberate searches for resistance to diseases and pests. The authors conclude from this that 'fringe' materials may be valuable for germplasm collections. These fringe materials have precisely the characteristics that are often the target of collection-wide searches.

The hedonic approach offers perhaps the most convincing measure of the value of genetic resources. By directly linking genetic materials – and specific types of genetic material – to levels of output, this approach provides strong evidence for the value of germplasm. The negative aspect of this approach is that it is extremely data intensive. The India study was carried out in conjunction with a broader study of the returns to agricultural research, which was in itself data intensive. Only in this context could the value of genetic material be disentangled from the value of other research inputs and increases in factor use. The need for a complete set of data on total factor productivity suggests that the hedonic approach may not be widely applicable. (See Chapters 10, 11 and 12 for further hedonic applications.)

Other Hedonic Approaches: Mapping Genetic Flows

A slightly less data-intensive hedonic approach involves estimating the effect of germplasm collections on the international process of varietal improvement. This approach (followed by Gollin and Evenson, 1997) is presented in detail in Chapter 13, as a case study of valuing germplasm. The general idea, however, is to measure the relationship between international flows of plant varieties and the stocks of germplasm in different countries.

By associating flows of germplasm with increases in productivity, it is possible to link increases in productivity with increases in the stock of usable germplasm. Thus, when a germplasm-poor country gains access to varieties from other countries, its agricultural productivity rises. Some portion of this productivity gain can be attributed to increases in the stock of germplasm available to scientists and to farmers.

Evenson and Gollin (1997) use this approach to assign a value to the IRGC at IRRI. They note that the size of IRGC influences the extent to which national rice breeding programmes are willing to collaborate with international genetic research trials (INGER); when countries think that IRRI is a source of valuable genetic material, they are more likely to participate.

This approach succeeds in assigning a value to genetic resources; its disadvantage lies in its indirectness. Instead of measuring the direct relationship between germplasm and productivity gains, this approach only measures the tendency of germplasm collections to induce changes in the rate at which varieties flow across countries.

Option Values

The concept of option value is widely used in financial economics and is readily adapted to a standard neoclassical or Arrow–Debreu framework. In financial markets, an option gives the purchaser the right to exercise a particular choice at a future date. For example, an option might assign the purchaser the right to buy a given quantity of wheat at a specified price at a time 3 months from the present. Environmental economists have borrowed this idea as a useful general framework for thinking about environmental goods: people may be willing to pay a certain amount today to guarantee their right to make choices in the future.

There is no question that option values exist and are important: options are widely bought and sold on financial markets. In principle, however, they do not confer values distinct from productive values. Option values exist only insofar as the goods or assets in question will have tangible value in the future. For genetic resources, that value could be presumed to be future value in producing new crop varieties or commercial products.

One interesting study that uses this concept was carried out by Brush *et al.* (1992). This study provides evidence that Peruvian peasants maintain certain thresholds of on-farm diversity even when the immediate advantages of switching to improved varieties are large. The authors suggest that the cost of maintaining these ‘emergency’ stocks of traditional varieties represents a form of option value. This is the amount that peasants are prepared to forego in order to maintain the option of switching to other varieties at a later date.

This form of option value is essentially a kind of insurance. Thus, this work is closely related to the study by Heisey *et al.* (1997) of on-farm diversification. Both approaches suggest that the value of *ex situ* collections can be estimated by looking at farmers’ willingness to pay for genetic diversity.

Production Losses Averted

Some economists have arrived at rough estimates of the value of *ex situ* collections by linking them to prevention of crop losses at a national or global level. *Ex situ* collections serve as a store of disease and pest resistance for crop plants. Thus, they reduce expected future crop losses. This benefit is weighed against the cost of operating a gene bank and of searching across the collection. Brown and Goldstein (1984) use a model of this type to argue that all varieties should be conserved for which the marginal benefit of preservation exceeds the marginal cost.

Other economists have implicitly focused on crop losses as a measure of value. Oldfield (1989), for example, cites figures showing that the 1970s epidemic of Southern corn leaf blight caused crop losses valued at $2 billion; the implication is that genetic improvement efforts that defeated the epidemic could be valued at the same amount.

From an analytic viewpoint, however, this argument depends on faulty reasoning. The effect of the leaf blight epidemic was to lower production of corn and thus to raise its market price. But numerous substitution possibilities were available to both producers and consumers. Although the value of corn production may have fallen substantially, it does not follow that the value of agricultural production fell by the same amount. Nor does it follow that consumers are badly hurt if they can readily purchase satisfactory substitutes at reasonable prices.[9] Thus, the magnitude of crop losses does not necessarily provide an indication of the true costs faced by producers or consumers and is, therefore a poor proxy for the value of genetic materials.

Use of Experimental Data to Estimate Value

In a few cases, the value of genetic resources can be measured directly. Mitchell *et al*. (1982) report an attempt to measure the value of genetic contributions to pig improvement in Great Britain. Using standard experimental protocols, they compared improved pigs with pigs from control groups to determine the heritability of important characteristics and to isolate the genetic contributions to improved performance.[10] Using these measures, they estimated the costs and benefits of pig improvement. This approach could have greater applicability: for most crops and livestock, there are abundant experimental data showing the productivity gains associated with genetic improvement. Although on-farm yield gains may not perfectly match experimental yield gains, controlled experiments offer one way to identify the genetic components of productivity gains.

An Overview of the Volume

The conference for which the papers in this volume were prepared (The Symposium on the Economics of Valuation and Conservation of Genetic Resources for Agriculture sponsored by the Centre for International Studies on Economic Growth, University of Rome Tor Vergata and held on 13–15 May 1996, at the University of Rome, 'Tor Vergata') was convened to address both economic valuation issues and economic policy issues associated with the conservation of genetic resources. An attempt was made to relate genetic resource policy to broader economic questions associated with biodiversity policy. Readers, we believe, will find that the papers in this volume show that policies for genetic resources based on economic principles are not in conflict with biodiversity conservation objectives. At the same time we recognize that the policy-making environment is influenced by the past history of agricultural land conversion and that our conclusion regarding the complementarity of agricultural genetic resource policy and biodiversity conservation is not widely held at present.

The volume is organized in five parts, as follows.

1. Part I includes four chapters which offer models (or partial models) of plant breeding and land conversion. These chapters contain at least some of the insights which guide the empirical work reported in the rest of the volume.

- Chapter 1 reports a plant breeding model based on the 'search model of research'. It addresses three issues that pervade analysis of plant breeding programmes. These are: periodicity, recharge and spill-overs.
- Chapter 2 presents a model that links conservation programmes for traditional varieties *in situ* to public benefits (producer and consumer surplus).
- Chapter 3 offers a 'biodiversity' perspective on the search for and collection of naturally occurring PGRs. It too stresses the diminishing returns aspect of search.
- Chapter 4 provides an analysis of the sources of value for genetic resources.

2. Part II includes two empirical studies of field diversity. Both are related to the analysis in Chapter 4 in Part I.

- Chapter 5 reports indicators of field diversity and of production and yield variability in modern bread wheats. It addresses the concern of many that modern varieties have reduced field diversity more than the varieties that they replaced. The question is whether fewer modern cultivars with more diversity per cultivar have lower field diversity than more cultivars with lower diversity per cultivar.
- Chapter 6 reports a study of farmer preservation of landraces in wheat production in Turkey and addresses the question of incentives required to achieve farmer preservation of PGRs.

3. Part III is the 'core' of the volume. It includes seven chapters addressing the breeding values of PGRs.

- Chapter 7 reports a case study of a pre-breeding programme for maize. While it does not calculate actual pre-breeding values, it covers an important dimension of plant breeding work that is often underappreciated.
- Chapter 8 applies the'genetic content' or hedonic trait value to durum wheats in Italy. Chapters 9–11 report estimates of 'trait' values in rice breeding. Chapter 9 summarizes the first study using these methods where it was applied to district data for rice in India. Chapter 10 reports further works on trait values using cultivar data for India. Chapter 11 reports a study of modern varietal adoption and traits or genetic content for rice, also in India. It concludes that the incorporation of single-gene traits based on PGRs enabled a major expansion of the area planted to the high-yielding semi-dwarf type rice varieties.
- Chapter 12 uses crop loss and pesticides as data, along with yield data, to estimate the values of traits incorporated into rice in Indonesia.
- Chapter 13 reports a 'breeding production function' study relating the

discovery and development of new rice varieties to the size of PGR collections and to the international nursery system used by rice researchers.

4. Part IV includes four chapters addressing the role of property rights in genetic resource policy. The expansion of IPR in recent decades and their extension via the recent GATT–WPO agreements raises a number of issues for the collection and exchange of PGRs. These are further complicated by the 1992 Biodiversity Convention calling for the recognition of 'farmers' rights'.

- Chapter 14 addresses the general question of incentives for genetic resource, discovery and preservation utilizing experience from pharmaceutical discoveries.
- Chapter 15 addresses the issue of 'farmers' rights' and provides historical insights into the development and potential enforcement of these rights.
- Chapter 16 provides analyses of the financial implications of farmers' rights and of IPR generally.
- Chapter 17 reports an example of valuation of farmers' rights for rice and shows, somewhat surprisingly, that developed countries (notably the US) have produced important farmers' varieties.

5. The final two chapters in the volume (Part V) are addressed to the implications of biotechnology breeding techniques for the value of PGRs. It is sometimes suggested that these new techniques will end up reducing the value of the traditional PGRs now in gene bank collections. This might occur because breeders will shift to non-conventional natural PGRs or to non-natural PGRs. Both chapters in this final part suggest that modern plant biotechnology techniques are likely to enhance, not reduce, the value of traditional PGRs.

- Chapter 18 examines the current 'state of the art' in rice breeding biotechnology work and applications in developing countries.
- Chapter 19 summarizes recent priority-setting work for rice that allows comparisons between the likely value of new biotechnology techniques and alternative research techniques.

Notes

1. Plant genetic resources for food and agriculture (PGRFA) consist of the diversity of genetic material contained in traditional varieties and modern cultivars grown by farmers, as well as crop wild relatives and other wild plant species that can be used for food, feed for domestic animals, fibre, clothing, shelter, wood, timber, energy, etc. These plants, seeds or cultures are maintained for the purposes of studying, managing or using the genetic information they possess. As a term, 'genetic resources' carries with it an implication that the material has, or is seen as having, economic or utilitarian value. In this paper we use the more general term PGRs to refer to PGRFA.

2. Inevitably, however, this line of argument leads us toward a slippery slope – namely, the relative 'uniqueness' of different species. Since all species are by definition unique, it is only from a peculiarly anthropocentric standpoint that we can claim elephants are 'more unique' than particular ant species. Once again, the utilitarian approach is to assess uniqueness from the perspective of consumers and producers.

3. Nevertheless, a number of economists have implicitly attempted to estimate the value of genetic resources on this basis (e.g. Brown and Goldstein, 1984).
4. Preserving habitat does not necessarily conserve farmer's varieties. Their conservation may require maintaining farmer's practices.
5. Pre-breeding refers to the systematic evaluation of genetic resources for use in varietal breeding programmes.
6. Landraces are distinct cultivar types of cultivated species selected for within-type uniformity by farmers for different production conditions.
7. Farmers' diversify risk by planting different crops as well as by planting different varieties of a crop.
8. At the farm level, they found evidence that traditional varieties had lower yield variance.
9. Suppose, for example, that farmers can grow either corn or sorghum on their land. The price of corn is higher than the price of sorghum, and yields may be higher as well. But if the yield of corn falls sufficiently, due to disease problems, farmers may choose to plant sorghum instead of corn. This will result in a large decrease in the value of corn produced on the farm, but not necessarily in a large decrease in farm income. For consumers, too, the disease outbreak in corn causes the price of corn to rise. This would harm consumers, but with good substitutes available (such as sorghum), the demand for corn is relatively elastic, and the higher price does not cause much loss of consumer surplus.
10. This offers an alternative approach to the ways that economists generally assess the genetic contribution to varietal improvement; economists typically rely on total factor productivity analysis to assess the gains from genetic improvement, since experimental yields may not be indicative of farm-level yields.

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1

Plant Breeding: a Case of Induced Innovation

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Models of induced innovation (or invention) were introduced a number of years ago. They represented an important part of the economics literature for a few years but then faded from the scene. The 'old' growth economics (i.e. models where technological change was treated as exogenous) was not well suited to bringing invention–innovation into the growth theory literature. The older applied growth literature (total factor productivity (TFP) accounting, estimating sources of growth, etc.) did incorporate some features of induced innovation (notably the contribution of Binswanger and Ruttan (1978)).

The 'new' growth theory of recent years (Romer, 1990; Barro and Sala-i-Martin, 1992; etc.) has opened up scope for a renewal of work on induced innovation. The field, however, has been hindered by several factors in the past:

1. The lack of case study and other evidence for a discovery function that actually guides invention (or innovation. The term invention is used here. The commercialization of inventions is taken as the definition of innovation).
2. Lack of clarity as to the 'periodicity' of discovery (e.g. must one stage be completed before another can begin).
3. Lack of clarity as to the 'recharge' mechanisms by which innovative scope is changed.

These issues will be discussed in the context of a particular form of invention, the breeding of improved plant cultivars. The standard 'search' model (Evenson and Kislev, 1975) is used in the discussion, and realism imparted by reference to the author's plant breeding experience. An important feature of this model is the 'recharge' of invention potential.

Agricultural Values of Plant Genetic Resources
(eds R.E. Evenson, D. Gollin and V. Santaniello)

The Simple One-trait One-period Model

Plant breeders have two search strategies in their research or inventive efforts. The first of these is the search for ‘quantitative’ plant traits such as yield. Quantitative traits are controlled by multiple genes (or alleles) and require complex strategies for crossing parental materials and selecting improved cultivars. The second is the search for ‘qualitative’ traits such as host plant resistance (HPR) to plant diseases or to insect pests. Host plant tolerance (HPT) to abiotic stress (drought, cold, etc.) are also qualitative traits. Qualitative traits are controlled by a single gene (or at least very few).[1]

Both breeding strategies rely on searching for genetically controlled traits in collections of plant genetic resources (PGRs) which include landraces of the cultivated species (distinct types selected by farmers over centuries from the earliest dates of cultivation and diffused across different ecosystems), ‘wild’ (related) species and related plants that might be combined.[2] PGR collections also include ‘combined’ landraces including varieties (officially recognized uniform populations of combined landraces often with many generations of combinations). The systematic combining of landraces and evaluation is termed ‘pre-breeding’.[3]

Consider the following representation of the single-trait one-period model.

In period 1, the existing breeders’ techniques and breeders’ PGR collections determine a distribution of potential varieties indexed by their economic value, x. Following Evenson and Kislev (1975), suppose this distribution to be an exponential distribution:

$$f(x) = \lambda e^{-\lambda(x-\theta)}, \theta \le x. \tag{1}$$

The cumulative distribution is:

$$F(x) = 1 - e^{-\lambda(x-\theta)} \text{ and} \tag{2}$$

$$E(x) = \theta + 1/\lambda \tag{3}$$

$$\mathrm{Var}(x) = 1\lambda^2. \tag{4}$$

The cumulative distribution of the largest value of x (z) from a sample of size (n) is the ‘order statistic’ (Evenson and Kislev, 1975):

$$H_n(z) = \left[1 - e^{-\lambda(z-\theta)}\right]^n \tag{5}$$

and the probability density function for (z) is:

$$h_{n(z)} = \lambda n \left[1 - e^{-\lambda(z-\theta)}\right]^{n-1} e^{-\lambda(z-\theta)}. \tag{6}$$

The expected value and variance of $h_n(z)$ are:

$$E_n(z) = \theta + \frac{1}{\lambda}\sum_{i=1}^{n}\frac{1}{i} \approx \theta + \lambda \ln(n) \tag{7}$$

$$\mathrm{Var}_n(z) = \frac{1}{\lambda^2} \sum_{i=1}^{n} \frac{1}{i^2}. \tag{8}$$

Evenson and Kislev discuss the applicability of equations (7) and (8) to plant breeding research. Equation (7) can be derived from a uniform distribution and this is a very general expression for a broad range of functions $f(x)$. Basically (7) can be thought of as the breeding production function with a very simple marginal product:

$$X_t^s = f\left(\mathbf{P}_t, \mathbf{Z}_t, \mathbf{h}_t, \tau_t \left[TE_{t-s}(E_{t-s}, I_{t-s}), TE_{t-s-1}(E_{t-s-1}, I_{t-s-1}), \ldots\right.\right. \tag{9}$$

When a measure of the units over which (z) applies is available (e.g. production in a specific ecosystem), V, the value of the marginal product can be computed and set equal to the marginal cost of search to solve for optimal n:

$$\lambda V / n = MC(n). \tag{10}$$

Figure 1.1 depicts $f(x)$ and $E_n(z)$ for two traits for a single period and shows the optimum.

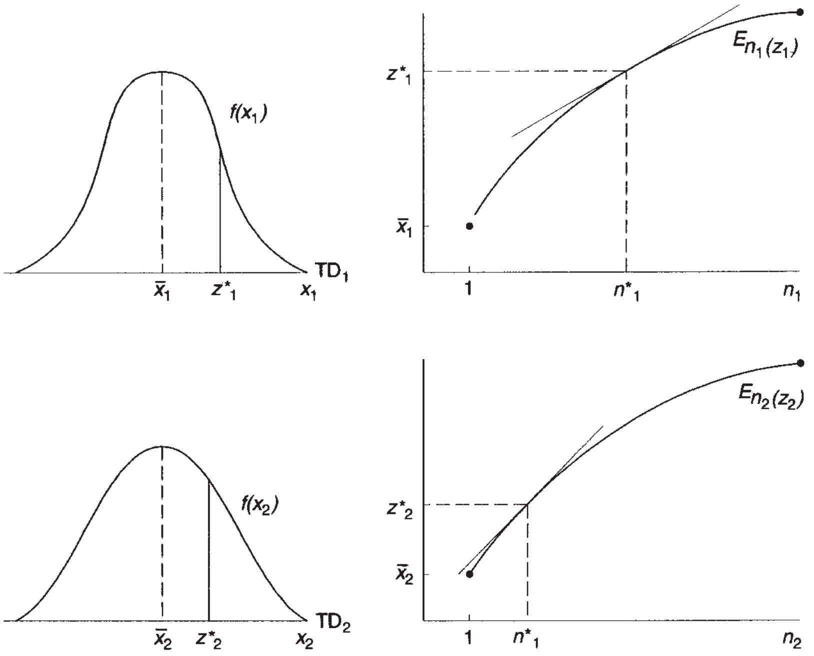


Fig. 1.1. Single-period search. TD, technological determination point.

The Simple Multiple Trait Invention Possibilities Frontier

For two or more traits, each can be characterized by Equation (7) with different parameters:

$$\begin{aligned} E_n(Z_1) &= t_1 = \theta_1 + \lambda_1 \ln(N_1) \\ E_n(Z_2) &= t_2 = \theta_2 + \lambda_2 \ln(N_2) \\ E_n(Z_n) &= t_n = \theta_n + \lambda_n \ln(N_n). \end{aligned} \tag{11}$$

When these traits are qualitative traits, breeders typically search for them independently because there are techniques enabling the breeders to incorporate only the single trait in a cultivar (i.e. by back-crossing and other methods, unwanted traits can be discarded). Thus even if traits are highly correlated, the breeder will search independently for them.[4]

Thus, if we set $N = N_1 + N_2$ at some level (say the optimizing level) where:

$$MC(N_1) = MC(N_2) = \alpha_1 V_1 N_1 = \alpha_1 V_1 N_1 = \alpha_2 V_2 N_2 \tag{12}$$

we have the standard invention (or innovation) possibilities frontier (IPF) depicted in Fig. 1.2. (Note the depiction is in terms of traits, but these can be translated into economic units through values.)

Multiple Periods Without Recharge

Now consider periodicity. In practice, we do not observe the single period optimal search implied by equations (7), (11) and (12). Typically we observe multiple-year R&D programmes even for narrowly defined objectives. Could we treat this multiple-year sequence as simply a long period instead of a sequence of periods? Certainly not in plant breeding. Plant crosses (genetic combinations) must be evaluated and selected over several generations. Plant 'types' (quantitative) are built with multi-generation crosses where the crossing decisions for the second generation can effectively be made only after the first generation has been observed.[5]

In addition to this periodicity, two related types of periodicity will be considered. In this section, periodicity associated with search field narrowing (elimination of unpromising search avenues) will be considered. In the next section, 'recharge' will be considered.

Consider first the search field narrowing case. This is depicted in Fig. 1.3 where a rightward shift in the mean of the distribution but not the right-hand tail of the distribution is depicted from period 1 to period 2. This shift can be thought of as the systematic elimination of unpromising search avenues. It may be possible to classify material in *n* groups. In period 1, sufficient sampling is undertaken to enable the estimation of the mean and variance for each of the *n* groups. On the basis of these estimates several groups may be eliminated, with the resultant distributional shift depicted in Fig. 1.3.[6]

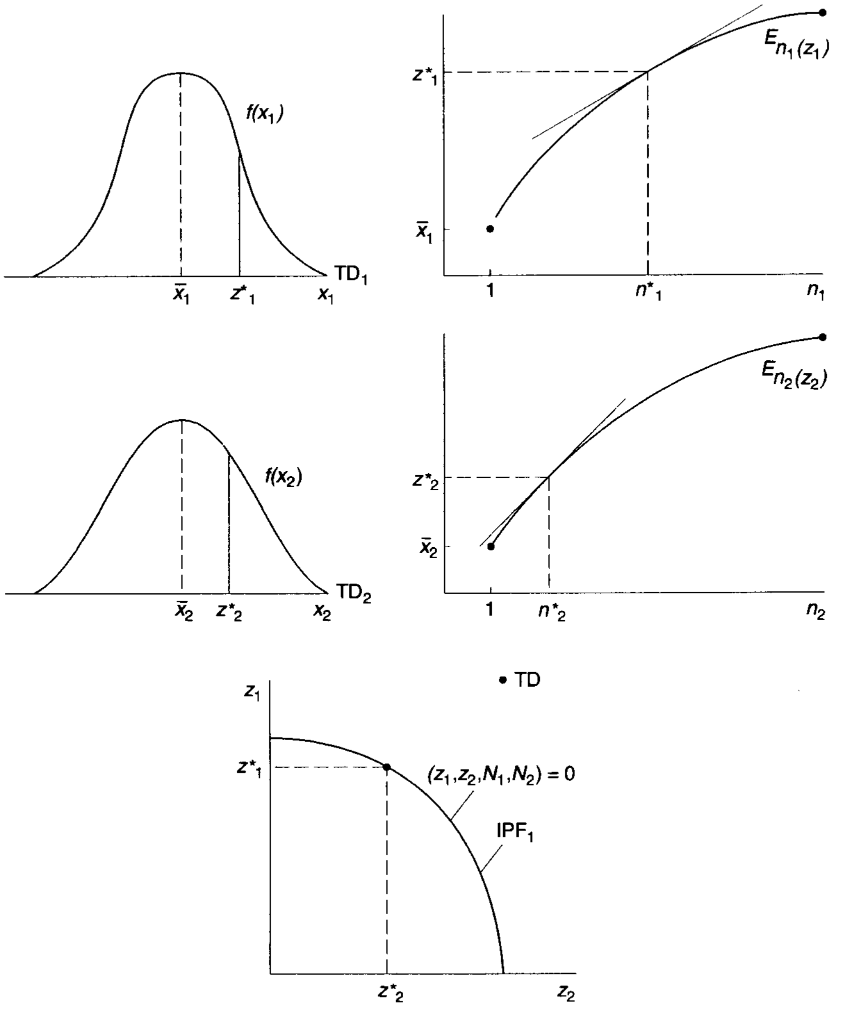


Fig. 1.2. Single-period invention possibilities frontier (IPF).

The shift in the mean as depicted for both trait distributions is proportional to the period 1 optimal discovery as depicted in the IPF diagram for the two traits. This IPF has two features designed to show how a multi-period invention process would proceed. The first is the period 2 IPF. The second is the 'technological determination' point, TD, which is determined by the location of the right-hand tails of the two search distributions. It is the point to which search would proceed if the marginal cost of search were zero.[7]

The period 2 IPF is determined by the period 2 means which locate the period 2 axis and the period 2 optimal search points n_{12} and n_{22}. The shape of

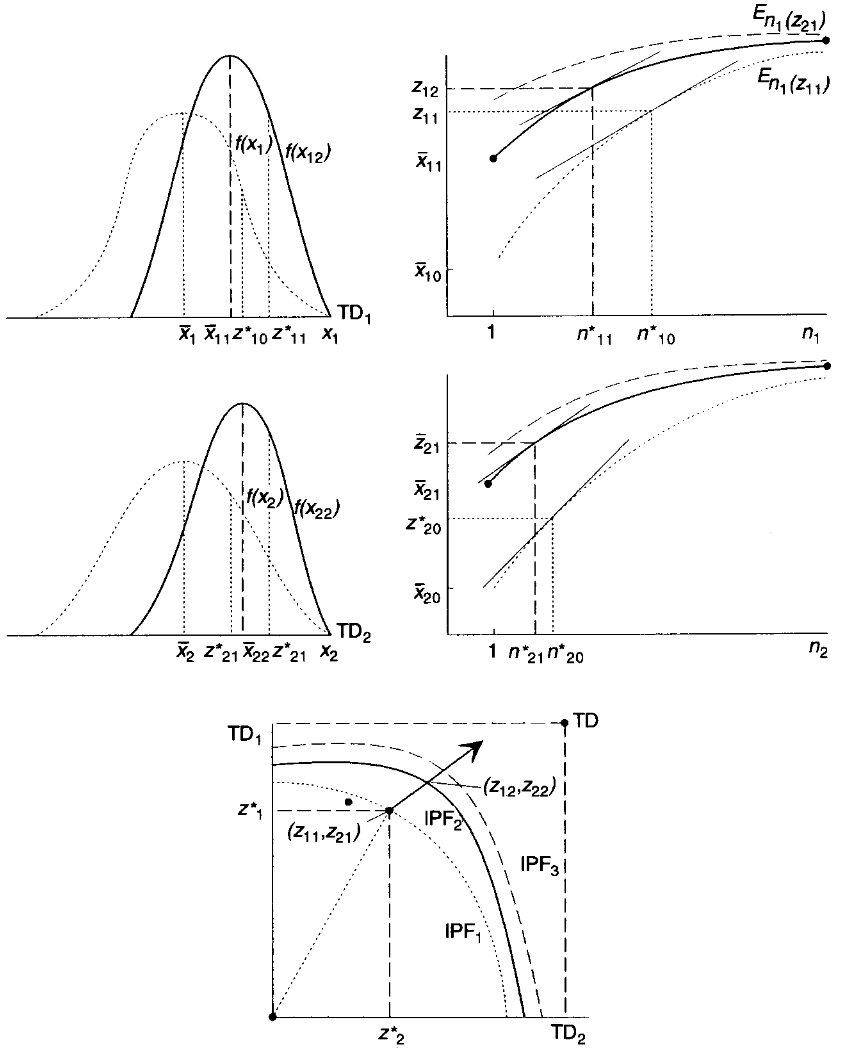


Fig. 1.3. Multi-period search with search field narrowing.

IPF_2 is affected by period 1 search. Because period 1 search was induced by values to produce more n_{11} search for t_1 than n_{21} search for t_2, there is more remaining exploitable search scope for t_2 in period 2. The resultant optimal point on IPF_2 is thus not on the same ray as was the optimal point on IPF_1. The search exhaustion phenomenon has moved the optimal point in the direction of the TD ray or ratio.

As depicted here, in period 3 the mean for t_1 shifted up but the optimal search point t_{13} is no higher than t_{12}. Thus, at existing prices and values no further search for t_1 will take place. Further search for t_2 will take place, but it too will stop at the end of period 3.

The implications of this search exhaustion case are that multi-period search can take place but that it will eventually stop. During the multi-period search, the ratio of inventions (presumably proportional to $t_{11} - t_{10}$, $t_{12} - t_{11}$, etc.) to search resources (R&D) n_1 will decline. A further implication is that after period 1 the t_1/t_2 ray will move in the direction of the TD ray.[8]

Multiple Periods with Recharge

Plant breeding programmes have developed several types of recharge mechanisms.[9] These include:

1. Genetic resource collection and evaluation programmes. These programmes are designed to discover uncollected materials and make them available to breeders.

2. Pre-breeding programmes where landrace materials are systematically combined into potential breeding lines by specialized research programmes. These programmes do not seek to develop 'final products' (i.e. new cultivars). Instead they seek to evaluate and produce 'advanced lines' that are then used by final product inventors.

3. Wide-crossing programmes where techniques for inter-specific combinations of genetic resources (between related species) are made possible. This expands the size and scope of the original materials that can be utilized in breeding programmes.

4. Transgenic breeding programmes where DNA insertion techniques allow traits associated with alien genes (i.e. from unrelated species) to be incorporated into cultivated plants.

These programmes are 'pre-invention' science or recharge science programmes. They provide recharge to the invention distributions by shifting both the mean and the right-hand tail of the search distribution.

Figure 1.4 depicts the nature of these shifts for search distributions and IPFs with recharge. Note that the TD point moves with recharge. The reader can readily see that one could have cases of 'super-recharge' for a number of periods where inventions per inventor might increase over time (e.g. in sugarcane breeding; Evenson and Kislev, 1975). But recharge science itself is likely to be subject to diminishing returns, unless it is also recharged by the more basic sciences. (See below for a discussion of this issue.)

These ideas can be clarified with a little algebra. Describe the breeding (invention) process as:

$$\begin{aligned}
&T_1 = T_1(G_1, B_1) = \theta_1 + \lambda_1 G_1 \ln(B_1) \\
&T_2 = T_2(G_2, B_2) = \theta_2 + \lambda_2 G_2 \ln(B_2) \qquad (13) \\
&\vdots \\
&T_n = T_n(G_n, B_n) = \theta_n + \lambda_n G_n \ln(B_n).
\end{aligned}$$

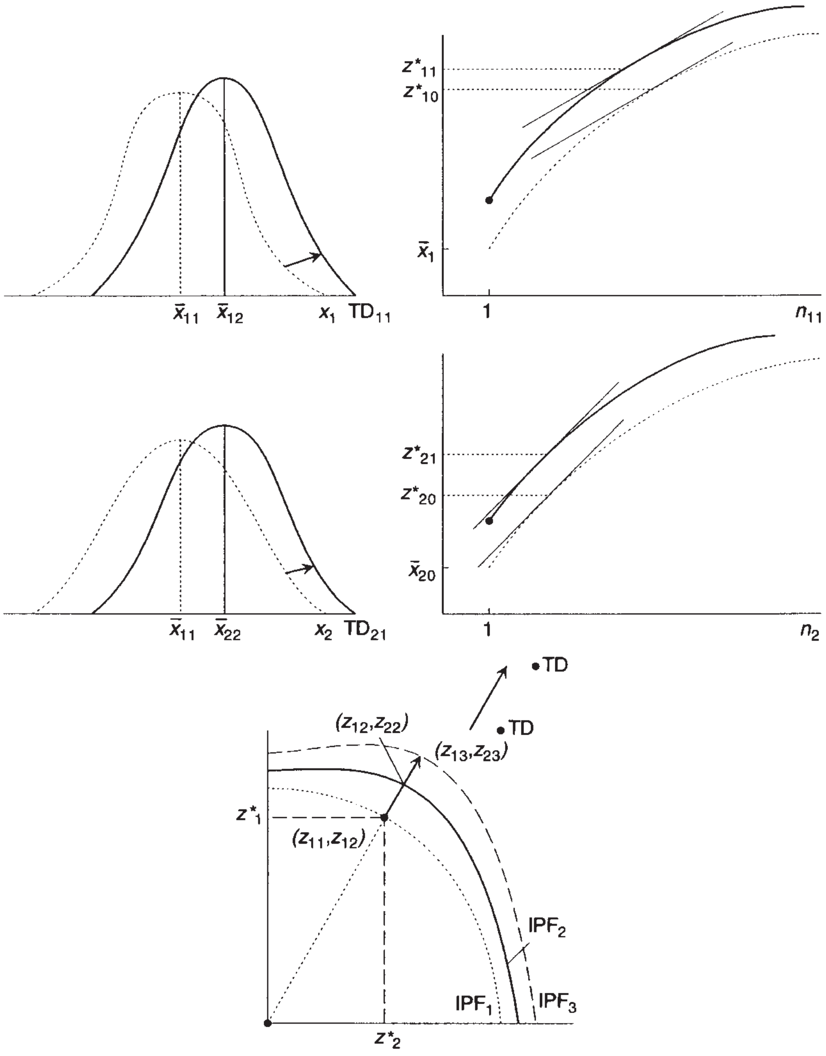


Fig. 1.4. Multi-period search with recharge.

This system of equations describes the incorporation of traits as a function of germplasm G_i and breeding activity B_i. The functional form is based on the search model.[10]

It is relatively straightforward to show that the first-order condition for allocating breeding research between any two traits is:

$$\frac{B_i}{B_j} = \frac{\lambda_i G_i V_i}{\lambda_j G_j V_j} \tag{14}$$

where V_i and V_j are measures of the marginal contribution to crop value of traits i and j. (Note that each trait may appear in several varieties and that each variety may be planted to different areas.)

Now consider the production of germplasm (G_i). This is characterized as being produced in a pre-breeding process:

$$\begin{aligned} G_1 &= G_1(G_c, PB_1) = \delta_1 + \phi_1 G_c \ln(PB_1) \\ G_2 &= G_2(G_c, PB_2) = \delta_2 + \phi_2 G_c \ln(PB_2) \\ &\vdots \\ G_n &= G_n(G_c, PB_n) = \delta_n + \phi_n G_c \ln(PB_n). \end{aligned} \tag{15}$$

In this pre-breeding process, pre-breeding activity converts evaluated genetic resources G_c into germplasmic breeding materials. This process is also a search process. Again, the first-order conditions for pre-breeding activities are straightforward:

$$\frac{PB_i}{PB_j} = \frac{\phi_i G_c \lambda_i V_i}{\phi_j G_c \lambda_j V_j}. \tag{16}$$

Evaluated germplasm is produced by the natural stock of genetic resources (G_n) and collection (C) and evaluation (E) activities

$$G_c = G_c(G_n, E, C). \tag{17}$$

The following features of this simple model can be noted:

In plant breeding, if the marginal search coefficients are equal ($\lambda_i = \lambda_j$), the breeding activity obeys ‘the congruence rule’ where inventive activity is proportional to the value of the units affected (see equations (14) and (16)).

$$\frac{B_i}{B_j} = \frac{V_i}{V_j}. \tag{18}$$

Departures from congruence (a strong form of induced innovation) are justified when search parameters differ.

It can be further noted that the optimal conditions for pre-breeding (or germplasmic recharge science) (equation 15) also imply that if the germplasmic search coefficients are equal, then congruence occurs for both pre-breeding and breeding. This is a strong form of multi-period-induced innovation. The multi-period invention path is a ray from the origin (if prices do not change) that is parallel to the TD expansion path. A change in prices (values) will result in a change in the invention path and in the TD path (Fig. 1.4). Both will have the same slope.

Implications for Incentives

The simple model sketched out above shows how recharge research is important to induced innovation. It does not address very directly the matter of incentives for undertaking R&D. Nor does it address inter-industry or geographic spillovers.

As the section on plant breeding and agricultural research below will show, both problems are central for this field of research. Perhaps it is because of the severity of both problems that we observe them being addressed as effectively as they have been. Public sector agricultural research systems have been built in most countries of the world. These systems were among the earliest cases where governments recognized that the incentive systems (chiefly intellectual property rights (IPRs) systems) were not sufficient to bring forth adequate invention. Colleges of agriculture and mechanics (A&Ms) were originally designed to train agricultural and engineering practitioners. Agricultural experiment stations were developed to facilitate inventions (especially plant breeding), and extension systems were developed to diffuse these inventions.

Over the years these institutions were continuously in tension over the relative weights to place on extension, invention, and pre-invention or recharge science. Equation (12) describes recharge activity and shows the resource allocation rule for breeding (equation 13). Pre-breeding (recharge) activity is described by equation (15), and equation (16) gives a simple allocation rule. Finally equation (17) describes the genetic resource allocation–collection activities.

There is thus a consistent system of derived demands for the relevant activities – breeding, pre-breeding, evaluation of CGRs and collection of CGRs – sketched out in the model. Empirical estimates of these derived demand equations are hampered by the lack of adequate markets for CGRs.

The simple breeding model sketched out above does provide guidelines as to the derived demand for various types of research activities. (Incentives affect the supply of such activities.) The demand for plant breeding research producing a single trait for a particular location is based on equation (7). Each new invention has an incremental value expressed by its value of marginal product $\lambda V/n$ (see equation (10). The optimizing level of trait search is determined by equation (10). For multiple traits, each has a demand function and optimization is governed by equation (12). These expressions describe the demand for inventive effort given the search distribution.

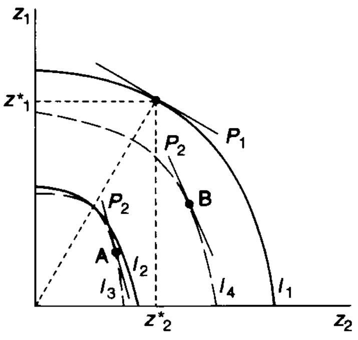
In the section ‘Multiple periods without recharge’, the demand for search field narrowing activities is developed. Some search field narrowing (SFN) is a by-product of search, but some is competitive with search. The value of the marginal product of SFN activity is based on its effect on the marginal product of search.

Implications for Spillovers

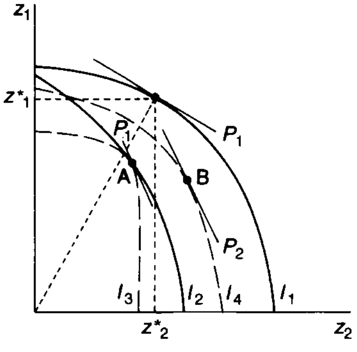
The dimension of spillovers was also recognized in agricultural research systems and is reflected in numerous locations of agricultural experiment stations around the world (see below for rice) with a high degree of germplasmic spillovers and adaptive invention for targeted ecosystems. It is well known that plants and animals perform differently under different ecosystems and that modern plant-breeding has only partially overcome the 'Darwinian' adaptation to ecosystem niches in nature. It is also well known that relative prices affect the real value of an invention (an improved rice harvesting machine is valuable in Texas but has no real value in Bangladesh where wages are low and rice is harvested by hand).

Figure 1.5 attempts to illustrate the price and non-price (ecosystem) elements of spillovers and incentives for two technology cases. Consider technology A. Four IPFs are illustrated.

- I_1 is for the origin location with prices P_1 and with adequate incentives inventions of (z_1*, z_2*) will be made.
- I_2 shows how non-price elements (ecosystem institutions, etc.) remediate the real performance of z_1 and z_2 in location 2 and leads to an interior IPF.
- I_3 is the real value IPF in location 2 given that location 1 produced (z_1*, z_2*). This lies below I_2. At location 2's price line P_2, location 2 will then have direct spill-in of point A.



Technology A



Technology B

Fig. 1.5. Spatial spillover.

- I_4 is the IPF now available to location 2 should it choose to undertake research. The difference between I_4 and I_3 is the germplasm potential afforded by location 1 to location 2. Location 2 has a choice between no research (point A) and research (point B).

Technology B has the same I_1 as technology A and lower non-price remediation. It, however, has less adaptability and germplasmic potential in the region of the IPF relevant to location 2 (a less developed country).

It is generally thought that agricultural technology is characterized by the A technology where non-price remediation (technology distance $I_1 - I_2$; see below) is high, and adaptive potential is good ($I_2 - I_3$ is low) and germplasmic potential ($I_4 - I_5$) is high. For biological traits, relative prices also may not differ between country 1 and country 2. This will lead to strong incentives to locate research capacity in both countries. These research programmes ‘feed’ off each other and sometimes on international recharge programmes. This produces a tendency for multiple period convergence of both paths toward the TD paths for the two countries which also converge. The history of public support (with World Bank and aid agency support) provides incentives for this system to reach many locations.

Mechanical technology is thought to be more like B where non-price remediation is low, price differences great, and adaptive and germplasmic potential low (at least at country 2’s prices). This combined with weak IPRs and public sector R&D experience in the poorer country leads to little R&D and a low rate of productivity growth in country 2.

Recharge and Spillovers in Empirical Studies

The empirical chapters in Part III of this volume report direct studies of PGR values. Several empirical studies of agricultural research have recognized recharge and spillover in a somewhat less direct fashion.

A recent review of these studies (Evenson, 1996) reported that several studies estimated the contributions of pre-invention or recharge science. The estimated economic contribution of these recharge science programmes was actually higher than the contribution of applied invention. Studies of science-linked invention where patent references to science (pre-invention science) are used are now being reported. This work is consistent with the above model.

Spillover modelling is still in its infancy, although a number of studies have now been reported. They are of two types. The first are of inter-sectoral spillovers chiefly from industry to agriculture. Evenson (1996) identifies ten studies of this type. The second are inter-regional spillovers. These are especially relevant to PGRs as shown in Chapter 11.

The key to inter-location studies is the identification of reasonably homogeneous regions or of technology distance measures of the form:

$$D_{ij} = \frac{C_{ij}}{C_{ii}} \tag{19}$$

where C_{ii} is the minimum cost of producing a commodity in location i using the cost minimizing technology (e.g. crop varieties) suited to location i, and C_{ij} is the minimum cost of producing the commodity in location i when producers in location i are constrained to use the cost minimizing technology for location j.

Measures of D_{ij} based on yield trial data have been developed for rice and used to estimate spillovers in India (Evenson, 1996). Similar estimates have been used for studies in Brazil (da Cruz and Evenson, 1989).

The D_{ij} measures tell us much about the optimal location of research programmes and about the value of CGRs. In crops planted on large areas, technology distances are great and within-species diversity is high. Plant breeders must exploit this diversity to target varietal development to the diverse regions that they serve.

Notes

1. Traits are controlled genetically and expressed phenotypically. Recent developments in biotechnology markers enable breeders to measure genetic components more accurately.
2. Gene bank collections for most cultivated crops are maintained and made accessible to plant breeders. Most collections are in the public domain. Private firms hold combined materials in a proprietary fashion.
3. The pre-breeding covers a range of activities including the development of inbred lines to be utilized in hybridization breeding.
4. Modern biotechnology techniques allow the breeder more refined means for transferring traits to plants.
5. The nature of pre-breeding requires selection which can be done only after the progeny for crosses can be observed.
6. Groups may be focused on the basis of phenotypic (observable) characteristics or with genetic markers. Breeders attempt to form groups with minimum within-group diversity and maximum between group diversity.
7. Actual search would never proceed to this point because it is costly. Genetic resources can also be classified by rarity (i.e., the size of the habitat). The cost of collection is related to rarity, but the cost of accessing collected materials is not. There is some evidence that the actual value increases with rarity.
8. This simple multi-period without recharge model characterizes many plant breeding programs that are ‘exhausted’ or ‘fished out’. In some cases this exhaustion has been there from the beginning in the sense that the CGR collections for the crop in that ecosystem have never been rich enough to enable breeders to improve upon the ‘farmers' varieties’ selected by farmers over centuries. In other cases, the original richness of the CGR collection has been exploited and breeders are near the TD point.
9. ‘Recharge’ refers to activities directed at changing the parameter of $f(x)$.
10. See Gollin and Evenson (1997).

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Part I
Modelling the Role of Genetic Resources in Plant Breeding

2

The Economics of Public Investment in Agro-biodiversity Conservation[1]

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In response to growing international concern that the threat to species and ecosystems caused by human activities is at an all time high, and that this threat may result in high costs to present and future generations, the United Nations adopted the Convention on Biological Diversity (CDB) in 1992 at the United Nations Conference on Environment and Development (the Rio 'Earth Summit'). While initially the concern was on biodiversity in general, by the third meeting of the Conference of the Parties to the Convention (COP) in 1996, it adopted decisions that included the development of a work programme on agricultural and forestry biological diversity, namely to 'establish a multi-year programme of activities on agricultural biological diversity aiming: first, to promote the positive effects and mitigate the negative impacts of agricultural practices on biological diversity in agro-ecosystems and their interface with other ecosystems; second, to promote the conservation and sustainable use of genetic resources of actual or potential value for food and agriculture; and third, to promote the fair and equitable sharing of benefits arising out of the utilization of genetic resources ... ' (paragraph 1, Decision III/11 in COP, 1997).

While the justification for this call to public action on agricultural biodiversity (from here on referred to as agro-biodiversity) has not been framed in an explicitly economic context, it may be considered as the value to society of avoiding irreversible decisions on the conservation of crop genetic resources (CGRs), i.e. the 'quasi-option value' (Arrow and Fisher, 1974) or 'option value' (Henry, 1974) of reducing the erosion in agro-biodiversity.[2] In particular, the loss of native landrace (or 'traditional' varieties) is irreversible. As first noted by Hanemann and Fisher in the context of option value, other varieties may be close, but not perfect, substitutes, so once a particular land race is extinct, its value for future plant breeding will remain unknown.[3]

Agricultural Values of Plant Genetic Resources (eds R.E. Evenson, D. Gollin and V. Santaniello)

This chapter presents a model for assessing publicly funded agro-biodiversity conservation programmes. It considers the tradeoff between *in situ* and *ex situ* conservation programmes and develops a methodology for assessing the economic returns associated with these programmes.

Methodology for Addressing Investment in Agro-biodiversity Conservation Projects

Genetic erosion is the loss of genetic diversity, including the loss of individual genes and combinations of genes. The main cause of genetic erosion in crops is the replacement of local varieties by improved or exotic varieties and species (FAO, 1996). Erosion can occur when a small number of new varieties replaces a larger number of older varieties and/or the newer varieties have a different gene base to the old one.

While some indicators of genetic erosion have been developed (FAO, Annex 1.1; Reid *et al*., 1993), there have been few studies with quantifiable estimates of the rates of genotypic or allelic extinction of CGRs. This chapter proposes a proxy measure for the rate of erosion of agro-biodiversity: the change over time in the number of potential accessions from *in situ* sources to *ex situ* collections. In addition to being a concrete measure, it has the benefit of making the link between *in situ* and *ex situ* conservation explicit.

This chapter assumes that genetic erosion takes place in poor countries but generates negative externalities for rich countries, which use agro-biodiversity as an input to breeding new crop varieties. It assumes further that rich countries bear the cost of agro-biodiversity maintenance, and that farms participating in *in situ* conservation programmes are price takers on the world market.

Let AM_0 be the estimate of the number of distinct existing cultivars uncollected at present. Chang (1993), for example, presents estimates of this value for various crops. Let AM_t be the number remaining at date t:

$$AM_t = f\left(I_t, S_t, AM_{t-1}\right), t = 1, \quad \ldots, T, \tag{1}$$

where I_t = investment by rich countries in agro-biodiversity conservation in target areas; S_t = vector of socio-economic factors in the programme area that are causing AM_t to decrease over time (see e.g. Brush *et al*., 1992); and I_t and $S_t \geq 0$. The expected signs are $\partial Am_t / \partial I_t > 0$ and $\partial Am_t / \partial S_t < 0$. It is assumed that $\partial AM_t / \partial t \leq 0$.

Let A_t be the number of these distinct cultivars collected (accessions) and put into *ex situ* collections in period t. In addition, it is likely that cultivars not existing at period 0 may be developed by breeding activities of the indigenous farmers in the programme target area. Let these new varieties be denoted by AN_t. The production of AN_t would be expected to be part of a conservation programme if the programme goes further than just paying farmers to conserve landraces they already have, but allows conservation to be a dynamic process and encourages the breeding of new varieties using their existing stock as a base. The accessions are functions of the following variables:

$$A_t = f\left(I_t, E_{A.t}, S_t, AM_t, A_0, A_1, \ldots, A_{t-1}\right), \tag{2}$$

$$AN_t = f\left(I_t, E_{AN.t}, S_t, AM_t\right), \tag{3}$$

where $E_{A.t}$ and $E_{AN.t}$ (both ≥0) are the collection efforts ($) (i.e. amount spent to collect CGRs during t in the programme area, on existing and new varieties, respectively). Note that $E_{A.t}$ and $E_{AN.t}$ are *ex post* accounting values: the search agent spends E_t over the period and then calculates how much was spent on A_t and AN_t in simple proportions to the amounts of each retrieved from the field. The expected signs are $\partial A_t/\partial I_t > 0$, $\partial A_t/\partial E_t > 0$ and $\partial A_t/\partial S_t < 0$. There is no reason to expect that AN_t would not behave in the same way as A_t in that investment I_t and E_t will turn up both existing and new cultivars, and hence $\partial AN_t/\partial I_t > 0$, $\partial AN_t/\partial E_t > 0$ and $\partial AN_t/\partial S_t < 0$.

Of course, AM_t, AN_t, and A_t cannot be known with certainty. Since AM_t is censored at 0 and discrete, the probability of these levels occurring is best modelled by a discrete distribution such as the negative binomial, at least in small samples.[4]

This approach differs from Simpson *et al.* (1996) in which biodiversity prospecting is modelled as a sequence of independent Bernoulli trials, where each species could either yield a 'hit' in the search for a new product, or prove useless. Here instead, in the sequence of independent Bernoulli trials that make up the negative binomial, a 'hit' is simply turning up a new (i.e. uncatalogued) distinct variety.

The probabilities of failure $P_{A.t}$, $P_{AN.t}$, and $P_{AM.t}$ are assumed to be a function of I_t and S_t. Since the true specification of P_t is unknown, P_t is chosen to be logistic, producing a tractable closed form specification. For a random variable x_t, this functional form is:

$$P\left(x_t \geq X\right) = \left[1 + exp^{\left(\frac{xt-mt}{kt}\right)}\right]^{-1}, t = 1, \ldots, T \tag{4}$$

where m_t and k_t are the mean and scale parameters, respectively. For simplicity, it is assumed that the transformation of $(x_t - m_t)/k_t = G_t = f(I_t, S_t)$, where $\partial G_t/\partial S_t > 0$, $\partial P_t/\partial E_t < 0$, $\partial P_t/\partial I_t < 0$, and $\partial P_t/\partial S_t > 0$. Given $\partial \Phi_t/\partial P_t < 0$, then $\partial_t \Phi \partial P_t/\partial P_t \partial I_t \geq 0$.[5]

Given that accessions in any period are negative binomial distributed random variables, mean AN_t is:

$$\varepsilon\left(AN_t\right) = \varphi_{AN.t} \exp\left(-G_{AN.t}\right). \tag{5}$$

As shown above, AM_t is non-increasing, so that $\varepsilon(AM_t) = \varphi_0[1 - \text{argmax}\{P_{AM.t-1},$

$P_{AM.t}\}]/\mathrm{argmax}\{P_{AM.t-1}, P_{AM.t}\}$. Given the logistic specification for P, $\varepsilon(AM_t)$ can be rewritten as:

$$\varepsilon\left(AN_t\right) = \mathrm{argmin}\left\{\varphi_0 \exp\left(-G_{AM.t}\right),\ \ \varepsilon\left(AM_{-1}\right)\right\},\quad t = 1,\ \ldots,\ T \tag{6}$$

where $\varepsilon(AM_{-1}) = \varphi_0$ (i.e. $P_{AM.0}$ is set equal to 50%).

Unlike AN_t, A_t is restricted by the previous levels of A_t and by AM_t. Let Ψ_t be the unrestricted value of A_t, and have a mean value of $\varphi_{At}Q_{A.t}/P_{A.t}$, then A_t is:

$$A_t = \begin{cases} \Psi_t, AM_t - \sum_{k=0}^{t-1} A_k \geq \Psi_t \\ AM_t - \sum_{k=0}^{t-1} A_k, AM_t - \sum_{k=0}^{t-1} A_k > 0 \text{ and } AM_t - \sum_{k=0}^{t-1} A_k < \Psi_t \\ 0, AM_t - \sum_{k=0}^{t-1} A_k \leq 0 \end{cases} \tag{7}$$

where $AM_t - \sum_{k=0}^{t-1} A_k$ is the uncollected CGRs from AM_t that are remaining on the field at time t. Note that since $\partial Am_t/\partial t \leq 0$, the uncollected CGRs can fall to 0 without $\sum_{k=0}^{t} A_k$ reaching the level AM_0, i.e. some potential accessions known at time 0 may be irreversibly lost.

Given annual accessions A_t and AN_t, the size of the *ex situ* collection at period t is denoted as TE_t and is simply:

$$TE_t = \sum_{k=0}^{t} A_k + \sum_{k=0}^{t} AN_k + TE_0 - \sum_{k=0}^{t} L_k \tag{8}$$

where TE_0 is the carryover stock at the beginning of period 0 and L_t are the losses of prior levels of TE_t due to spoilage and other factors each period, and where '*ex situ* collection' refers to the aggregate of all *ex situ* collections.

Methodology for Assessing Economic Returns to Gains to Investment in Agro-biodiversity Conservation Projects

Crop breeding research relies on the availability of genetic resources as an input. In general, given a larger stock of genetic resources, the gains to research will be higher.

The general form for a supply response function for agricultural crop output with respect to gene bank size can be written as:

$$\begin{aligned} X_t^s = f\Big(&\boldsymbol{P}_t, \boldsymbol{Z}_t, \boldsymbol{h}_t, \tau_t\Big[TE_{t-s}\left(E_{t-s}, I_{t-s}\right), TE_{t-s-I}\left(E_{t-s-I}, I_{t-s-I}\right),\ \ldots, \\ &TE_0\left(E_0, I_0\right), \boldsymbol{h}_t\Big], \boldsymbol{U}_t\Big) \text{ for } t = s,\ \ldots, T \end{aligned} \tag{9}$$

where X_t^s is output given the vector of expected prices $\boldsymbol{P}_t$, vector of inputs $\boldsymbol{Z}_t$, vector of uncontrolled factors $\boldsymbol{U}_t$, vector of state of technology (excluding breeding research technology), $\boldsymbol{h}_t$, state of crop breeding research technology, τ_t, and s, the lag before accessions have impact. Note that $\boldsymbol{h}_t$ appears outside the brackets as well as inside, as much research on CGRs is done using only the private collections of the breeding firm. For τ_t, $\partial\tau_t / \partial TE_{t-s-i} \leq 0$, and $\partial X_t / \partial\tau_t \geq 0$, $i = 0, \ldots, t-s$. Assuming that crop breeding research technology exhibits diminishing marginal returns with respect to TE, $\partial^2\tau_t / \partial TE_{t-s-i} \leq 0$. At the farm level, crop breeding research related technical change can be modelled using the common specification (Norton *et al.*, 1992) for the profit function for a perfectly competitive farm unit j as $\pi_t = g[P_t(\tau_t), \boldsymbol{Z}_{tj}, \boldsymbol{h}_{tj}, \boldsymbol{U}_{tj} \mid \omega_{tj}]$. For this specification τ_t can represent either output or input augmenting technical change. Crop breeding research can be either.

In the literature on measuring gains to agricultural research, a common practice is to assume that agricultural research induces shifts in the supply function, which then translate into changes in producer plus consumer surplus (de Gorter *et al.*, 1992; Alston *et al.*, 1995). While the policymaker may have objectives other than maximizing producer plus consumer surplus and while no measure is completely subjective, this criterion has the benefit of being reasonably general and objective. Fisher and Hanemann were the first to apply this criteria in the context of agro-biodiversity. In a two-period model for measuring the option value of saving an identified native landrace, they model the benefits of saving a native corn landrace by assuming this *a priori* identified landrace impacts the corn supply curve through the intercept. This chapter will use the criterion of producer plus consumer surplus (denoted as W) maximization as the policymaker's objective function, but in a more generalized form that formally models the change in accessions as a function of conservation investment, models the impacts of the change in agricultural supply as a function of the change in accessions, and allows for economic uncertainty as well as multiple time periods.

Suppose that due to the new biodiversity conservation investment I'', the supply curve shifter γ_0 decreases to γ_1, i.e. $\gamma_1 = f[\tau_t(TE_t \mid I_t - I'')]$ and $\gamma_0 = f[\tau_t(TE_t \mid I_t - I'])$, where I' is the base level, $I'' > I'$ (where γ_1 and γ_0 are the intercept results from the summation (whether vertical or horizontal) of the supply functions of each farm unit maximizing π_j above, and γ_1 and $\gamma_0 > 0$). Considering for the moment only the welfare of developed countries making this expenditure, their change in welfare in period t when γ_0 decreases to γ_1 is denoted as ΔW_t.

Since one would expect that the benefits of the investment I_t would be felt in successive periods, the net present value in rich countries of an agro-biodiversity investment I_t can be written as:

$$NW\left(I_0, \ldots, I_{T-s}; \beta, \delta, \alpha\right) = \sum_{t=0}^{T-s} \left\{ \sum_{j=0}^{T-s-t} \Delta W_{s+j+1}\left(\gamma_{s+j+t,1}\left(A_t, AN_t \mid I_t = I''\right); \gamma_{s+j+t,0}\left(A_t, AN_t \mid I_t = I'\right)\right)\left(1+r\right)^{-(s+j+t)} - I_t\left(1+r\right)^{-t} \right\}. \quad (10)$$

Another way to treat the problem is explicitly write γ_t as a function of TE_{t-s} from equation (8), the total size of the *ex situ* collection at time *t-s*, which in turn is a function of past levels of $I_{t-s}, I_{t-s-1}, \ldots, I_0$. Doing so also allows consideration that desired traits may be drawn not only from one accession, but also from a combination of accessions. Net present value is then:

$$
\begin{aligned}
&W\left(I_0, \ldots, I_{T-s}; \beta, \delta, \alpha\right) \\
&= \sum_{t=0}^{T-s} \frac{\Delta W_{s+t}\left(\gamma_{s+t,1}\left(TE_t \mid I_t = I''; I_0, \ldots, I_{t-1}\right); \gamma_{s+t,0}\left(TE_t \mid I_t = I'; I_0, \ldots, I_{t-1}\right)\right)}{\left(1+r\right)^{s+t}} \\
&- \sum_{t=0}^{T-s} \frac{I_t}{\left(1+r\right)^t}
\end{aligned}
\tag{11}
$$

The summation over ΔW_{s+t} in equation (11) is the value associated with keeping alive the option of being able to use existing uncollected CGRs that would be lost without the investment plus the value of new CGRs that are developed due to the investment.

Assume that the government body is given an amount:

$$
I = \sum_{t=1}^{T} \frac{I_t}{\left(1+r\right)^t} \tag{12}
$$

that it can spend on field programmes to reduce the erosion of biodiversity. In a world without uncertainty and irreversibility, the policymaker uses the net present value (NPV) rule and makes the investment now if the present value of the benefits minus the costs is greater than zero. However, as stated earlier, the standard NPV rule ignores the fact that expenditures are largely irreversible, i.e. they are a sunk cost that cannot be recovered. It also ignores the investor's option to delay and to wait for new information about markets and agro-biodiversity conditions before making the investment. This aspect of the problem is incorporated into the model by borrowing the approach used in much of the commodities literature to address investment under uncertainty and irreversibility. In the context of this paper, irreversibility refers to both irreversible loss of genetic resources as well as potentially irreversible conservation investments. The specific approaches are too lengthy to discuss in this chapter and are covered in detail in the paper that this chapter is drawn from.

Biodiversity Investment Under Uncertainty and Irreversibility: a Numerical Simulation

Given that even with a linear supply and demand system, ΔW_t is a non-linear function of the variables, evaluating ΔW_t at the means of A_t, AN_t and AM_t is not the same as $\varepsilon(\Delta W_t)$ given the distributions of these variables. Given these non-linearities, the most tractable method for evaluating the net present value of a particular set $\{I_{j.0}, I_{j.1}, \ldots, I_{j.t-s}\}$ for each $j = 1, \ldots, J$ *in situ* conservation areas is with a simulation approach in which repeated draws are made, as illustrated in the following section.

Obviously, maximizing equation (11) over I_{jt} in this simulation framework would be laborious and require a complex non-linear programming application. However, given the lack of availability of the data necessary for estimating actual values, developing such an application would be overkill in the short term. Instead, several simplifying assumptions will provide a more tractable maximization problem that will be sufficient towards the chapter's basic goal of generating a conceptual framework for economic discussion of agro-biodiversity conservation. First, let $j = 1$ *in situ* region. Second, it is unlikely to be politically feasible to vary I_t (in real terms) greatly from period to period. Whether or not the programme lasts for a fixed number of years, once a programme starts, the payments are likely to continue at some fixed rate until the programme is stopped. It is unrealistic to turn on and off conservation programmes from year to year. For instance, the US farmers enrol in the Conservation Research Program under 10 year contracts at rates that are fixed for the contract period. Next, assume that the budget of the biodiversity programme is a given I that must be used in its entirety. Then, whether or not the programme enrolment is to last an indefinite period or for a predetermined number of years, the choice variable is the starting period. This strict equality constraint eliminates the trade-off between biodiversity conservation and other activities, but still allows for intertemporal tradeoffs within the sphere of this conservation activity. Given these assumptions, the maximization problem is:

$$NW = \underset{d(k)}{\operatorname{argmax}} \left[0, \sum_{k=0}^{T-s} \left\{ NW(k) d(k) \right\} \right] \tag{13}$$

where k is an index referring to one of $T-s$ programme starting points and where $d(k) = 1$ when k is chosen and: 0 otherwise, where I_k, the fixed programme payment per year is chosen such that:

$$\sum_{t=k}^{T-s} I_k / \left(1+r\right)^t = 1, k = 0, \ \ldots, T-s.$$

On the other hand, if the public agent plans an m period contract to start at some point t during the evaluation period, then I_k is chosen such that:

$$\sum_{t=k}^{k+m-1} I_k / \left(1+r\right)^t = I, k = 0, \ \ldots, T-s-m. \tag{14}$$

For the simulations, two scenarios are examined: (i) conservation programme costs that are constant per period over the planning horizon T; and (ii) a 10-period long conservation programme, starting any time from $t = 0$ and

Table 2.1. Base parameters used for simulation runs

$T = 50$	Simulation time span coverage[a]
$r = 0.04$	Interest rate per period
$PV = 4500$	Discounted cost of conservation contracts (over time span T) at $t = 0$
$\varphi_0 = 100$	Bernoulli parameter for the number of estimated total CGRs uncollected at $t = 0$
$\varphi\Psi_{At} = \varphi_{ANt} = 20$	Bernoulli success parameter for yearly accessions given constant E_t, both for existing uncollected CGRs, and new CGRs
$v_2 = 0.08$	Rate of loss of *in situ* CGRs
$v_1 = v_{1.A} = v_{1.AN} = -0.001$	Transformation of conservation investment into change in number of accessions
$\omega_1 = 0.05$; $\omega_2 = 0.8$	Parameters for conversion of total accessions into agricultural supply intercept coefficient change[b]
$s = 3$	Research lag, i.e. periods before new accessions to *ex situ* collections have economic impact
$\alpha_0 = 23.7$	Agricultural demand intercept (source: Chambers and Just)[c]
$\beta = 8.6$	Agricultural demand price coefficient
$\gamma_0 = 420$	Agricultural supply intercept coefficient
$\delta = 213.2$	Agricultural supply price coefficient
$\eta = \zeta = 0.01$	Agricultural supply and demand intercept drift parameters
$\sigma_\alpha = \sigma_\gamma = 0.1$	Volatility of drift parameter
$\theta_t \sim \mathrm{Beta}(1,50)$	Impact of new varieties on γ_t

[a] To increase precision of predictions, each period divided into 12 subperiods for estimation of the Brownian motion equations but is converted back to the original units elsewhere.
[b] For the simulations, a Cobb–Douglas type functional form is assumed fr λ_t, the average number of varieties adopted by farmers in period t that used accessions from TE_{t-s} in the breeding process. Normalizing inputs other than TE_{t-s} in this process to 1, $\lambda_t = \omega_1(TE_{t-s})^{\omega_2}$.
[c] Supply and demand coefficients are from Chambers and Just and are also used in Fisher and Hanemann and are for a simplified version of US demand and supply curves for corn (price coefficient is in dollars/bushel and quantity is measured in billions of bushels per annum).

$t = T - 10$. In all cases, the discounted costs of programmes are the same. Table 2.1 lists the values and the simplifying assumptions used for the simulations. Programming of the simulations was done using the GAUSS computer programming language and each of the 40 possible payments paths was simulated 500 times over the range of the planning horizon.

Simulations were conducted to examine the path of total accessions over time, with and without a 10-period conservation programme starting at $t = 0$, using the functional forms from the first section plus the parameter values from Table 2.1. For the simulation, the variables are drawn stochastically, where, according to equation (7):

$AM_t \sim \mathrm{NB}(\text{Bernoulli success parameter} = \varphi_0, \text{probability of failure}$
$= \mathrm{argmax}\{P_{AM.t-1}, P_{AM.t}\})$
$AN_t \sim \mathrm{NB}(\text{Bernoulli success parameter} = \varphi_{AN.t}, \text{probability of failure}$
$= P_{AN.t-1}, P_{AN.t})$
$\Psi_t \sim \mathrm{NB}(\text{Bernoulli success parameter} = \varphi\Psi_{.t}, \text{probability of failure}$
$= \boldsymbol{P}\Psi_{.t-1}, \boldsymbol{P}\Psi_{.t})$

The results of the simulations show that the *in situ* accessions eventually fall to the same level whether or not the conservation programme is funded. However, the conservation programme succeeds in delaying genetic erosion. Thus, under the scenario in which the conservation programme is funded, more accessions move from *in situ* to *ex situ* collection before they disappear.

In computing benefit streams, the simulation results show that while the median discounted present value of the conservation investment is relatively constant over time, the upper bounds of the confidence interval around benefits become many times higher than the median or mean values. The upper bounds are more sensitive to the specification of the price volatility parameter than they are to the erosion in biodiversity coefficient.

Of the 40 possible 10-period long investment plans, the simulations show that the welfare-maximizing plan is the one starting at the present time, a result that is no doubt influenced by the linear-over-time specification of the erosion in agro-biodiversity coefficient used here. This specification implies that the biodiversity erosion rate is high enough at present that potentially valuable accessions are being lost. The results can change if the impact of accessions on the agricultural supply is a function of age cohorts (i.e. newer accessions have a greater impact than older stocks). The same result holds with investments evaluated at their mean values of the simulations. However, if one considers the relatively large width of the 90% confidence intervals as well as their relatively flat path with respect to the median paths, the gains to starting the programme in the first period are less clear cut.

Conclusion

This chapter is the first to present a formal discussion of framing models for measuring gains to publicly funded research as investments under uncertainty and as irreversible decisions. This framework, which borrows from the commodities literature, can have applications in other resource topics, such as publicly funded pest control. One observation drawn from the simulation results is that mean benefits estimates may be inappropriate as they will give little idea of the large spread. Perhaps an analogy can be drawn with investments on flood control projects, for which planning decisions are not generally based on mean potential damages but on costs of extreme floods (e.g. the 100-year high vs. the yearly high).

Given the modelling framework presented in this chapter, the key areas for empirical research necessary to implement this model include:

1. Estimates of AM_t, the number of existing cultivars uncollected at time t. These data are necessary to allow estimation of the rate of loss in potential accessions over time.
2. Estimation of the number of accessions obtained from both *in situ* stock existing at $t = 0$ as well as from new varieties not yet in existence at $t = 0$ obtained per dollar of collection expenditure (E_t). As collection activities have gone on for some time, some of these data should be available, although it may be difficult to separately identify A_t (the number of cultivars collected from the base value AM_0) from AN_t, which are the cultivars not existing at period 0, but which may be developed by indigenous breeding activities subsequent to $t = 0$.
3. Estimation of the impact on the change in accessions obtained at time t from both *in situ* stock existing at $t = 0$ as well as from new varieties introduced after $t = 0$ per dollar of *in situ* biodiversity conservation expenditure (I_t). Since major *in situ* agro-biodiversity programmes have not yet been implemented, this estimation may have to wait some time.
4. Estimation of $\tau_t[TE_{t-s}(E_{t-s}, I_{t-s}), TE_{t-s-1}(E_{t-s-1}, I_{t-s-1}), \ldots , TE_0(E_0, I_0), h_t]$ from equation (9), i.e. the impact on the agricultural supply function of publicly available accessions. Perhaps this section can be addressed through extensions of research that have been done on valuing the traits of accessions in *ex situ* collections (Evenson, 1996).[6] Estimates of the mean arrival rate of a disease or pest-related production shocks as a function of total accessions can be included here as well, but this is probably not feasible to estimate. Another avenue of research is on research investments that can change the parameters in τ.
5. Estimation of agricultural output price and quantity prices, as well as the price volatility term.

When sufficient data have been collected to make empirical estimation possible, the logical research extension is to apply the model discussed in this chapter in a multi-country, multi-crop partial equilibrium framework that can account for substitution effects and cross-price linkages. Given that farmers participating in agro-biodiversity conservation programmes may have lower output than if they were not, and to the extent that this participation increases local prices, consumers in the conservation regions may require compensation, which would be an additional component of the cost of *in situ* conservation programmes. In the developing country regions hosting the agro-biodiversity conservation programmes, the costs of these distributional impacts may be addressed through an application of the model in a computable general equilibrium framework.

Notes

1. This chapter is excerpted from a more detailed manuscript of the same title; contact the author for further particulars.

2. Although the term CGR is used for brevity, the same economic principles discussed in the chapter should hold for animal genetic resources for agriculture as well. Note that the term agro-biodiversity covers all plants and animals, whether wild or domestic, that are important to food and agriculture.

3. To some extent, this latter form of irreversibility (loss of genetic resources) may be analogous to asset depreciation in the case of an asset for which there may not be perfect substitutes, such as the pitching arm of a potential major league draft pick. If the arm of this player is not carefully nurtured and is damaged before the player makes the majors, whether or not he will be the next superstar is unknown.

4. The other possible discrete distributions include the Poisson and the negative binomial. The variance of a negative binomial distributed variable is greater than its mean, while the variance of a Poisson distributed variable equals its mean.

5. In calibrating the coefficients in $P(\theta_t)$ in an empirical application of this model, it may be useful to note that with the logistic specification, the value of I_t where $P(I_t \leq \mathrm{I}) = 0.5$ is $I_t = -a/v_\mathrm{I}$, where $a = v_0 + v_A A_{\mathrm{t}-1} + v_S S_t$, which is positive if $a > 0$. Furthermore, for $0 < P < 1$, $\ln((1-P)/P) = a + v_I I$.

6. Since the hedonic method estimates values over a path of tangencies of supply and demand, the cited study cannot be used directly to identify the supply shifter.

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3

The Value of Genetic Resources for Use in Agricultural Improvement

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One of the most frequently mentioned arguments for preserving biological diversity is that it may serve as a great reservoir of genetic information useful in crop improvement programmes (see, e.g. Wilson, 1992). Most of the world depends on only a relative handful of crops to meet its nutritional needs. Genetic diversity within these crops is narrowing. Vast stretches of agricultural land may be sown with virtually identical seeds, resulting in potentially extreme susceptibility to pests and disease.

In this paper we consider the economic valuation of genetic diversity for use in crop improvement programmes. While genetic improvement has featured prominently in studies of farm productivity since Griliches's seminal work (1958, 1964), if not before, only recently has the focus turned to the value of genetic resources *per se*, as opposed to the value of research on genetic resources. The former and the latter may be considerably different, research expertise could be a relatively scarce (and hence valuable) resource and genetic diversity could be relatively common (and hence of little economic value in this context). While some work has been done by non-economists on these matters, the formal tools of economics have not often been applied to these issues.[1]

In this paper we consider research in crop improvement as a problem in search theory. Agricultural researchers seek to find genetic combinations that offer higher yields and/or display greater resistance to environmental stresses. Casual empiricism, as well as common sense, suggests that the effort and expense dedicated to these searches depend on the cost of search, the expected rewards to be earned and the best alternative identified to date. In what follows we describe a simple search model, similar in many ways to models that have been developed in the labour economics literature (see, e.g. Lippman and McCall, 1981). An important difference, however, is in the emphasis of our

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approach. Unlike the typical case in the labour context, the number of search opportunities is not an exogenous variable. The economically relevant question in the valuation of genetic diversity for use in agricultural improvement concerns the gain to be expected from an additional search opportunity, what we will call the 'value of the marginal genotype'.

This approach parallels that developed in Simpson *et al.* (1996) in the context of 'biodiversity prospecting' for products for use in pharmaceutical applications (see also Pearce and Puroshothamon, 1992; Aylward, 1993; Artuso, 1994; and Mendelsohn and Balick, 1995). In our earlier paper, we modelled the new product research process as a sequence of independent Bernoulli trials: each species could either yield a 'hit' in the search for a new product, or prove useless. By restricting the distribution to two points under the Bernoulli assumption, we generated a very simple search model: search is suspended (with respect to any particular product demand) as soon as the first effective product is identified. In this model we were able to demonstrate that an upper bound on the value of the 'marginal species' is relatively modest. If there is a high probability of making a hit in any single Bernoulli trial, it is also very likely that the 'marginal species' will prove redundant, and hence of no incremental value. Conversely, if there is a low probability of making a hit in any single Bernoulli trial, it is unlikely that two or more species will prove redundant in the search for any particular new product. It is also unlikely, however, that *any* species will yield the desired new product. We found in our earlier paper that, for fixed values of the number of species over which search can be undertaken, the payoff in the event of a success, and the cost of determining whether a species yields a 'hit', there exists a probability of success in each Bernoulli trial that maximizes the value of the 'marginal species'. Even when evaluated at this probability of success, the upper bound on the value of the marginal species appears to be modest given evidence on the number of species that might be the subject of search, the cost of search and the payoff to success.

An analysis of the value of genetic resources in agricultural research will differ in several important respects from our earlier analysis of biodiversity prospecting in pharmaceutical research. One of the most important of these differences concerns the assumption of Bernoulli distributions. This assumption is, of course, not exact in the pharmaceutical context. Different natural products may have greater or lesser efficacy in particular applications, and different natural products may require greater or lesser expense in converting them to pharmaceutical uses. As a general approach, however, it may be appropriate to assume Bernoulli trials. The great majority of natural materials tested for pharmaceutical applications simply 'don't work', as opposed to working at higher or lower levels. Thus, treating the testing process as having a binomial outcome does not seem too great an abstraction from reality.

In agricultural research, on the other hand, most genotypes tested are neither complete failures nor unqualified successes. In fact, genetic principles might lead us to suppose that many attributes of interest would be (approximately) continuously distributed. Thus, the search is not for one genotype that 'works' to replace others that do not 'work', but rather, for a genotype that 'works best' in the circumstances under which it is to be cultivated.

A consequence of the assumption of continuously distributed outcomes in sample evaluation is that we must also consider more carefully the nature of payoffs realized. Improvements in, for example, the yield of a crop do not translate on a one-for-one basis into improvements in economic welfare. The demand for any food crop is limited, so the benefits of increased yield will be limited by consumers' willingness to pay. In this paper, in contrast with our earlier work on biodiversity prospecting for pharmaceutical products, we will focus on the social, rather than the private, value of genetic diversity.

The remainder of this paper is laid out in four sections. In the first section following, we consider what a very general model of optimal search might look like. We conclude that no tractable model can be entirely realistic. We then proceed to construct a simpler but tractable model, and argue that, despite its simplifying assumptions, it may provide some useful insights about values. We briefly discuss some specific functional form assumptions for demand and cost functions, and for probability distributions. We conclude with a discussion of the steps necessary to generate an empirically relevant and useful model.

We must emphasize, and it will soon become apparent to the reader, that the model we describe remains incomplete and the work we report here is very much in progress. We have not yet performed the types of simulations that might allow us to draw policy-relevant conclusions from this model. We can, however, identify some important considerations in framing policy-relevant questions, and, by drawing analogies to other work in related contexts, draw some conjectures as to the answers in this context.

A General Framework for Optimal Search in Crop Improvement

It may be helpful to think first about how the problem of valuing genetic material for use in crop improvement could be addressed at a very abstract level. We will not be able to proceed very far at this level of generality, but it will be useful to point out where we will need to make simplifying assumptions if we are to develop a tractable approach.

Let us first posit a vector of attributes ϕ drawn from a distribution $g(\phi)$. We will refer to ϕ as the 'state of the world', i.e. the set of conditions that will determine the demand for genetic improvements, the technological possibilities, etc. It is important to note that the 'state of the world' may also, for our purposes, include the parameters of other probability distributions.

Let S be the set of all genotypes available for testing. Let Σ be a feasible testing strategy. That is, Σ is a plan that calls for testing some subset $s \subseteq S$ initially, then proceeding to either test or not test, and if the former, test in a certain sequence, the remaining elements of S. Let $V(\Sigma, \phi)$ be the expected value of a testing programme following the strategy Σ given that the vector of attributes ϕ is observed.

Define $\Sigma^*(S, \phi)$ as:

$$\sum{}^*\left(S, \phi\right) \in \underset{\Sigma}{\operatorname{argmax}}\, V\left(\Sigma, \phi\right). \tag{1}$$

Define also:

$$V^*\left(S, \phi\right) = V\left[\Sigma^*\left(S, \phi\right), \phi\right]. \tag{2}$$

Now suppose that we have a set of genotypes $S^+ \supset S$; that is, S^+ is a larger set containing S. Now we might also define:

$$\sum{}^*\left(S^+, \phi\right) \in \underset{\Sigma}{\operatorname{argmax}}\, V\left(\Sigma, \phi\right). \tag{3}$$

and

$$V^*\left(S^+, \phi\right) = V\left[\Sigma^*\left(S, \phi\right), \phi\right]. \tag{4}$$

What is the expected value of having a larger number set of genotypes, S^+, as opposed to the subset, S, conditional on a state-of-the-world obtaining? Denote it as:

$$V^*\left(S^+, S, \phi\right) = V^*\left(S^+, \phi\right) - V^*\left(S, \phi\right). \tag{5}$$

It may be difficult to define a measure by which strategies differ from one another, but it is clear that if optimal strategies are not altered greatly by reducing the size of the set over which research can be done, there is no great loss in expected value from reducing the size of the set.

Finally, we would like to note that the unconditional expectation of the value of having the larger set, as opposed to only having S is:

$$\int_{\Phi} v^*\left(S^+, S, \phi\right) g\left(\phi\right) d\,\phi, \tag{6}$$

where Φ is the support of ϕ. Heuristically, if the measure of the set of states-of-the-world in which the optimal strategies differ by much is small, we might expect the value of having a larger set of genotypes to test also to be small.

Optimal Search Under an i.i.d. Assumption

It would prove completely intractable to work with a model at the level of generality that we have outlined above. The major problem with the more complex model concerns the distributional assumptions made on the potential of each sample tested. If we assume distributions that are not statistically independent, the search strategy will depend on the history of search, and the calculation of values becomes intractable. In order to arrive at any meaningful results, then, we will have to assume that the values of genotypes sampled are independently distributed. We will make the further simplifying assumption that these values are independently and identically distributed (i.i.d.).

Of course, 'simplifying the mathematics does not simplify nature'; assumptions adopted for analytical convenience need to be justified by reference to real-world facts. It seems reasonable to suppose, however, that the set of alternative genetic resources from which researchers sample in undertaking crop improvement programmes might be at least approximately i.i.d. There is little sense in bearing the expense of sampling two things that are likely to yield the same outcome.[2]

We will, then, consider a crop-improvement programme in which researchers seek to improve crop yields by finding a genotype with the highest value of some parameter θ. This random variable could represent yield per hectare, resistance to drought, pests or infection, nutritional content, pleasantness of taste, and/or any of a number of other attributes. We will treat θ as a scalar for simplicity, but it could as easily be a vector. Suppose that each of a collection of n distinct genotypes varies in its value of θ. Suppose that the θ of each genotype is independently drawn from the i.i.d. probability density $f(\theta)$, which has a cumulative density $F(\theta)$. Finally suppose that it costs c to determine the actual θ of any genotype.

We will suppose that a genotype of type θ can be quickly replicated in limitless quantities. Suppose that, at the beginning of a crop improvement programme, the *status quo ante* value of θ is θ_0. Without loss of generality, suppose that $\theta_0 \geq 0$. To determine the social benefits of an improvement in θ, let us make the simplifying assumption that higher-θ varieties provide a greater yield per hectare planted, but that the crop is qualitatively identical regardless of the yield per hectare of the variety from which it is grown. Let $q(\theta)$ be the output of the crop as a whole when a variety of type θ is cultivated, let $p[q(\theta)]$ be the inverse demand for the output, and let $C[\theta, q(\theta)]$ be the cost of growing quantity $q(\theta)$ of the θ variety.

Social welfare can, then, be represented as the difference between consumer surplus from the consumption of the crop and the costs of growing the crop:[3]

$$W(\theta) = \int_0^{q(\theta)} p(x)\,dx - C[\theta, q(\theta)]. \tag{7}$$

Note that:

$$\frac{dW(\theta)}{d\theta} = \left[p - \frac{\partial C}{\partial q}\right]\frac{\partial q}{\partial \theta} - \frac{\partial C}{\partial \theta}.$$

Let us suppose that the crop is grown in a competitive farm sector, so that price is equated to marginal cost, so we have:

$$\frac{dW(\theta)}{d\theta} = -\frac{\partial C[\theta, q(\theta)]}{\partial\theta}. \tag{8}$$

Thus, welfare is increasing in θ if an increase in θ induces a reduction in total cost. This would be the case, for example, if θ induces an increase in yield per unit planted, keeping other things equal.

In what follows we will treat the problem we are describing as a simple search problem. The objective is to search until a sufficiently valuable species is identified as to render the expected gain from further search less than the cost.[4] It is well known (see, e.g. Lippman and McCall, 1981) that the solution to such problems is of the form of an 'optimal stopping rule'. This stopping rule is of the form 'if, with *m* species remaining to sample, the greatest value encountered to date is at least as large as θ^*_m, stop sampling and commercialize the species with the greatest value thus far encountered, otherwise, continue'. Moreover, if the distribution of values among species is independent and identical, the optimal stopping rule is myopic and constant. By myopic we mean that the decision to stop can be made based solely on a comparison of whether to cultivate the species with the greatest value thus far encountered, or to sample only one more time (see, e.g. Rosenfield and Shapiro, 1981). Given the myopic property, it is immediate that the optimal stopping rule is independent of the number of species remaining to be sampled.

Suppose that in each period the best variety thus far identified is planted and harvested. If this variety is sufficiently good as to motivate the suspension of search, welfare will be maintained at the same level in perpetuity. Let the discount rate be $1-\delta$.[5]

Thus, we can implicitly state the optimal stopping rule as that value of θ that satisfies:

$$\frac{1}{1-\delta} W(\theta^*) = W(\theta^*) + \frac{\delta}{1-\delta}\left[\int_{\theta^*}^{\infty} W(\theta) f(\theta) d\theta + F(\theta^*) W(\theta^*)\right] - c, \tag{9}$$

or

$$\frac{\delta}{1-\delta}\int_{\theta^*}^{\infty}\left[W(\theta) - W(\theta^*)\right] f(\theta) d\theta = c. \tag{10}$$

We are deriving an expression for the value of having an additional genotype that might be the subject of continuing search. We can derive the value of this 'marginal genotype' by noting that having an additional genotype available for testing proves valuable only if: (i) a variety so successful as to motivate the suspension of testing has not been found before reaching the end of the collection; and (ii) when the final genotype is tested, it is found to be better than those tested previously.

Somewhat more formally, the value of having an $n+1^{\text{st}}$ genotype to test is equal to the expectation of the improvement over the best genotype identified among the first *n* samples tested, conditioned on the value of that best genotype, less the cost of testing, and then summed over all the probabilities of all possible values the best genotype could take on. Putting this all in a mathematical expression:

$$v(n) = \delta^n \int_{\theta_0}^{\theta^*} \left[\frac{\delta}{1-\delta} \int_{\tilde{\theta}}^{\infty} \left[W(\theta) - W(\tilde{\theta}) \right] f(\theta) d\theta - c \right] n f(\tilde{\theta}) F(\tilde{\theta})^{n-1} d\tilde{\theta}. \tag{11}$$

Integrate by parts to find:

$$v(n) = \left[\frac{\delta^{n+1}}{1-\delta} \int_{\tilde{\theta}}^{\infty} \left[W(\theta) - W(\tilde{\theta}) \right] f(\theta) d\theta - c \right] F(\tilde{\theta})^n \Bigg|_{\theta_0}^{\theta^*}$$
$$+ \frac{\delta^{n+1}}{1-\delta} \int_{\theta_0}^{\theta^*} \int_{\tilde{\theta}}^{\infty} \frac{\partial W(\tilde{\theta})}{\partial \tilde{\theta}} f(\theta) d\theta F(\tilde{\theta})^n d\tilde{\theta}.$$

By the definition of θ^*, the first term inside the larger parentheses is zero. As the welfare derivative is independent of the variable over which the inner integration is taken in the second term, we have, using equation (7)[6]:

$$v(n) = -\frac{\delta^{n+1}}{1-\delta} \int_{\theta_0}^{\theta^*} \frac{\partial C\left[\tilde{\theta}, q(\tilde{\theta})\right]}{\partial \tilde{\theta}} \left[1 - F(\tilde{\theta}) \right] F(\tilde{\theta})^n d\tilde{\theta}. \tag{12}$$

Let us continue by considering a specific example. A reasonable, if admittedly very simplified,[7] specification of an agricultural production function might be:

$$q(\theta) = \theta T(\theta); \tag{13}$$

that is, output, q, is the product of yield per hectare, θ, times the total hectares planted in the crop, $T(\theta)$. Let the rental price on a unit of farmland be r, so, if yield per hectare is θ, the total cost of producing q units of output is:

$$C\left[\theta, q(\theta)\right] = rT(\theta) = \frac{rq(\theta)}{\theta}. \tag{14}$$

The marginal cost of producing another unit of output when θ is fixed is:

$$\frac{\partial C\left[\theta, q(\theta)\right]}{\partial q} = \frac{r}{\theta}, \tag{15}$$

and the reduction in the cost of producing a fixed amount of output induced by an increase in θ is:

$$\frac{\partial C\left[\theta, q(\theta)\right]}{\partial \theta} = -\frac{rq}{\theta^2}. \tag{16}$$

Equilibrium in the competitive farm sector requires that price be equal to marginal cost. Let us suppose that the inverse demand curve is of the constant-elasticity form:

$$p(q) = aq^{-1/\eta}. \tag{17}$$

Equate price to marginal cost:

$$aq^{-1/\eta} = r/\theta, \tag{18}$$

so

$$q = \left(\frac{a}{r}\right)^{\eta} \theta^{\eta}. \tag{19}$$

Thus, the partial derivative of the cost function with respect to yield is:

$$\frac{\partial C[\theta, q(\theta)]}{\partial \theta} = -r\left(\frac{a}{r}\right)^{\eta} \theta^{\eta-2}. \tag{20}$$

Using expression (20) in (12), we have:

$$v(n) = \frac{\delta^{n+1}}{1-\delta}\left(\frac{a}{r}\right)^{\eta} \int_{\theta_0}^{\theta^*} \theta^{\eta-2}\left[1 - F(\tilde{\theta})\right] F(\tilde{\theta})^n \, d\tilde{\theta}. \tag{21}$$

Conventional wisdom has it that demand for agricultural production is relatively inelastic.[8] If this were the case, η would be less than one. While we again hesitate to draw conclusions inasmuch as equation (21) is an implicit expression, the value of the marginal genotype will be smaller to the extent that relatively large realizations of θ have relatively low values to society.

Expression (21) might be calculated under different assumptions on the probability distribution for the θs. Analytical solution for the optimal stopping rule, θ^*, is, in general, difficult; thus, analytical solution for the value of the marginal genotype will be difficult as well. We might, however, illustrate a simple case by supposing that θ is distributed uniformly on the interval [0,1] (i.e. we are normalizing by the maximum value of θ) and that $\theta_0 = 0$. Finally, suppose that c is negligible, so the search will continue so long as no value of $\theta = 1$ is identified. It can be shown under these assumptions that:

$$v(n) = \frac{\frac{\delta^{n+1}}{1-\delta}\left(\frac{a}{r}\right)^{\eta}}{(n+\eta)(n+\eta-1)}. \tag{22}$$

In other words, under the assumption of a uniform distribution, the value of the marginal genotype varies approximately inversely with the square of the number of genotypes over which testing can be done.

Some Conjectures on the Distribution Function

It seems reasonable to suppose that the yield of different genotypes would follow a limiting distribution. It is, in fact, common in the literature on selective breeding to suppose that the distribution of valuable traits among a genetically diverse population is normally distributed. It would appear (to lay-people, at least) that there is an intuitive argument for this limiting behaviour: traits are determined by genetic makeup, and many traits (such as yield under a host of different environmental factors) depend on a combination of many genes. At least in situations in which the expression of traits is determined by the matching of dominant or recessive genes, one might suppose that the expression of a complex trait such as yield would be determined by the (more or less) additive combination of several more (more or less) independent random variables – that is, that the conditions for the application of the central limit theorem would obtain.

These considerations suggest that the value of the marginal genotype could be negligible. On the one hand, with relatively high probability, the marginal genotype might prove to be no better than another sample previously tested. On the other hand, even though the tails of the normal distribution may reach far, they are relatively thin, suggesting that the expected gain to further search might be small.

There are, however, situations in which the normal approximation might be inappropriate. Some traits, such as resistance to particular pests or diseases, might be linked to a single gene. If this were the case, the appropriate distributional assumption would be a Bernoulli trial. It can be shown, in fact, that the value of the marginal genotype is maximized (given a finite and fixed support) under a Bernoulli (i.e. two-point) distribution. Of course, even if the only chance for improvement lies in the identification of a single gene, the value of the marginal genotype would depend on the frequency of that gene among the set of things available to be sampled and the improvement it offers over other genotypes.

We have not discussed aggregation. An important consideration concerns not only how important a marginal genotype is in the improvement of any given crop with respect to any given attribute, but also with respect to the entire set of crops and the time-series of environmental stresses they may face. With respect to the former, it is clear that any particular genotype will be more valuable to the extent that it may be used in the improvement of a wider variety of crops. At the same time, however, any particular genotype will be *less* valuable to the extent that genotypes from other subspecies, or, increasingly, with developments in biotechnology, other species (and, in at least one example, even another *kingdom*) can substitute for it in crop-improvement research.

Our discussion above suggests a way of incorporating aggregation in a fuller treatment: we could derive the aggregate, discounted present expected value of the marginal species by considering a time series of draws from the parameters of the distribution function that enters our expressions above.

Requirements for Empirically Meaningful Work

We are, at present, contemplating whether to extend the modelling exercises described above to derive estimates of the value of the marginal genotype in crop improvement. It would seem that there is little hope of conducting formal econometric estimation of the values generated by search models.[9] We could, however, conduct simulations using data from crop breeding programmes, agricultural output, *a priori* arguments concerning probability distributions, etc., to derive estimates of the value of the marginal genotype.

Such exercises are only as reliable as the data they employ, and we are somewhat sceptical as to the quality and availability of such data. We would need data on the demand for agricultural output, the cost of its supply, the number of genotypes available to testing programmes, and, perhaps more elusively, the cost of crop improvement research. With respect to the latter, the better source for information may not be in directly recorded costs *per se*, but rather in inferences from research practices. Brian Wright (1995; see also Note 4) makes a particularly telling observation: crop improvement researchers make very little use of the vast majority of the material available to them. We might infer from this that the costs typically exceed the benefits of expanding the research effort. There are, however, other possibilities. Perhaps only a relative handful of sources survive an initial pre-screening; perhaps *social* incentives to conduct more broadly based searches are greater than are the incentives to which researchers respond.

In recent papers on biodiversity prospecting in the pharmaceutical industry (Simpson and Sedjo, 1996a, b), we have developed models that are more detailed in some aspects at the expense of being narrower in others than has been the model we developed here. In the first of these other papers, we considered a situation in which researchers can decide how many samples to evaluate simultaneously in their search for a new product. Explicitly incorporating this intensity-of-search variable places further restrictions on the values generated by biodiversity prospecting, and has led to some more concise, and we would argue, plausible estimates. In our second paper, we considered capital investments in biodiversity prospecting facilities, which affect the intensity of search. Again, the results suggest more concise (and pessimistic) estimates of the values generated by biodiversity prospecting.

Let us conclude this report on work in progress with a final conjecture. While we have not studied the agricultural context as closely as we have the pharmaceutical, our impression is that the underlying features may be more similar than they first appear. If the question is ‘what is the value to society of maintaining the current range of *ex situ* biodiversity for use in agricultural improvement’, the answer we think is likely to emerge is the same as that we derived in considering the private willingness to pay for biological diversity in pharmaceutical research: it is negligible. This is not to say that biodiversity is not valuable; it may be of great value for any number of other ecological, ethical and aesthetic reasons. All we are saying is that our inference from the numbers of genotypes extant and the simple (albeit arguably too simple) analytical exercises we have performed is that genetic resources may simply not be scarce, and for that reason not of much economic value.

Notes

1. A notable exception is the work of Evenson and Gollin, Chapter 13, and more recent work by Evenson, Chapters 11 and 12. Wright (1995) has also surveyed work on the economics of genetic resources.
2. Of course, things are selected for testing in the first place because they are closely related to food crops, but conditional on the traits that motivated selection, the samples might be i.i.d.
3. It might be objected that this is a situation in which the approximation implicit in measuring social welfare by consumer surplus is inappropriate. Catastrophic crop failure might induce important income effects. Some who foresee the possibility of imminent doom may regard our reliance on such an incomplete, partial equilibrium welfare measure as avoidance of the 'real' issue: that genetic diversity provides insurance against crop failures of apocalyptic proportions. We are, frankly, sceptical of such claims, but might also add that any far-reaching crop failure might well result from causes for which no genetic remedy might be available.
4. In fact, the search for better crop varieties is ongoing – a variety so completely satisfactory as to motivate the suspension of all further research will never be found. Wright (1995) has noted an extremely interesting fact, however: most crop improvement research is conducted using only a very small number of the possibilities available, the *intensity* of research effort varies in relation to the perceived need. Reducing this intensity-of-effort variable to a dichotomous choice is intended as a simple way of reflecting this feature.
5. In fact, improved varieties are likely to lose their qualities as climatic conditions change, different pests arrive, etc. We can incorporate these considerations, however, by combining in the discount factor, δ, both the rate of time preference and the probability that adverse conditions will motivate resumption of search.
6. Note the similarity of equation (12) to the difference in the expected values of the first-order statistics from samples of size $n+1$ and n, to which (12) could be reduced if c were zero and welfare linear in θ.
7. The principle simplifications here are that we suppose that land of the same quality is available in sufficient quantities and that there is no extra effort or expense required to collect greater harvests. The latter assumption might be justified by supposing harvest expenses to be negligible in comparison with sowing, cultivation, irrigation, etc.
8. It may be noted that the solutions derived here depend on demand being inelastic; unitary elasticity will imply infinite welfare, and an elasticity greater than 1 will imply negative utility. In the context of agricultural commodities, however, a restriction to inelastic demands may not be troubling. Those agricultural commodities for which demand is elastic might be supposed to have so many substitutes as to make the question of their continuing supply of little importance to society.
9. Evenson (1995a, b) and Gollin and Evenson (Chapter 13) have estimated what we might regard as reduced form models of the value of additional accessions to germplasm collections. While we are somewhat sceptical of the results of these exercises, our work does leave us with a profound appreciation of the difficulties involved.

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4

The Source of Genetic Resource Values and the Reasons for Their Management

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There is a fundamental problem that lies at the base of the need for genetic resources. This is the contest of innovation that exists within any predator–prey system: a Red Queen race.[1] Agriculturalists must continue to supply new forms of resistance within modern agricultural systems, otherwise they will be overwhelmed by the continuing selection of those pests which are adapted to those varieties which are in use. Genetic resources have value as potential solution concepts to this fundamental problem.

The importance of public management in this context is restricted to the set of those problems which the private sector cannot or will not address. Genetic resources exist as a stock of potential solution concepts, and they can also provide a flow of potential solutions in the future. The important question for public policy purposes is: What sorts of public intervention are required in order to ensure the set of solutions that agriculture will require in the future?

This chapter develops these ideas concerning the fundamental nature of the values of genetic resources, and the fundamental nature of the public management required to conserve them.

The Ecological Dynamics Within Agriculture: the Source of Genetic Values

Ever since agriculture was first developed, there has been a race implicit within it, as pests and pathogens erode the resistance of the crop varieties currently in use and new varieties are devised to replace them. This race can never be won with finality by agriculturalists, and the correct formulation of the question

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concerning agricultural sustainability must be: 'Is it possible to remain a player in this race indefinitely?' Genetic resources as inputs into agriculture play a prominent role in the continuation of this contest, and the optimal conservation of these resources – in order to ensure an optimal supply of resistance into the indefinite future – is at present a necessary condition for the continuance of agriculture. This chapter examines the meaning of the optimal management of these resources, as important inputs into both the improvement of agricultural productivity and the maintenance of agricultural sustainability.

In ecological terms, the stable dynamics witnessed in agriculture are known as a 'Red Queen race'. It is necessary to continue to make moves in order to stand still. In co-evolutionary settings of predator–prey models, it is possible to show that the populations of hosts and pathogens will reach an ecological steady-state where virulence, or its mirror image susceptibility, do not change. In other words, the system converges to a long-run equilibrium of host off-take, and stable population levels. This does not imply that the underlying dynamics have stopped: in fact, both pathogen and host populations continuously update their strategies in order to cope with the constant increase in the opponent's ability to improve its growth parameters (Schaffer and Rosenzweig, 1978).

How has the development of agriculture impacted upon these evolutionary contests within the biosphere? The choices formerly made by evolution have been supplanted by human choice in certain spheres of activity, but the general nature of those forces remains. Humans have selected the crops and crop varieties that are most easily appropriated by themselves (and hence denied to competing pathogens), but this simple act of selection introduces genetic drift within the competing pathogen population that renders them increasingly competitive. This harvest's appropriation generates next harvest's competition, and the race is on. Ever since human societies interjected themselves into the role as selector, the innovation contest between human societies and the pathogens of their crops has been ongoing.

This contest is apparent in the studies of declining resistance in agriculture. Agriculture has witnessed the steady erosion of the productivity of the best performing and most widely used crop varieties due to evolutionary pressures from pathogens. This depreciation in the effectiveness of prevalent varieties has been addressed by agriculturalists by means of the periodic interjection of new varieties into agriculture, and the consequent decline of those varieties. A cycle of introduction and subsequent decline is documented for a range of crops and crop varieties (Evans, 1993; Smale, 1996; Rejesus *et al.*, 1996). A recent empirical analysis has even estimated the impact of 'age' of a variety (i.e. years in agricultural use) on its productivity, and found that it is significantly negative (Hartell *et al.*, 1997).

Therefore human choice has altered the setting for the evolutionary contest quite a lot, but the basic nature of the problem remains unchanged: humans (in their management of crops and crop varieties) continue in a contest of appropriation and innovation with the natural predators and pathogens of those crops. In order to maintain stability within agriculture, it is necessary to continue to develop strategies of resistance to meet the new strategies continually evolving within pest populations. It is as inputs into this ongoing contest of innovation that genetic resources have value. The remainder of this chapter shows how this is the case, and what is necessary to manage these values optimally.

The Informational Nature of the Problem: Information and Agriculture

How is it that the agricultural industry attempts to address the ecological problem identified above? Of course industry has an incentive to address this problem, because these instabilities contribute to lost production in agriculture. In order to assess the management of genetic resources, it is necessary to create a framework for understanding how the private sector uses genetic resources and for what purposes; then it will be possible (see following section, ‘The public good nature of the problem’) to identify which of the functions of genetic resources are not being managed privately.

In order to maintain stability within modern agriculture, it is necessary for society to continue to search for, identify and utilize strategies that are successful in the continuously evolving biological environment. This is embodied within the research on the traits conferring improved resistance, and the development of these traits into new varieties usable in modern agriculture. Research and development (R&D) is the term used generally to describe the industrial process by which new ideas are developed into applications to problems. When a new solution concept is successfully developed within the R&D process, it will then be marketed, usually embodied within some novel product. Economists have long analysed the research and development process as one of information creation, application and diffusion (Arrow, 1962; Nordhaus, 1969). The theoretical concept of the R&D process is usually presented as a production process, itself dependent upon the application of various factors of production (machinery, labour, etc.) for the production of useful ideas. The base of information so produced is applied by researchers to the solution of the economic problems presented by society.

‘Innovations’ are then the products which embody those solution concepts when applied to address these problems (Rosenberg, 1974; Kamien and Schwartz, 1985).

Certain industries by their nature expend substantial proportions of their total available resources on the R&D process. For example, the computer software, plant breeding and pharmaceutical industries are all R&D-intensive industries, with over 10% of their gross revenues invested in the development of solution concepts. R&D will always constitute an important part of the agricultural industry because of the contest of innovation described previously. Much of the R&D concerned with the problems generated by the biological world are dealt with by the plant breeding sector of that industry. In the plant breeding industry, one recent survey found that the proportion of annual turnover spent on breeding and research programmes ranges from 0.5–66%. The breeders allocate, on average, 18% of annual turnover to breeding and research activities. Most breeders (73%), however, spend between 0.5 and 15% of annual turnover on research and breeding (WCMC, 1996).

This same survey found that R&D in this sector is becoming increasingly focused on the problem of the maintenance of resistance to pests. A breakdown of properties of new germplasm incorporated into new varieties shows that 45% of the germplasm develops disease/pest resistance, 35% increases yield, 10% improves stress resistance, and 9% improves quality (WCMC, 1996). The majority of plant breeders mentioned 'resistance' as the primary focus of their research activities.

This study (and others) identifies a continuing cycle of declining crop resistance – crop varieties often have a commercial life of about 5–10 years (Swanson and Luxmoore, 1997). Plant breeders act as the sector that continues to address this problem, primarily through the breeding and introduction of varieties with restored characteristics of resistance.

Therefore, it is possible to identify the sector (plant breeders) that addresses the ecological problem outlined above, and how these breeders formulate the problem (developing new varieties to reintroduce resistance into the crop). The remainder of this section identifies the role of genetic resources in this process.

Stocks and Flows of Information in Agricultural R&D

Genetic resources are an important input into this R&D process, but only to the extent that they are an output from the same evolutionary process that is generating the problems to be solved. Genetic resources operate initially as 'flows' of information as well. Whenever the evolutionary process generates a new problem, it simultaneously generates information relevant to the identification and isolation of that problem, in the form of those organisms which have relatively better survival prospects within the new environment. The implied, naturally supplied 'resistance strategies' constitute information themselves, and they are often useful in the identification of the traits and characteristics most effective in the new environment. Genetic resources that have been used and useful in the past contain information on strategies that have worked successfully as solution concepts in the past, even if the precise nature of the problem that they solved has long been forgotten. They contain information in the sense that there is an enhanced probability (over randomness) that this particular combination of traits contains resistance to some sort of agricultural problem.[2]

Biodiversity operates as an input into the agricultural industry, as both a provider of stocks and as a flow of information into agricultural R&D. The screening of landraces previously in use in traditional farming practices is an example of the use of existing *stocks* of naturally generated information. Often, all that is required for the industrial application of the stock of information accumulated within a landrace is for this information to be transported into the modern sector.

In this instance the idea and its application are naturally generated, and the local community has accumulated the information as a stock within the plant varieties already in use. Sometimes these selections may have occurred hundreds or even thousands of years ago, but they may still retain some residual of their then-existing beneficial effect. Thus a landrace may be conceptualized as an organism in which a series of beneficial selections have occurred in response to environmental changes (pests, climate stress). The landrace then accumulates a stock of previously successful strategies. The screening of such landraces functions as an important part of the agricultural R&D process; that is, this stock of information provides immediately identifiable innovations for use in agriculture. The extent of the accumulated value of these selections within landraces is indicated by their relative value within the plant breeding industry.

The information generated by nature always arrives initially as a flow, however. This happens, for example, whenever a particular type of pest invasion eliminates a large proportion of an existing crop. The survival of some individuals of any such crop variety is indicative of the presence of a strategy of resistance that is successful within the current environment. Analysis of these individuals might allow for the isolation of the trait or characteristic which confers this resistance and which might then be incorporated within modern agriculture. In this instance the retention of a diversity of plant genetic resources is generating a flow of information for use within the R&D process which, after careful analysis, may result in successful innovations in terms of plant varieties. When a particular plant variety has been subject to years of use and farmer-based selection (as in the case of a landrace) then this flow of information may accumulate in the form of a stock of ‘resistance strategies’, but the informational value of genetic resources must always originate as a flow.

Consider how the plant breeding industry makes use of naturally generated information in the undertaking of its R&D efforts. Effective characteristics for new plant varieties develop naturally through the process of ‘natural selection’: only those which are able to survive existing threats (pests and pathogens) remain. Since the set of threats is constantly changing, the natural environment continuously produces a flow of new information on the characteristics that are relatively fit under current environmental conditions. This naturally generated flow of information continues to flow from nature so long as some portion of land use is dedicated to the use of a wide range of plant varieties with relatively unknown genetic characteristics.

With appropriate management, it is possible for these flows of information to accumulate over time. ‘Traditional farmers’ have themselves survived by means of a process of observing this naturally produced information and the consequent selection and use of the traits and characteristics that have aided survivability. In this way traditional plant varieties (landraces) are transformed into the accumulated history of the information which nature has generated and that farmers have observed and used. The landraces that traditional farmers use constitute a stock of information on naturally generated resistance strategies that have been successful in varying environments over the years.

In general the modern plant breeding industry has operated primarily through the collection and utilization of the set of landraces, and hence the stock of naturally produced information that is encapsulated within them. That is, modern agriculture has then been based on the development of a particular crop variety that is an amalgam of some subset of the traditional varieties and its widespread use. The remaining stock of information derived from the landraces is then retained to deal with subsequently arising problems (occasioned by further mutations of pests and pathogens).

This discussion indicates that the nature of the R&D industry in agriculture is one that has relied heavily upon the accumulated stocks of naturally generated information within the landraces, but that it is the supply of information generally which is essential, not the conservation of any given stock. There is no value to maintaining a particular set of resources at least cost if these are not the resources that will be needed to solve a problem that arises at a future point in time. The optimal conservation mechanism must conserve the mechanisms which supply solution concepts for time-dependent problems, not a particular set of germplasm.

The Extent of Agricultural Reliance upon Biodiversity: a Case Study

To what extent does the agricultural industry rely upon biological diversity as an informational input? Table 4.1 lists the results from a study conducted on this question. A quick glance at this table might create the impression that wild resources play a relatively unimportant role in the agricultural R&D process; this is not the case. Landraces and wild species together contribute only 6.5% of all genetic resources. The figure of 6.5% is not a measure of relative importance of diverse compared with other sources of germplasm; it is instead an indicator of the rate of input from diverse resources required over time in order to sustain the existing system of R&D.

The vast majority of R&D (here, 82.9%) will always be undertaken on those varieties which are already standardized and well understood, and within the system. This is not a substitute for the input of new germplasm; it is merely the continuation of a programme of research on germplasm that was input into the system at an earlier point in time. This is R&D at the end of the pipeline: it represents an attempt to produce the maximum number of useful innovations from a given stock of information.

Genetic diversity serves a distinct function within the R&D process. It acts as a source of new stocks of information, which can then serve as the base from which to develop new innovations. Once brought within the process, it is assimilated bit by bit into the commercial sector and investigated as such. However,

Table 4.1. Source of germplasm used for all development of new varieties.

	Crop group				
	All	Potatoes	Cereals	Oil	Vegetables
Commercial cultivar	81.5	50.0	87.0	78.8	95.7
Related minor crop[a]	1.4	8.0	0.6	1.2	0.3
Wild species					
ex situ gene bank	2.5	19.0	12.0	1.0	1.4
maintained *in situ*	1.0	0.0	0.7	0.1	0.1
Landrace					
ex situ gene bank	1.6	1.7	1.7	2.3	1.7
maintained *in situ*	1.4	0.0	0.7	2.8	0.4
Induced mutation	2.2	3.3	0.7	7.2	0.3
Biotechnology	4.5	17.7	3.5	6.8	0.1

Source: WCMC (1996).

Note that all columns are percentages, but that not all columns sum to 100% as some innovations defied categorization under a single source.

[a] 'Related minor crop': minor crop cultivated on a small scale with some improvement over wild ancestors.

all stocks of information must originally derive from outside of the process, and it is essential to input new supplies at the optimal rate necessary in order to sustain the R&D process. This is what the rate of input from non-commercial species represents: the need for inputs from outside the system.

The stock of existing commercial varieties may be seen as the information base from which bio-industries develop innovations whereas the sources of new diversity (wild species, induced mutation) may be seen as the sources of increments to that information base. Then the figure of 6.5%, relative to 82.9%, indicates that at present the R&D system is requiring annual injections of 'new' genetic material from natural sources amounting to approximately 7% of the stock of material currently within the system. This material both replenishes 'depreciated' germplasm and adds to the stock of available genes.

In sum, the stock of germplasm relied upon by society for the maintenance of its agricultural system may be seen as a continuously eroding asset. R&D is constantly required in order to maintain the current production system against the forces of biological invasion; this is what the industry terms research into 'resistance' and 'stress'. The industry reports that the life cycle of any given product is only about 5 years in duration, with pests and disease being primary factors for the obsolescence of the product (WCMC, 1996). The primary result of this study is that it has estimated the industry's current annual rate of utilization of diverse germplasm at 7% of the germplasm base.[3]

The Public Good Nature of the Problem: Externalities and Agriculture

To what extent does the agricultural industry itself manage optimally all of the values of genetic resources for agriculture? The previous discussion indicates that the plant breeding industry is both addressing this fundamental problem and supplying and using genetic resources in order to do so. Stability has been maintained for thousands of years of agriculture, without the need for intervention from the public sector; why would it be necessary to do so now? This section sets out a broad framework for the conceptualization of all of the values of genetic resources, and then compares the private sector's management objectives with those of society generally.

There are two broad forms of values which best describe the role of genetic resources in agriculture: *insurance* and *information* (Swanson, 1992). *Insurance* refers to the value of genetic diversity in providing a broad base of independent assets on which to build production. It is the motivation to which the individual isolated farmer responded when planting a wider range of varieties to ensure his crop. In the past, if the crop failed, then the society depending upon it faced collapse as well. Investing in diversity provided the portfolio of different assets which insured against complete crop failure.

Information refers to the uncertainty that exists about the future and what will be revealed with the passage of time. In the context of agriculture, information arrives whenever the nature of the next invading pest or disease is revealed, or when the nature of the best strategy for resistance is identified. Diversity is useful in this context because it acts as a receiver, capturing information on the nature of successful resistance strategies through the process of selection. A greater diversity of plant varieties increases the prospects for the survival of at least one variety when a pest or disease passes through, and this provides the necessary information for the development of a successful resistance strategy against the prevalent pest. It signals the traits and characteristics that are successful in the new environment. When these signals are used, or accumulated, they provide the basis for continuing stability in agriculture.

How well does the agricultural industry address these fundamental values in their broadest sense, and how well does it manage genetic resources for these purposes? It is necessary to outline these various values and to consider the management implications of each.

Externalities in Agriculture

We will assume that the supply of genetic resources in agriculture will correspond directly to the objective function of the producers in agriculture. We will look to the individual decisions that are determining the production choices in agriculture and attempt to identify which, if any, of the values of genetic resources are external to this process. These external values determine the public interest in conserving biological diversity for agriculture.

Expected Agricultural Yields

Expected (average) yield is the fundamental criterion used in the determination of the vast majority of crop choice and land use decisions in recent times. The beneficial impact of this decision-making criterion is unquestionable. The impact in aggregate has been the 'green revolution': the increase in worldwide grain yields at a rate of nearly 3% per annum over a period of 30 years. What has been the impact of this criterion on genetic resource supplies? Empirical studies indicate that there is an opportunity cost implicit in the retention of a diversity of genetic resources in production (Hartell *et al*., 1997). Nevertheless, many times local demands of consumers and producers lead to the retention of some amount of diverse genetic resources (Altieri and Merrick, 1987). In sum, with the dissipation of the need for diversity as an individual insurance good, there has been an increasing focus of production choices and land use decisions on a small set of the highest yielding varieties across the globe.

What other values might be left out of the calculations of so many decentralized choices concerning crop varieties and land use?

Portfolio Value

This is the static value (available in a single growing season) derived from the retention of a relatively wider range of assets within the agricultural production system. It is the value which individual farmers formerly pursued when they had few other assets to rely upon. Now that individual farmers rely upon other assets for their insurance needs (access to markets, crop insurance programmes, etc.), the public sector must consider the cumulative impact on yield variability deriving from individual farmer's land use decisions. So long as society is averse to risk and thus has a distaste for yield variability, there will be value to investing in a greater diversity of production methods than would any individual farmer. Yield variability is smoothed by reason of non-conversion because this implies: (i) a broader portfolio of assets (varieties) within the species; (ii) a wider portfolio of assets (agricultural commodities) within the country; and (iii) a wider portfolio of assets (available methods of production) across the globe.

A topical example of a harmful 'portfolio effect' is the current bovine spongiform encephalitis (BSE) problem in the UK. Disease within the food chain is problematic in any event, but when disease becomes endemic within a crop in which a country is heavily invested, the costs of the pathogen become extremely heavy. 'Mad cow disease' is a portfolio problem because it is the UK's investment strategy that has made it possible for this single pathogen to have such a substantial impact on such a large proportion of the agricultural industry. The country is so heavily invested in this single species that it is difficult for it to absorb alone the costliness of the eradication campaign that is probably necessary to restore consumer confidence.

The most important level at which this externality operates is the global one. Any given country has the same incentives as the individual farmer to rely upon other national assets for insurance in times of crop failure. The level at which this obviously does not work is the global one; if all countries plant common varieties expecting to rely upon one another's harvests in the event of a national crop failure, then the fallacy of their reasoning would be revealed only in the context of a global crop failure. This would occur, for example, if the four primary carbohydrate crops (rice, wheat, potatoes and maize) which now provide the majority of the world's diet were subject to severe pest invasions in the same year. The continued narrowing of the range of production methods, crops and crop varieties in use across the globe continues to enhance the cumulative probability of such an occurrence.

There is another more fundamental level at which this portfolio value operates. One of the ecological functions of diverse genetic resources is to perform as 'fire breaks' in the event of pest and pathogen epidemics. As agriculture intensifies, these breaks are removed, enhancing the risks of the mutation of virulent strains of pests. The ecological portfolio value of genetic resources is positive by reason of the manner in which it reduces this contagion effect.

There is empirical evidence that demonstrates that modern intensive agriculture has had a systematic impact on correlated yields across the globe. The studies of crop yield variabilities have indicated that there has been a corresponding increase in variability going hand-in-hand with the increased average yield. The coefficient of variation in global grain yields has nearly doubled when comparing the experience of the 1960s with that of the 1970s (Anderson and Hazell, 1989). The vast majority of this enhanced variability is traceable to the reduced portfolio effect across space (international and intranational) rather than within species; that is, it is the adoption of a smaller number of crops and methods (rather than genetic uniformity itself) which is most contributing to the increase in variability. This is indicative of the externality that exists across countries when they are making their land use decisions.

Quasi-option Value

This is the value of retaining a wider portfolio of assets across time given that the environment is constantly changing and rendering known characteristics far more valuable than they are currently considered to be. That is, this is the value of retaining options currently thought to be of little value, when it is known that circumstances may change to alter that valuation (Arrow and Fisher, 1974; Conrad, 1980; Hanneman, 1989). For example, this is the value of the retention of certain varieties of cultivated species not known to be of any substantial expected value, but which are found to be of enhanced value when a particular form of pest or disease becomes more prevalent. It is the change in the value of a known characteristic by reason of an unforeseeable change in the environment. Clearly, this is a value that is not addressed by means of expected (mean) yield forms of decision making.

There is also an ecological quasi-option value. This is the value of the retention of some manner of evolutionary process intact, in the event that some trait for resistance might be identified via natural selection. That is, it is the basis for a distinct value to *in situ* conservation. For example, the continued cultivation of a wide range of varieties of wheat within a natural environment would allow natural selection to signal which of these varieties has the characteristic providing resistance to a newly invading pest. *In situ* conservation allows nature to signal this information and identify the important trait in the most direct fashion.

Although individual farmers utilizing the expected yield form of decision making do not consider these values, there are other parts of the agricultural industry which do. It was argued above that these sorts of quasi-option values are one of the driving forces within the plant breeding industry. Plant breeders retain genetic resources and continue to breed them into their lines of high-yielding varieties, for the express purpose of addressing this recurring problem of declining resistance.

Are there any externalities at work within this process? One thing is certain: society would supply a much wider range of genetic resources than those which would be perceived as imminently profitable by a plant breeder. This is indicative of the difference in the discount rates in use in evaluating supply decisions. Clearly a business firm will use its financial rate of return (usually in the range of 10–20%) in order to evaluate investment options. Most economists agree that a social investment decision should be evaluated at a rate nearer to 2–5% (Pearce and Ulph, 1995) while there is an argument to be made that the social discount rate should be even lower (or possibly zero) when the survival of future generations is at stake (Broome, 1995). This difference in discount rate will make a huge difference in the amount of genetic resources that would be supplied by the public sector which would not be supplied by the private. It means that a business firm would be considering a time horizon of not more than 5–10 years in making its decisions, while the public sector should be considering possible problems arising well beyond this time period.

It is also important to note that private firms are less likely to focus on a range of information-generating mechanisms than would an idealized public sector. This is both on account of the need to have the information in immediately appropriable form (since appropriation after 10 years would be discounted to nothing) and investments in information production must be relatively secure from the standpoint of the private investors concerned (i.e. they are concerned about the distribution of any informational gains as much as the production). These sorts of considerations mitigate in favour of conservative forms of investments in the industry. Information is difficult enough to generate and appropriate without making investments which are relatively insecure. A public sector which was less concerned with issues of distribution and appropriation would probably invest in very different methods. This is one reason (explored further below) for the investment in storage methods of supply rather than the usage-based methods of supply of information.

There is no doubt that change will occur over time (in the environment, in technology), and one of the values of genetic diversity is the flexibility it allows for response to future changes in circumstances. The agricultural industry definitely recognizes this value and provides against many eventualities, but there are clear instances in which there is a difference between what the private and the public sector would supply in terms of this value of genetic resources. These differences identify one of the most important public interests in the conservation of genetic resources.

Exploration Value

This is the value of retaining a wider portfolio of assets across time given that the exploration and use of little-known assets will generate discoveries of currently unknown traits and characteristics (Pindyck, 1991). This is a ‘Bayesian’ sort of value, where information derives from the process of converging expectations. Long analysed resources will no longer divulge as much information as will those that are little analysed, even though the former might have much higher expected yields. For example, this can be conceived of as the value of the retention of a given land area in ‘unused’ status, because it is possible that certain wild relatives of cultivated varieties will be found within that area, and these relatives may generate new and valuable characteristics if investigated. The same idea may also be applied at the field level and the species level. Any non-modern production method or crop will be relatively unknown (compared with the heavily researched crops and crop varieties). It is important to continue to hold on to some of these little-known wildernesses, crops and crop varieties, if only because we must admit that these have received little exploration while the other paths have been much pursued.

Once again there are good reasons to expect that private industry will take some of this value into account in its approach to conserving genetic diversity, but there are also good reasons why their approach will be inadequate. As with individuals, private industries (even those focusing upon informational values) will be using a criterion based on expected profitability, yet an argument could be made that the appropriate objective should be to maximize the amount of information derived per unit of expenditure (see e.g. Weitzman, 1993). The public sector has a much wider range of social objectives that it may consider than the private sector, and one focused on the informational rather than the current production value of the resource would favour a much greater supply of genetic resources.

Another reason is based more on national externalities. Even if private companies should wish to invest in the conservation of certain land areas in certain countries, they may find it very difficult to obtain any return from doing so across political boundaries. The absence of universally recognized property rights in informational values renders investments across borders highly dubious. Most of the plant breeders mentioned ‘insecurity of investment’ as the primary reason that more investments in *in situ* conservation did not occur. This is one of the primary reasons why private firms place relatively little effort into *in situ* conservation strategies (Swanson, 1996). This property right failure is another example of a private sector failure that implies the necessity of public sector intervention.

The Public Interest in Genetic Resource Conservation for Agriculture

This section has demonstrated the values of genetic resources which the private sector probably will and will not take into account systematically in making their conservation and use decisions. It is then the role of the public sector to intervene to conserve genetic resources for agriculture for those values which are under-appreciated by the private sector.

This framework helps to identify the values of genetic diversity which should be the subject of public interest and investment in order to insure the future of modern agriculture. The nurturing and advancement of the green revolution has been an important event in human history, but it is equally important that a scientific basis for conservation is developed in order to ensure the sustainability of this advance.

Conclusion

The fundamental values of genetic resources for agriculture lie in their contribution to the solution of the fundamental ecological problem underlying the system. They provide the source for the strategies required to address the evolving problems of pest resistance (virulence) which develop naturally through the process of natural selection. Genetic resources are not uniform in their informational value, however. Previously selected varieties are valuable on account of the resistance that such selection connotes, and stocks of these varieties are valuable as wells (i.e. stocks) of potentially useful information on resistance. On the other hand, varieties that are being selected now, or at some time in the future, provide *flows* of information. They provide information on the nature of the current threats to the system, and the nature of the traits and characteristics which currently provide the best response to these problems.

Both types of information should be conserved, and the plant breeding industry has incentives to do so. The interesting question is whether this industry and the public sector together have the complete incentives for supplying all of these values. For this reason, we look at the sector closely in order to identify any gaps or ‘market failures’ that might prevent some of these values from registering. This is the fundamental nature of the public interest in genetic resource conservation: supplying those values which the private sector has little or no incentive to pursue. We have attempted to identify here the potential gaps in the framework used by the private sector in conducting this research, and we have indicated briefly the nature of the public sector policies (property rights, conservation strategies) that are required to redress them.

Notes

1. Named after the Red Queen in *Alice in Wonderland*, who said that it was necessary to keep moving just to stand still.
2. Smale (1996) identifies a certain level of such 'background resistance' in the wheat landraces held by CIMMYT. These are general traits of resistance which are unidentified but are found to exist at greater than random rates within previously used varieties of wheat.
3. A similar finding (of 7% wild input requirements) was reported by a survey undertaken by CIMMYT in relation to wheat genetic resources utilized in the modern plant breeding industry (Rejesus *et al*., 1996).

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Part II
Empirical Studies: Plant Breeding and Field Diversity

5

Indicators of Varietal Diversity in Bread Wheat Grown in Developing Countries

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In this chapter, several indicators that social and biological scientists have used to describe varietal and genetic diversity in farm fields are applied to data for bread wheats grown in developing countries. The discussion is based on patterns that can be observed in farm fields rather than those developed from population genetics or molecular measurements. This emphasis reflects both our interest in factors that shape farmers' choice of varieties and the difficulty of assembling genetic or molecular data on such a large scale.

Spatial Diversity

Empirically, there is an inverse relationship between area sown to modern bread wheats in developing countries and the numbers of distinct varieties[2] grown per million hectares. South Asia, the Southern Cone, and West Asia, which contain the largest areas planted to bread wheats in the developing world, have the lowest number of crosses per million hectares sown (Table 5.1).[3]

The percentage of area planted to the top five crosses ranges between 43% in the Southern Cone and 71% for Mexico and Central America and the Andean region. West Asia also has a relatively low concentration of area under leading crosses, which may in part reflect the importance of traditional bread wheat varieties in that region.

While these percentages appear high, it is important to recognize that the concentration of wheat area under modern cultivars is probably less today than in earlier decades of this century for major wheat-producing regions of both the industrialized and developing world (see data in MacIndoe and Brown, 1968; Reitz, 1979; Lupton, 1992; and Thomas, 1995). Since the beginning of

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Table 5.1. Indicators of spatial diversity among bread wheats grown in the developing world in 1990.

	Sub-Saharan Africa	North Africa	West Asia	South Asia	Mexico and Guatemala	Andean region	Southern Cone	Developing world[a]
Number of modern cultivars	39	28	51	64	42	27	64	310
Number of crosses from which cultivars are selected	30	23	47	51	36	25	54	234
Area in modern cultivars (Mha)	0.7	1.8	8.4	29.2	0.9	0.2	8.8	49.8
Modern cultivars as percent of area in bread wheats	86	83	53	93	94	87	93	82
Crosses Mha^{-1} modern cultivars	45	13	5	2	41	145	6	5
Top five crosses as percent of area in modern cultivars	64	62	48	59	71	71	43	36.4

Source: calculated from CIMMYT Wheat Pedigree Management System and data from CIMMYT Wheat Impacts Survey, summarized in Byerlee and Moya (1993).

[a] Regional numbers of cultivars and crosses do not total to Developing world because the same cultivar or cross may be grown in more than one region. The Developing world category excludes China.

the green revolution the concentration of planted area among leading bread wheats has also changed. The number of cultivars released in developing countries that were derived from the CIMMYT variety Veery is at least twice that of the cultivars derived from the II8156 (Mexipak) cross, but the area planted to all of them is small compared with the area once sown to II8156 alone (Byerlee and Moya, 1993).

Estimates suggest, for example, that the area planted to a single cultivar was high in the Indian Punjab in the late 1950s prior to the green revolution: a tall bread cultivar called C591 may have covered most of the irrigated area and some of the rainfed area. Semi-dwarf wheat varieties generally replaced the tall, modern varieties (such as C591) that were released by the Indian national breeding programme from the early 1900s. Since the late 1960s, the percentage of area in leading cultivars has fluctuated, but if any long-term trend is observable since independence in 1947, it has not been upward. In the Pakistani Punjab, for the shorter period from 1978, the percent of wheat area in the dominant and top five cultivars has been only slightly lower than in the Indian Punjab, and the pattern over time also appears to be cyclical. The cyclical pattern reflects the replacement of older varieties with newer releases, or the decline and rise in popularity among leading cultivars. For both the Indian and Pakistani Punjabs, however, the concentration of planted area among modern wheats still appears to be relatively high (Smale, 1995).

Temporal Diversity

The average age of crosses in farmers' fields, weighted by area planted, is a measure of the *temporal diversity* of cultivars, or diversity in time (Duvick, 1984). The average age of crosses grown in farmers' fields, weighted by area planted, ranges between about 8 years for Mexico and Guatemala and about 15 years for the North Africa region (Table 5.2). The rapid rate of change among crosses grown in Mexico and Guatemala reflects in part the rapid rate of change in the virulence of rusts in that zone.

As a point of comparison with these figures, Brennan and Byerlee (1991) have estimated the weighted average age of cultivars for a number of specific wheat-producing zones of the industrialized and developing world over several decades. Among the zones they studied, the Yaqui Valley of Mexico had the highest temporal diversity (a weighted average age of only 3.1 years over the 1972–1986 period) and the Punjab of Pakistan had the lowest (a weighted average age of about 11 years over the 1978–1986 period). The Punjab of India had a weighted average age of 5.3 over the 1970–1986 period. Brennan and Byerlee found that the commercialized wheat-producing zones in Brazil, Argentina, the US, Australia, New Zealand and the Netherlands had an average age of 7–10 years. By contrast, Canada has a relatively low level of temporal diversity for an industrialized major wheat producer, ranging from about 10 to 13 years over the past 20 years (see Thomas, 1995).

Table 5.2. Temporal diversity among bread wheats grown in the developing world in 1990.

Region	Weighted average age of crosses[a]
Sub-Saharan Africa	11.3
West Asia	10.6
North Africa	14.7
South Asia	12.8
Southern Cone	9.2
Andean region	13.7
Mexico and Guatemala	8.0

Source: calculated from CIMMYT Wheat Pedigree Management System and data from CIMMYT Wheat Impacts Survey, summarized in Byerlee and Moya (1993).

[a] Weights are percentage area planted to cultivars derived from same crosses.

The weighted average age of crosses has implications for resistance to both known and unknown pathogens. Using data from a number of countries, Kilpatrick (1975) estimated an overall average of 5–6 years' cultivar longevity for leaf and stripe rusts, when resistance is monogenic. Using that estimate alone, the rate of turnover among crosses would be less than desirable for all of the regions of the developing world in 1990. But the longevity of cultivars in terms of rust resistance is very environment specific, and the socially optimal period for cultivar replacement is a function of many economic and biological factors, of which resistance to pathogens is only one (Heisey and Brennan, 1991).[4] Generally, there is a need for higher rates of varietal turnover in more favourable production environments, because the conditions that are conducive to high productivity are also conducive to the development of disease.

Diversity Indicators Based on Genealogical Characteristics

Latent Diversity

As calculated from the coefficients of parentage, the *latent diversity* of the top ten cultivars planted in the developing world in 1990 appears to be fairly high, although the average coefficient of diversity varies by geographical region (Table 5.3).[5] Among regions of the developing world, the average coefficients of diversity are significantly higher among the top ten lines grown in West Asia, and the Southern Cone of Latin America, than in South Asia, Mexico and Guatemala.

As a point of comparison, the same indicators are presented for three of the

Table 5.3. Latent diversity of the top ten bread wheat crosses grown in regions of the developing world and in selected industrialized nations in 1990.

Region/country	Average coefficient of diversity	Average coefficient of diversity weighted by cultivated area	Minimum pairwise coefficient of diversity	Maximum pairwise coefficient of diversity	Genealogical distance
Developing world	0.78	0.70	0.43	0.98	8.18
Sub-Saharan Africa	0.79	0.77	0.28	0.99	8.29
North Africa	0.79	0.73	0.57	1.00	7.12
West Asia	0.84[a]	0.80	0.67	0.99	8.11
South Asia	0.72[b]	0.63	0.35	0.96	7.70
Mexico and Guatemala	0.69[b]	0.63	0.57	0.88	5.80
Andean region	0.80	0.72	0.41	0.99	7.89
Southern Cone	0.82[a]	0.80	0.69	1.00	7.78
Selected major industrialized bread wheat producers					
Canada (spring wheats)	0.48[c]	0.22	0.01	0.80	4.71
Australia (spring wheats)	0.74[b]	0.72	0.30	0.98	8.63
US (hard red spring wheats)	0.84[a]	0.79	0.53	1.00	8.71

Source: calculated from CIMMYT Wheat Pedigree Management System and data from CIMMYT Wheat Impacts Survey, summarized in Byerlee and Moya (1993).
Notes: coefficient of diversity = 1 − coefficient of parentage. Genealogical distance measured as total branch length of dendrogram constructed from Ward's cluster analysis of coefficients of diversity (see Weitzman, 1992). Average coefficients of diversity with different letters are statistically different, using a non-parametric test. China is excluded from the Developing world category.

four major bread wheat producers of the industrialized world, also for the top ten crosses, and for spring wheats. In Australia average and weighted coefficients are almost equal which implies that the top ten crosses are distributed equally as a percent of national area. Each state of Australia has a different set of leading cultivars, and the environment is more heterogeneous than in the US or Canada. The top ten lines grown in Canada are statistically less diverse than the top ten in any of the developing or industrialized regions considered. The minimum diversity among pairs of crosses is also near zero in Canada, while the maximum diversity is lower than for the other industrialized producers and the developing regions.

An estimate of genealogical distance suggested by the work of Weitzman (1992)[6] is also shown in Table 5.3. In comparison with a simple average of the coefficients of diversity for each group of ten cultivars, this indicator represents the sum of the distances of each cultivar from all other cultivars in the set based on the pairwise coefficient of diversity as a measure of distance. Once again, Canada's leading spring wheats appear to be markedly less diverse than those of either the other major industrialized wheat producers or the developing regions. Mexican wheats, grown in a small relatively homogeneous production environment, also appear to be considerably less diverse – a result that is not as clear with a simple average of coefficients of diversity. The top ten bread wheats of West Asia appear among the most diverse for developing regions.

The data demonstrate clearly how the factors affecting the spatial distribution of planted area among cultivars can influence latent diversity. For all developing country regions, weighting by area planted to the cultivars in 1990 reduces the average coefficients of diversity, although not by a very large magnitude. In Canada, weighting by percent of area halves an already low average coefficient of diversity.

The difference between the weighted and unweighted measures of diversity crudely reflects the effects of factors related to varietal adoption, such as seed distribution systems. Farmers will choose to grow the variety that is most attractive to them (in terms of profits or other measures of economic value), but the range of their choice is often limited by the few seed types that are locally available. Policy factors that affect the rate of release of cultivars, and the policy, institutional and behavioural factors that determine the varieties that farmers plant and their rate of varietal replacement, are principal determinants of wheat diversity in farmers' fields. These are generally outside the influence of plant breeders and are those in need of more careful study by social scientists.

In the Indian Punjab, both the average and weighted average coefficients of diversity of the leading cultivars grown in farmers' fields have increased significantly over time since the late 1970s. The movement around the trend line is greater for the weighted average coefficient of diversity, reflecting changes in area planted among leading cultivars. The upward trend is greater for the weighted average than the average coefficient of diversity, and no trend is perceptible over the period for the average coefficient of diversity among all wheats released by the national programme.[7]

Landrace Use

In a sample of 800 wheats released by breeding programmes in developing countries over the past 30 years, the average number of *different* landraces per pedigree has continued to increase. This is an important finding. Although we can expect the frequency of landrace use to increase over time as pedigrees grow longer, it is not necessarily true that the number of different landraces also increases. For example, in the early part of this century, plant breeders in many regions of the world used a few landraces from the former Soviet Union, Europe and India extensively (see information summarized in Smale and McBride, 1996). When advanced materials were later exchanged among breeding programmes, the frequency of many of these landraces in the pedigrees of wheat releases increased, but not necessarily the number of different landraces.

Among wheat breeding programmes in developing countries, wild relatives and landraces are entered less frequently in crossing blocks than other germplasm materials – but breeders do use them (in roughly 14% of all crosses), and particularly when they make crosses for biotic resistance, tolerance to abiotic stress or quality (Table 5.4). Other results reported in Rejesus *et al*. (1998) suggest that turnover of wild relatives and landraces in wheat breeders' crossing blocks is also lower than for other types of materials.

Turnover of landraces in crossing blocks and the representation of landraces among active parental stocks probably reflect closely the way in which they are used and breeders' perceptions of expected returns from their investment. To determine which landraces 'combine' well with modern germplasm and transmit the trait(s) of interest requires several breeding cycles and several hundreds of crosses. Verifying that a desirable trait has been transferred to, and is stable in, the progeny requires further testing. Transferring desirable genes without also transferring deleterious genes represents a further challenge. As Harlan (1992, p. 154) has stated, the plant breeder 'wants the genes not the linkages'.

Landraces are infrequently the direct parents of leading wheat varieties grown in farmers' fields. Gerek 79, a major Turkish wheat variety and one of the top ten wheat varieties grown in the developing world in 1990, is an exception – one of its parents is a Turkish landrace. When new materials are brought into a wheat breeder's programme, most are advanced materials with long pedigrees. Many have similar genealogical backgrounds to materials previously used by the breeder. Some have landrace ancestors that are not found in materials previously used by the breeder. Very few are landraces that have never been used before in wheat breeding. (See pedigrees shown in Smale and McBride, 1996.)

Table 5.4. Type of parent materials used in crossing, by breeding goal, wheat programmes in developing countries in 1994.

	Percent of crosses, by goal				
Parent material	Yield	Biotic resistance	Abiotic resistance	Quality	All
Wild relatives and landraces	4.7	15.4	22.1	20.9	14.4
Advanced materials	69.0	54.6	51.2	55.1	59.2
CIMMYT International Nurseries	23.2	26.6	22.3	20.4	23.0
Others	3.1	3.4	4.4	3.6	3.4
Total	100	100	100	100	100

Source: survey conducted for CIMMYT World Wheat Facts and Trends (1996).
Note: includes responses from 70 wheat breeders. Advanced materials included released varieties and advanced lines from respondent's programme or other national programmes. Others category includes materials from other, sub-national programmes in the respondent's nation, or materials from other international nurseries.

Yield Stability

The *yield stability* of wheat in the developing world is compared over four decades in Table 5.5. For every region, variation was greater in the decade preceding 1965 (the year that marks the early phase of the green revolution) than in the most recent decade. In regions where the largest proportion of wheat area is planted to modern wheats (South Asia, Mexico/Guatemala, and the Southern Cone of South America) the variation in wheat yields has declined since 1965. In West Asia and North Africa, where modern wheats cover a smaller proportion of area, yield stability has not worsened over the past three decades. Only in the Andean region and sub-Saharan Africa, two regions with very small wheat areas and with distinctive growing conditions, does the variation in wheat yields appear to have increased since 1965. In both of these regions, however, the overall level of variation is quite low.

As explained previously, because most of the year-to-year variation in aggregate yields is caused by differences in weather, use of irrigation, and pathogens, the factors explaining the largest proportion of variation in aggregate yields are probably associated less with plant stature or genotype than with input supply and pricing policy. The balance of general evidence concerning the relationship between mean yields and yield variance in farmers' fields over time suggests that yield stability has increased even as mean yields have increased, from the 1950s through the 1980s, across the world, in major wheat-producing countries of the developing world, and in India (Anderson and Hazell, 1989; Singh and Byerlee, 1990). In particular, Singh and Byerlee (1990) showed that technological variables such as the level of adoption of high-yielding varieties and levels of fertilizer use had no effect on differences in wheat yield stability across countries.

Table 5.5. Yield stability of all wheats grown from 1955 to 1994 in the developing world.

	Coefficient yield of variation adjusted for trend (%)						
	Sub-Saharan Africa	North Africa	West Asia	South Asia	Mexico and Guatemala	Andean region	Southern Cone
1955–1964	10.8	13.4	8.7	6.5	12.3	9.8	12.9
1965–1974	4.3	10.3	8.0	9.1	7.9	2.4	8.1
1975–1984	7.1	12.1	4.0	3.0	5.6	5.6	12.2
1985–1994	8.8	11.0	7.5	4.0	5.5	4.8	5.0

S*ource:* constructed from FAO yield data using the Cuddy–Della Valle index (Cuddy and Della Valle, 1978).
Note: China is excluded.

Conclusions

The findings summarized here suggest that the percentage of area planted to leading cultivars in major bread wheat-producing zones of the developing world and industrialized world is high, although less so than in earlier periods of this century, when the first products of scientific plant breeding were widely distributed across Europe, Australia, North America and India. Evidence from India also indicates that the concentration of area among the top cultivars is lower now than in the green revolution period. These findings are not inconsistent, however, with the generally held view that the ancient patterns of genetic variation in farmers' varieties have been replaced during the past 200 years by patterns based on modern plant breeding. Further, broad perspectives such as those presented here cannot capture the effects of important changes in the micro-centres of diversity. Such changes must be studied in detail on a case-by-case basis.

Notes

1. Numerous CIMMYT scientists have contributed to the work summarized here.
2. By 'modern', we denote both improved tall and semi-dwarf varieties – or all varieties with known pedigrees that are the products of a scientific breeding programme. We contrast the number of distinct varieties with the number of cultivars, because the same variety can be released under several names. This happens, for example, when national programmes re-release a variety obtained from an international research institution or another national programme under a new name. Many lines can also be selected from one cross. The most precise level of detail for identifying a variety is given by a combination of cross and selection information. In these tables, and in the reported calculations of coefficients of parentage, selections from one cross have been treated as the same cross and called a 'variety'. This slightly overstates the similarity of parentage and understates the diversity.
3. The People's Republic of China is the largest national producer of wheat in the developing world, but the CIMMYT Wheat Impacts Survey (summarized in Byerlee and Moya, 1993) contains wheat cultivar data from only one of its regions. CIMMYT Economics and Wheat Programs are currently engaged in improving the coverage and quality of data on wheat releases and pedigree information for China. Some preliminary findings are reported in Yang and Smale (1996).
4. Recall that historically, some single cultivars dominated the wheat areas of industrialized countries for decades, such as Wilhelmina and Juliana in the Netherlands, the Vilmorin crosses in France, and Federation in Australia (MacIndoe and Brown, 1968; Lupton, 1992). In more recent years, in Canada, the fact that Neepawa occupied over 50% of wheat area for years has contributed to a relatively low measure of temporal diversity (see Thomas, 1995).
5. Souza *et al*., (1994) have defined (1-COP) as an indicator of latent genetic diversity. In wheat, the coefficient of parentage measures the probability that two cultivars are identical-by-descent for a character (observable or unobservable) that varies genetically and is not expressed as a result of intensive selection by plant breeders.

6. The sum of the branch lengths of the dendrogram constructed from Ward's cluster analysis of pairwise, ultrametric distances. Here, the pairwise distance measures are coefficients of diversity. Any pairwise distance measure that satisfies ultrametric properties can be used as the basis of analysis.
7. Data reported in Smale (1995) show a constant or slightly positive trend among wheats released by the national programme over the last 80 years.

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6

The Value of Wheat Genetic Resources to Farmers in Turkey

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Although attempts to formally assign a value to crop genetic resources have been a relatively recent phenomenon, the long-term use and conservation of these resources by farmers, as well as by scientists and other interested parties, provide evidence that value was attributed to them long before a formal valuation process began. Until recently, proponents of genetic resource conservation have been able to provide only anecdotal and rather vague estimates of the value of genetic resources. There are abundant examples of the economic contribution of exotic crops or crop varieties to societies around the world, but these examples do not furnish estimates of the value of crop resources that remain in farmers' fields, in forests and pastures, or in gene banks. The burden of being more specific about the value of genetic resources comes from two directions. Crop resource conservationists need measures of value to justify budgets. Farmers' rights activists want measures of the value of crop resources to back up their attempts to obtain compensation for farmers or for less developed countries. These reasons for specifying the value of crop genetic resources are given legitimacy in the 1992 Convention on Biological Diversity. Different methods for valuing non-market resources exist, but it is questionable whether a single method is available to value the vast array of genetic resources.

Estimation of value suffers from lack of data and, in some cases, lack of methodology. We assert that genetic resources for agriculture present a unique and separate set of problems and characteristics that must be acknowledged in any valuation exercise. Our approach is to examine the use value of landraces to farmers, as a means of assessing the likelihood of genetic resource loss in landraces and to explore the possibility of *in situ* conservation of genetic resources by farmers in the agricultural systems where landraces are maintained. We view landraces as a proxy for crop genetic resources because landraces have historically been an important source of germplasm in crop improvement programmes. In the collections of the CGIAR centres, 59% of all

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accessions are landraces, 14% wild and weedy relatives, and 27% advanced cultivars and breeders' lines, where the last category derives largely from the first (FAO, 1996).

As a source of raw materials for the crop development process, landraces are a public good with social value. However, to the farmers who choose to cultivate them, landraces are also private goods. Farm households benefit directly from their production and consumption, and dedicate valuable resources to make their cultivation possible. Because private value affects the supply of genetic resources, it also affects their social value. Therefore, consideration of the social value of genetic resources must address the value of these resources to farmers. An attempt to examine the value of a landrace to the farm household should be preceded by the identification of what exactly farmers perceive to be advantageous and therefore valuable about the traditional varieties they choose to cultivate. These characteristics presumably will be the same as, or similar to, factors ultimately influencing the farm household in its land allocation decisions.

The objective of this chapter is to propose a practical alternative for valuation by focusing on the private value of landraces in centres of agricultural diversity.

The Loss and Conservation of Crop Genetic Resources

The definition of crop genetic resources has grown increasingly broad and now includes germplasm from both cultivated and wild plants, as well as the ecosystems that contain the germplasm. The germplasm resources of agriculture are found in wild relatives of cultivated plants, weedy forms, locally selected crop varieties (landraces), modern cultivars, and the breeding lines used in crop improvement. The first three have been targeted for conservation due to both their threatened status and their contribution to the development of the latter two types. Moreover, these three sources of crop germplasm are the basis for demands for compensation (Mooney, 1979).

Landraces were the initial target for conservation, and hundreds of thousands of individual accessions have been assembled into national and international collections, stored in gene banks, botanical gardens, and breeding programmes around the world (*ex situ* conservation). Gene bank collections exist in 130 countries, with approximately 6.2 million accessions, including over 2 million cereal accessions (FAO, 1996). Half (50.4%) of the accessions are located in developed countries, more than one-third (38%) are in developing countries, and a smaller fraction (11.6%) are in international centres of the CGIAR (FAO, 1996).

As conservation of crop genetic resources has progressed, conservationists have concluded that *ex situ* maintenance alone is not sufficient and that *in situ* conservation is needed to complement gene banks and botanical gardens. *In situ* conservation serves not only as a back-up, but it also covers types of genetic resource which cannot be protected in gene banks, such as local knowledge and ecosystem interactions (Oldfield and Alcorn, 1987; Brush and Stabinsky, 1996). *Ex situ* conservation simply cannot capture or conserve all of the diversity in agricultural systems. *In situ* conservation does not directly provide genes for crop improvement, but it preserves evolutionary processes which will yield new germplasm in the future (Brush, 1995).

For nearly as long as the crop breeding industry has existed, scientists have worried that the ultimate source of crop germplasm in centres of crop origins and evolution is threatened by modern conditions – especially the size and growth of the human population, technological change and markets (Frankel, 1970). While threat of genetic erosion came into sharp focus in technical conferences of the FAO in the 1970s, scientific understanding and measurement of this problem is weak. The lack of a firm estimate for genetic erosion and uncertainty about the supply of genetic resources has a potentially large impact on our ability to measure the value of these resources. Diffusion of modern crop varieties (MVs) is the process most widely used to indicate genetic erosion, but this is an indirect measure. The experience in developed countries is that diffusion of MVs can have a devastating effect on the diversity of local crops (Griliches, 1958; Duvick, 1984). While the spread of semi-dwarf wheat and rice in Asia convinced many agricultural scientists that genetic erosion experienced in temperate industrial countries was about to repeat itself in tropical, less developed ones, some evidence suggests that a different pattern may prevail in centres of crop diversity.

Genetic erosion in less developed countries was expected to follow two of the trends observed in developed countries. First, it was believed that the diffusion of MVs would be rapid and thorough. Second, MVs were expected to completely replace landraces. This extrapolation from developed to less developed countries was supported by aggregate data (e.g. Dalrymple, 1986), but more detailed studies suggest that the two trends may not apply broadly in diverse, less developed countries (Brush, 1995). The diffusion of MVs in the latter is complex, with a rate and extent that is context specific. In many situations, farmers decide to plant both MVs and landraces on their farms. Regions thus exist in several countries where landraces either persist as the major type of cultivar or where landraces have been decreased but not eliminated by MVs.

From the observed cultivation of landraces, we can infer that these varieties hold some value for the households that cultivate them, and this household value is one component of the overall value of the genetic resource. Estimating their value to farm households involved in their cultivation can provide a lower-bound estimate of the total value of these resources to society. The change in focus from private, on-farm value for farm households to broader measures of value for society is not necessarily straightforward. In the context of valuing biodiversity for pharmaceutical research, Simpson *et al.* (1996) point out that previously estimated values have probably been overestimated due to the failure to account for issues of scarcity and redundancy. They emphasize that an accurate assessment will value a marginal species on the basis of its incremental contribution. A similar precaution should be applied to any valuation of landraces.

Additional information about specific varietal characteristics that the farmer finds important will provide insights into household preferences and behaviour. Ideally, the availability of the appropriate information of preferences, both in terms of crop varieties as well as production and consumption characteristics, could facilitate the estimation of household value of landraces. Improved knowledge of preferences and behaviour will also assist in assessing the likelihood that farm households will continue to include traditional varieties in their production decisions. If continued cultivation of landraces appears uncertain and if on-farm maintenance of a specific target level of diversity is a stated policy objective, then the accurate valuation of these genetic resources from the viewpoint of the farm household could provide crucial information for the development of policies to guarantee their existence in the future.

Farmer's Valuations of Crop Resources in Turkish Wheat

Several theories of behaviour have been developed to explain the varietal choice of farm households. The desire to diversify and shield against risk (Just and Zilberman, 1983; Clawson, 1985; Finkelshtain and Chalfant, 1991; Fafchamps, 1992), transactions costs restricting households access to markets (Strauss, 1986; Falchamps, 1992; Goetz, 1992), and the presence of environmental constraints (Richards, 1986; Bellon and Taylor, 1993; Zimmerer, 1996) have all been advanced as important influences in the land-use decisions of farm households. Each of these theories has been empirically tested separately, and alone can explain to some extent the occurrence of the partial adoption of improved crop varieties by farmers in developing countries. Factors such as production stability, joint production, performance in different agroclimatic zones and fit to household schedules may lead to the selection of landraces instead of or in addition to MVs. The presence of consumption risk and the demand for specific quality characteristics can also result in a household decision to cultivate a traditional variety if transportation costs, search costs or other transaction costs prevent household access to markets. Field research on the maintenance of landraces in regions where MVs are grown confirms the multiple objectives of farmers and the importance of heterogeneity in the physical, economic and cultural contexts of local agriculture (Brush, 1992).

As a centre of domestication and diversity for wheat (Zohary and Hopf, 1993), the cultivation of wheat in Turkey for over 8000 years has resulted in a large number of traditionally grown wheat varieties in addition to the existing wild and semi-domesticated wheat relatives. Modern (dwarf) varieties have been available in Turkey since the early part of the century and semi-dwarf varieties were introduced from Mexico in 1966. However, the level of adoption in the country varies greatly from region to region. The spring wheat regions of Thrace and the largely winter wheat areas of the Anatolian plateau are extensively planted in MVs, but CIMMYT (1993) reports that only 31% of Turkey's wheat area was planted in MVs in 1990. The western transitional zone, located between the major wheat-producing Anatolian Plateau region and the western coastal plains, was selected for this research due to its considerable variation from village to village in percentage of area cultivated with MVs. Our surveys show that the adoption of modern wheat varieties varies within as well as between provinces.

Our data were collected in 1992 from a household-level survey covering 287 households, in 24 villages selected from the three provinces of Eskisehir, Kutahya and Usak. Villages also vary with respect to agroclimatic zones, which can be divided into three categories: valley land, hillside land and mountain land. Valley land is more likely to have irrigation and to be connected with urban markets, while mountain land is most distant from markets and situated in or around forested zones. Hillside land shares attributes of both valley and mountain land. The socioeconomic survey covers a broad range of information regarding household characteristics, detailed production data and consumption preferences. Households in the sample include those that cultivate only MVs, those that cultivate both modern and traditional varieties, and those that cultivate only traditional varieties. Differentiation between households also exists with respect to percentage of production output marketed. Table 6.1 summarizes several household characteristics by province and agroclimatic zone for the surveyed sample.

In our Turkish research, we find evidence that environmental heterogeneity, risk and the high household transaction costs of obtaining desired qualities in wheat contributed to the continued cultivation of landraces in specific areas of a nation which has successfully promoted MVs. An econometric analysis of the factors influencing plot-level households varietal selection decisions in the Turkish data confirms the importance of acknowledging multiple household motivations for cultivating traditional varieties (Meng *et al*., 1995). The probability of cultivation of traditional varieties in a given household plot significantly increases, for example, when the plot is situated in less fertile soil or when distance to market and bad road quality increase a household's cost of accessing markets.

A household's ability to access markets plays a significant role in its decision to cultivate traditional varieties. Table 6.2 shows the relationship between the percentage of household wheat sales and selected household characteristics. Households with little or no wheat sales are often located furthest from markets and experience the least amount of interaction with extension agents. Moreover, these households are likely to be the smallest landowners, both in terms of overall area and irrigated area.

Our survey also reveals that a substantial percentage of households participate in some kind of market, but that market integration and efficiency are not fully represented by road quality and distance to market. Once the market is accessed in Turkey, the sale of any wheat variety is guaranteed since it is the stated policy of the government state purchasing authority, the Toprak Mahsulleri Ofisi (TMO), to accept all varieties. The purchase of a specific variety,

Table 6.1. Household characteristics.

	n	Off-farm income (%)	Age	School	Household size	Total land (ha)	Total irrigated land	Total plots	Mean plot size	No. of household wheat plots	Distance from market (km)
All households	285	26.5	49.1	4.1	4.5	12.3	2.6	12.4	13.1	7.0	16.6
Eskisehir	96	21.9	48.2	4.6	4.4	15.5	6.7	13.2	18.0	7.2	20.4
Kutahya	96	22.7	49.7	3.8	4.6	10.4	0.9	20.3	7.1	10.8	12.9
Usak	93	35.1	49.5	3.9	4.3	10.8	0.1	8.5	14.3	2.8	16.6
Valley	100	17.0	50.1	4.4	4.7	15.0	6.7	15.8	16.9	7.3	10.6
Hillside	101	22.5	49.1	4.3	4.3	13.9	0.6	16.2	12.1	8.4	13.5
Mountain	84	42.4	48.0	3.4	4.4	6.9	0.02	9.5	9.9	4.8	24.0

Table 6.2. Household characteristics by percentage production sold.

Household sales	No. of households	Total land (ha)	Total wheat land (ha)	Total irrigated land (ha)	Percentage of land in: Modern varieties	Traditional varieties	Home bread (% households)	Market distance (km)	Extension visit (%)	Off-farm income (%)
0	91	7.4	2.7	2.1	9.1	90.9	98.9	18.1	19.8	36.3
		(10.1)*	(2.1)	(1.6)				(7.3)		
0<S<25	34	10.8	5.4	4.3	13.2	86.8	97.1	18.4	23.5	35.3
		(10.7)	(4.3)	(4.4)				(7.5)		
26<S<50	49	13.4	8.3	5.8	34.6	65.4	87.0	15.9	36.7	12.2
		(13.3)	(7.9)	(6.6)				(7.8)		
51<S<75	51	13.9	10.4	5.5	43.8	56.2	74.0	15.7	19.6	31.4
		(10.0)	(13.0)	(5.8)				(8.4)		
76<S<99	60	17.4	11.9	4.2	63.0	37.0	80.7	14.8	43.3	11.7
		(16.2)	(15.5)	(5.6)				(8.2)		
100	4	14.7	3.5	0.8	75.0	25.0	75.0	12.8	50.0	25.0
		(10.9)	(4.4)	(1.2)				(9.9)		

*Standard deviation.

Table 6.3. Location of sales by variety type.

Variety type	No. of households cultivating variety type	No. of households with sales	Total quantity sold (kg)	Percent of sales of total wheat production	Percent of sales of total variety production	Location sold (%) Local	Merchant	Not local
Modern	136	108	2,899,478	76.3	74.3	1.5	24.4	73.3
Traditional	221	127	901,955	23.7	46.7	5.8	65.3	28.0

Table 6.4. Seed acquisition.

Activity	Yes (%)	No (%)
Purchase seed	35.4	64.6
Borrow seed	11.2	88.8
Purchase government seed	7.7	92.3
Purchase government seed (previous years)	42.6	57.4
Sell seed	15.8	84.2
Sell seed (previous years)	31.9	68.1

	Location purchased		Location purchased (previous years)	
	No.	Percent	No.	Percent
Village	45	31	20	13.8
Merchant	21	14.5	10	6.9
Neighbour	16	11	8	5.5
Cooperative	12	8.3	6	4.1
Government	5	3.4	5	3.4
No purchase	46	31.7	64	44.1
Total responses	145	100	113	100

however, is much more difficult. Private and public wheat buyers categorize the grain by colour and hardness, a policy that results in a mixture of varieties in each market class. Quality aspects that might be attributed to specific varieties are not included in the market classes, so that search costs and other transaction costs for obtaining a specific local variety are likely to be high. Table 6.3 gives a breakdown of sales of modern and traditional varieties by location sold and shows that sales of traditional varieties make up only a small percentage of wheat sales. Half of the production in traditional varieties is sold in contrast with the high percentage of sales in modern wheat varieties. Local sales at the village level amount to only 9% of traditional variety sales, indicating that these varieties are primarily used to meet consumption needs. A slightly higher percentage (12.4%) of wheat sales to the TMO take place outside the village. While merchant sales take place in or near the village, the percentage of this wheat remaining in the local community is unknown. In conclusion, it appears that if the household wishes to consume a specific variety, on-farm cultivation appears to be the most certain method of guaranteeing availability.

Similarly, a secure supply of seed of traditional varieties for a particular household can best be obtained through on-farm cultivation. A market for traditional variety seed is hard to detect in our survey. Table 6.4 shows that just over a third (35.4%) of the households purchased any wheat seed and even fewer (11.2%) borrowed seed. The bulk of seed that is sold and bought locally is seed of MVs.

Table 6.5. Variety attributes by household type.

		Attribute*				
Household type	*n*	Yield	Drought resistance	Disease resistance	Baking quality	Taste
All	352	2.13 (0.87)	2.24 (1.07)	1.86 (0.87)	1.93 (0.87)	1.86 (0.78)
Modern varieties	133	1.73 (0.67)	2.72 (1.02)	1.97 (0.81)	2.22 (0.92)	2.15 (0.81)
Traditional varieties	219	2.37 (0.89)	1.95 (1.00)	1.79 (0.90)	1.75 (0.79)	1.69 (0.72)

*1 = best quality, 5 = worst quality.

Traditional varieties are often attributed with more attractive characteristics than MVs. An examination of household rankings of specific attributes on a scale from 1 (best quality) to 5 (worst quality) from the Turkish survey data sheds light on the association of these characteristics with individual varieties. Households ranked each variety cultivated with respect to taste, bread quality, milling quality, yield, disease resistance and drought resistance. These characteristics reflect important considerations for the household on both the production and consumption side. Table 6.5 presents the average scores among all households of five characteristics for both traditional and modern varieties. In general, yield attributes are ranked higher for MVs while traditional varieties are ranked higher in terms of taste and baking quality. Traditional varieties also appear to be associated with better drought resistance.

Unfortunately, information is not available from individual households ranking the characteristics of the available varieties against each other. However, particularly for households that cultivate only one variety, it is reasonable to assume that the qualities most characteristic of the chosen variety are the ones that the household considers the most important relative to other varietal traits. Data on varietal rankings from households that did not grow the variety are likewise unavailable. Nevertheless, we are able to examine the rankings assigned to modern and traditional varieties by the subsample of 71 households cultivating both types of varieties. As shown in Table 6.6, households that grow both modern and traditional wheat varieties exhibit no marked differences relative to other households in the sample with respect to variables such as age and education of household head, number of household members or total land in wheat. The number of household plots, distance to market and percentage of households baking bread at home for these households, however, fall outside the range found for other household types. The attribute rankings for the households cultivating both modern and traditional varieties that are presented in Table 6.7 exhibit a pattern of rankings similar to that of the other households in the sample.

Additional information on the relative importance of varietal attributes comes from the responses given by households regarding their reasons for discarding a previously cultivated variety. Table 6.8 gives similar information for

Table 6.6. Selected household characteristics by household types.

Household type (by type of variety cultivated)	*n*	Total land (ha)	Total wheat land	Total irrigated land	No. of household plots	Home bread (% households)	Livestock (no.)	Market distance (km)	No. in household	No. of varieties	Age	Education (years)
Both varieties	71	15.7	9.6	5.9	23.8	75.7	3.8	14.6	5.9	2.3	48.6	4.6
		(16.2)	(11.3)	(6.7)	(21.3)	(43.2)	(2.8)	(7.7)	(2.2)	(0.9)	(11.2)	(1.7)
All households	285	12.1	7.3	4.0	16.5	88.5	3.7	16.6	5.9	1.6	49.1	4.1
		(12.7)	(10.4)	(5.0)	(16.6)	(32.0)	(3.7)	(7.9)	(2.6)	(0.8)	(11.9)	(2.3)
Only modern varieties	63	15.6	12.4	3.6	16.0	84.7	4.7	17.7	5.8	1.7	47.1	3.9
		(14.6)	(15.9)	(5.5)	(17.5)	(36.3)	(6.3)	(7.7)	(2.8)	(0.9)	(11.9)	(2.2)
Only traditional varieties	147	8.9	4.0	3.1	13.2	95.9	3.3	16.9	6.0	1.2	50.1	3.6
		(8.6)	(3.8)	(3.1)	(12.3)	(20.0)	(2.2)	(7.7)	(2.7)	(0.4)	(12.2)	(2.4)

Table 6.7. Attribute rankings for households growing both variety types.

		Attribute				
Variety type	*n*	Yield	Drought resistance	Disease resistance	Baking quality	Taste
Modern varieties	71	1.65 (0.61)	2.78 (0.89)	2.17 (0.88)	2.35 (0.96)	2.29 (0.88)
Traditional varieties	71	2.71 (0.85)	1.71 (0.82)	1.74 (0.93)	1.96 (0.89)	1.76 (0.78)

Table 6.8. Reasons given for ending cultivation of traditional varieties.

	All households responding (*n* = 163/285)		Households cultivating MVs (*n* = 88/118)	
Reason	No.	Percent	No.	Percent
Yield	124	38.8	78	38.8
Cold susceptibility	38	11.9	20	10.0
Production-related	27	8.4	16	8.0
Quality problems	26	8.1	6	3.0
Drought susceptibility	24	7.5	20	10.0
Lodging	23	7.2	21	10.4
Other	18	5.6	14	7.0
Seed availability	16	5.0	10	5.0
Marketing problems	12	3.8	9	4.5
Disease susceptibility	5	1.6	1	0.5
Price	4	1.3	4	2.0
Climate adaptability	2	0.6	1	0.5
Soil adaptability	1	0.3	1	0.5
Total responses	320	100	201	100

all households that have given up the cultivation of traditional varieties and also for those households that continue to grow MVs and have recently discarded a traditional variety. Yield is the most frequent reason given for their decisions. Quality-related reasons decrease sharply between the sample of all responding households and the subsample of households that currently cultivate MVs. These findings suggest that quality issues are no longer of great importance for those households that have given up traditional varieties. Table 6.9 presents the reasons provided for opting against the cultivation of MVs. Two sets of responses are presented: firstly, for all households responding to the question, and secondly, for those households that continue to cultivate traditional varieties and have given up the cultivation of a MV. Again, yield remains the most important reason in both cases, but different reasons may pertain here than for those households that listed yield as the primary reason for giving up a traditional

Table 6.9. Reasons given for ending cultivation of modern varieties.

	All households responding (*n* = 100/285)		Households cultivating traditional varieties (*n* = 54/217)	
Reason	No.	Percent	No.	Percent
Yield	43	25.4	22	25.9
Drought susceptibility	26	15.4	19	22.4
Production-related	20	11.8	7	8.2
Quality problems	14	8.3	10	11.8
Disease susceptibility	13	7.7	1	1.2
Seed availability	12	7.1	3	3.5
Cold susceptibility	10	5.9	10	11.8
Price	10	5.9	3	3.5
Other	9	5.3	4	4.7
Lodging	4	2.4	1	1.2
Climate adaptability	4	2.4	4	4.7
Soil adaptability	4	2.4	1	1.2
Marketing problems	0	0.0	0	0.0
Total responses	169	100	85	100

variety. For MVs, it is more likely that the yield response reflects a failure to attain expected yield. In addition. the percentage of households listing quality and drought resistance as reasons for giving up MVs increases for the subsample of households that continue to grow traditional varieties. These results further suggest that influence of both consumption demand and environmental constraints in variety choice and the advantages of consumption quality and adaptability to climate hardships associated with landraces.

An understanding of farm households' perspectives about landraces is relevant for the effective design, implementation and cost estimation of *in situ* conservation. Information about varietal selection is useful in identifying households that value landraces the most, those likely to carry on *de facto* conservation, and the ones least costly to incorporate into conservation programmes. Socio-economic surveys can link the probability of cultivating certain varieties or types (e.g. traditional or modern) with the household costs of production and the profitability of different varieties. In combination with genetic assessment, these surveys provide a way of determining the most cost-effective way to conserve diversity in an agro-ecosystem. Given the difficulty of estimating the total benefit of landrace conservation to society, this cost-side approach provides a method for estimating the cost of *in situ* conservation of landraces. The costs of such a conservation programme depend largely on the scope of the programme – the number of landraces targeted, the area needed to conserve these, and the number of households deemed necessary to maintain these in cultivation. While cost estimation does not necessarily require specific knowledge of how households value landraces, this knowledge can be helpful in reducing costs.

The Cost of On-farm Conservation

As long as farmers continue to select landraces for cultivation, the *in situ* conservation that we currently observe will continue, and it is possible that the establishment of a formal *in situ* programme might not be necessary. In this scenario, an estimate of the value of the resources to the farm households could instead provide a basis for responding to demands for farmers' rights and for the acknowledgement of the roles of farmers in the conservation process rather than them being used as a mechanism to ensure cultivation. However, if the continued cultivation of landraces appears uncertain and if on-site maintenance of a specific target level of diversity is indeed a stated objective, then information on valuation or some other method ranking the landraces from the viewpoint of the farm household could provide crucial information towards estimating the cost of policies to guarantee their existence in the future.

The cost of *in situ* conservation is the cost of assisting the necessary number of farms in key farming systems to maintain local resources and knowledge in order to maintain the crop evolutionary system of the centre of agricultural biodiversity. It is difficult to estimate the cost because of uncertainties regarding the social and biological status of farming systems and prerequisites for maintaining crop evolutionary systems in some semblance of their natural or historic order. The goal of *in situ* conservation is not to preserve a given number of alleles or genotypes (i.e. diversity *per se*) but to maintain an agricultural system which generates crop genetic resistance in a manner similar to the historic system. An object of *in situ* conservation should be to locate sites to represent a sample of the general ecogeographics zones of the crop in its centre of origin. The lower bounds of such a programme are not known and are probably both crop- and region-specific.

Both biological and socioeconomic data are important for estimating costs of *in situ* conservation. The dimensions, composition and distribution of landrace populations needed to maintain a crop's evolutionary system comprise the biological data. Obtaining and analysing this type of data for farming systems is likely to be as problematic for agricultural scientists as it has been for biogeographers and ecologists of 'natural' populations (MacArthur and Wilson, 1967; Tilman and Pacala,1993). A starting point is to identify major ecogeographic patterns of crop populations, but the conservation biology of crops needs to address finer spatial levels. In Turkey, for instance, geographers conventionally divide the country into nine major agricultural zones. It is, therefore, possible to imagine *in situ* conservation of wheat in Turkey as requiring nine or more locales, depending on the heterogeneity of wheat within each of the nine zones. The number of farms involved in on-farm conservation depends on the degree of diversity that is found within crop populations at various levels (e.g. farms, villages, micro-region, etc.) as opposed to between populations. The exchange of seed between farms and communities is also an important factor to consider. The number of farms necessary to support *in situ* conservation may be relatively small if most of the diversity at a single location is found within the individual farm store.

On the socioeconomic side, information on any future comparative disadvantages, if any, for a farm household that selects landraces over MVs, other crops, or economic pursuits, is necessary to estimate the costs of *in situ* conservation. The pressures against landraces may include lower unit costs of production, broad resistance of MVs, and commercial and official factors which favour MVs. How disadvantageous are landraces? Currently, for those farmers selecting them, they are not disadvantageous; on the contrary, landraces are the optimal choice given the multiple criteria used in the varietal selection process. Yield is certainly a primary consideration, but it is only one of several. Bellon (1996) describes how farmers' concerns are met by infraspecific diversity within a crop. He cites five general concerns, environmental heterogeneity, pests and pathogens, risk management, culture and ritual, and diet, which are met by infraspecific diversity. Bellon (1996) details specific concerns which explain the persistence of maize landraces in Chiapas, Mexico: drought, lodging, uneven (poor) soils, labour availability, fertilizer availability, yield, storage, use and taste. These concerns can be satisfied in other ways, for instance by purchased inputs (e.g. irrigation, fertilizer, pesticides), but markets in peasant agricultural systems are often unreliable or too costly to change household production strategies (de Janvry *et al*., 1991). The conclusion from Bellon's and other research (Brush, 1995) is that landraces occupy specific niches in peasant economies and that these niches are difficult to close altogether. Environmental heterogeneity and high household transaction costs for substituting market goods and services for those provided by landraces are important factors in the observed inertia of peasant cultivators who keep selecting landraces.

Currently, there are no costs to bear for *in situ* conservation in centres of diversity such as Turkey and Mexico because numerous farmers continue to plant landraces, a form of *de facto* on-farm conservation. Wheat landraces are reported in eight out of nine major agricultural zones in Turkey, with Thrace being the single exception. This *de facto* conservation could be eliminated if all farmers chose to stop planting landraces or if sufficient numbers stopped, making seed supplies of traditional varieties all but impossible to obtain. However, this scenario depends on investment to create viable substitutions for landraces for the households that now rely on them. These investments include crop breeding for the marginal areas where landraces persist, improving the physical infrastructure such as irrigation, and improving the market infrastructure so as to lower the transaction costs of households. There is also a threat to landraces from farmers shifting out of staple crops or exiting from crop production altogether.

These scenarios for the replacement of landraces appear unrealistic. At present, many of the farmers who cultivate landraces are minimally affected by crop improvement programmes, largely because they till small parcels of land for home consumption in marginal agroeconomic zones. This farm sector can be reached by agricultural development, but most national agricultural research programmes in countries with important genetic resources, including Turkey, lack the means to accomplish this. Public investment historically favours prime production zones rather than marginal ones, and the costs to upgrade the physical and market infrastructure in these marginal and heterogeneous agro-ecosystems are relatively high. At a local level, peasants may have multiple and different reasons for keeping landraces.

Both aggregate and local factors serve to maintain landraces, as much as the pressures of population, technology and market favour their replacement. The future of landraces may depend on relatively small advantages, rather than the strong yield advantages seemingly offered by MVs. Consequently, a relatively small investment in landraces may suffice to maintain their advantage in a particular farming system. The cost of *in situ* conservation can thus alternatively be expressed as the cost necessary to raise the comparative advantage of landraces above that of competing varieties, crops or off-farm activities. This cost may require a subsidy to one agricultural sector (e.g. producers of landraces in selected regions) but it need not be a direct payment to farmers. Indirect methods are arguably more sustainable for meeting long-term conservation and agricultural development goals.

Conclusions

A puzzle of biological diversity is why numerous species persist in the same habitat. Tilman and Pacala (1993) observe that multiple species are found in places where two or more environmental factors are binding constraints and where unavoidable trade-offs exist among the responses to these constraints. Our research on the wheat agro-ecosystem in Turkey suggests that similar principles hold. Numerous environmental factors constrain the fitness of a particular wheat variety (e.g. soil, water availability and altitude), and farmers appear to confront unavoidable trade-offs as they select for one trait (e.g. yield, stability of yield, taste). Variety selection involves a complex interaction of factors at several levels (plot, household, region, nation), but our analysis suggests a positive outlook for the maintenance of landraces in Turkish agriculture. Turkey may alter its wheat breeding and promotion programmes to achieve a greater effect in marginal agro-economic zones where landraces prevail, but improving yield, reducing yield variance, and meeting quality expectations is a daunting and expensive task with uncertain returns for public investment.

The private value of landraces for farmers remains positive, leading to their continued cultivation in many places in the world. The social value of landraces is also positive, because of their contribution to the pool of genetic resources. Moreover, local knowledge about landraces and their production in centres of crop origins and evolution has positive social value because of its use to crop breeders and agricultural scientists in the formal sector. Although a high percentage of the genetic diversity of landraces of major crops is reported in *ex situ* collections, landraces and the knowledge and production practices associated with them continue to possess *in situ* value. This value derives from the landraces, both as a source of new diversity and for new collection, should there be a failure in the *ex situ* system. For science, peasant farming systems with landraces in centres of crop origins are an important crop evolutionary laboratory. Investing in on-farm conservation to maintain the comparative advantage of landraces in selected areas is a way to integrate the private and social values of landraces. The future of landraces is unknown, but we currently have the opportunity to understand the biological and social dynamics of these crop populations, to forecast the demise of landraces, and to devise methods to increase their private value.

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Part III

Empirical Studies: Breeding Values

7

Maize Breeding and Genetic Resources*

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The environment is subject to increased pressures that endanger the sustainability of life. Rapid growth in human populations, poverty and inefficient agriculture all contribute to the endangerment of sustainable biological cycles that are essential in order to maintain quality of life.

The uncertainties about the very origins and foundation of human civilization illuminate two enduring and fundamental truths. First, agriculture requires more effort per unit area to produce food than did the previous practice of hunting and gathering. Also, increased planning and management of the environment is needed for food production to be successful. Second, agriculture is the fundamental activity upon which all society depends for its industry, lifestyle and economic well-being.

A second agricultural revolution began in the mid-17th century in Europe. During this and the next century, new arable rotations, new crops (potato, maize, marigolds, sugar beet, coleseed), and new seed drills, hoes and ploughs were introduced. The 18th and 19th centuries witnessed the use of improved fertilizers and mechanization.

The effective improvement of yield by plant breeding came late during this revolution. However, as early as 1813 John Loraine presented a paper on maize in Philadelphia that presaged future events by more than a century: ‘The pollen is wafted far by high winds ... (and) ... if nature be judiciously directed by art, such mixtures as are best suited for the purpose of farmers, in every climate in this country where corn is grown, may be introduced’. Anderson and Brown

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Agricultural Values of Plant Genetic Resources (eds R.E. Evenson, D. Gollin and V. Santaniello)

(1952) have commented upon the activities of farmer–breeders in the latter half of the 19th century as they continued to develop open-pollinated varieties of maize: 'The controlled breeding of new varieties by farmers themselves was more frequent than anyone would believe who has not looked into the record. ... We have been struck by the high proportion ... who began their work by deliberate crossing of two or more varieties. Some had highly elaborate methods of selection'.

Maize, with a global harvest in 1994 of 467 Mt from 128 Mha, ranked second to wheat among the world's cereal crops (USDA, 1995). Some 70 countries produce maize on 100 kha or more; 53 of these are developing countries that contributed in production with 40% of the global harvest. Worldwide, about 25% of all maize is used for human consumption, 66% for feeding livestock and 9% for industrial purposes and as seed. In the developing world, however, roughly 50% of all maize is consumed by humans as a direct food source, 43% is for livestock feed, and the 7% for industrial and seed purposes. The most accessible resource to improve maize is the utilization of their genetic resources. However genetic erosion is happening rapidly, reducing the biodiversity, the pillar for survival.

Very little attention was put in genetic resources through the years, and this is indicated by the approximately $55 million that was spent worldwide on plant genetic resources work in 1982. In order to carry out conservation, evaluation and utilization of genetic resources the work must be coordinated, and joint action between national, international and private industries is needed. It also needs enough financial support from governments and donors along with the commitment to carry the process through the utilization; which demonstrates practically the importance of the genetic resources.

The Bases of Achieving Improved Agricultural Productivity Through Plant Breeding

The term 'genetic diversity' is in common parlance. However, for genetic diversity to be useful in plant breeding to serve farmers and consumers, it must encompass genetic variability that is not present in the materials with which breeders are currently working. It is necessary to have new sources of germplasm for present and future uses since environmental conditions, disease pressure, technologies and demands from the farmer and consumer are constantly changing. New sources of germplasm must have yield potential with other useful traits so that breeders can be encouraged to use sources of new genetic diversity.

Despite their best efforts, by the late 1920s, farm breeders in the US had not been able to raise average maize yields above 1880 kg ha^{-1} (30 bushels per acre). Plants remained very susceptible to heat and drought stress, and ravages by pests and diseases continued to be disastrous. As a result of research and practical experience gained by breeders from the early part of the 20th century, yield gains for maize increased to 3136 kg ha^{-1} during 1930–1960, due to the use of double-cross hybrids. The rate of yield gain due to genetic change alone tripled again after 1960, due to the utilization of single-cross hybrids. These yield gains are due solely to plant breeders achieving increased managerial control over germplasm-producing hybrids. Effective plant breeding requires vastly more effort to improve crop yields than mass selection and seed saving which are the strategies of informal breeders.

Modern corn agriculture in the US uses hybrids from a cross of two inbred lines, which gives the current average yield of about 8152 kg ha^{-1} (130 bushels per acre). The improvement in yield is due to years of selection by breeders to improve agronomic characteristics such as: reducing plant height, selection of the plants to stay alive until maturity, improvements in stalk and root lodging, selection for upright habit, tolerance to European corn borer, and greater stress tolerance that allows consistent yields at high plant densities.

The history of plant breeding is one of a continual increase in the range and capabilities of techniques that have come from basic and applied research in genetics, physiology, statistics, molecular biology, etc. Plant breeding exemplifies the continuing adaptation by humans to meet the increasing food needs of growing populations. And like the first agricultural revolution some years ago, which demanded more effort per unit area to provide more food, successful and sustainable plant breeding requires yet more effort to increase food production.

The bases for successful and sustainable progress in plant breeding are: (i) the ability to find useful genetics affecting traits of agricultural importance; and (ii) the ability to recombine genetics favourably affecting agronomic traits into new varieties that are overall better adapted to the target environment of the farmer and the demands of the consumer or processor.

Key resources that are necessary to achieve these objectives are:

- available sources of useful genetic diversity;
- adequate knowledge of these genetic resources to facilitate sourcing of useful germplasm;
- adequate availability of technologies and skills to enable sourcing, manipulation and effective transference of germplasm from exotic sources into adapted and improved varieties;
- adequate knowledge of customer needs and target environment;
- adequate funding to support the relatively long-term programmes of research and product development that are required in plant breeding (10–15 years) and in effective sourcing of exotic genetic diversity (15–25 years).

Sources of Useful Germplasm

Latin American countries are a very important source of maize for gene banks since the crop originated in this area. The largest germplasm accessions are in

INIFAP in Mexico and ICA in Colombia. The germplasm bank in Mexico is holding accessions from Mexico, Central America and the Caribbean; some of the foreign accessions are not duplicated in any other germplasm bank. Colombia is holding accessions from Colombia, the Caribbean and South America; again some of the foreign accessions are not duplicated in other gene banks. The other Latin American countries are holding the germplasms that was collected in their own country. The concern is that the equipment for these cold storage facilities is very old, and since a large number of these accessions are not duplicated in another storage facility, they could be lost forever.

Under the support of International Plant Genetic Resources Institute (IPGRI), new accessions were collected in several countries of Central and South America. In most of the countries the number of accessions collected is known, but there are a few that are unknown.

According to the reports presented by the maize curators of Latin American countries (CIMMYT, 1988) the total number of accessions held in these gene banks is 31,159. The number of duplicate accessions is 3996, so the total number of unique accessions is 27,163.

More than 27,000 accessions exist in the germplasm bank of America, classified into about 250 races, with some overlap (Goodman, 1983; Goodman and Brown, 1988). Most recent estimates following critical re-examination of morphological, cytogenetic and molecular marker data are that maize germplasm of the western hemisphere can be classified into about 130 racial complexes.

In areas below 1800 m of elevation, some examples of non-native usage of maize germplasm are: Bolivia is using Caribbean material; Brazil is using Cateto, Tuxpeno and Caribbean germplasm; Colombia is using Tuxpeno, Caribbean Flints and ETO; Mexico, Central America and the Caribbean area form their hybrids on the basis of Tuxpeno, ETO, Cuban Flint and Coastal Tropical Flint; Paraguay is using Caribbean germplasm; Peru based its hybrids on crosses between Perla (the formerly predominant flint variety) and the exotic Caribbean flint–dent complex; Venezuela is successfully working the Tuxpeno × ETO, in addition to the formation of native varieties (Salhuana, 1995).

In contrast, Goodman (1985) estimated that only 1% of the genetic material in US commercial hybrids traced to exotic sources. ‘Fewer races have been identified in the United States and many of the open-pollinated varieties that constituted the Corn Belt Dents were discarded during the first half of this century before it became apparent that they might still harbor useful germplasm for future corn improvement’. However, the origin of the Corn Belt Dents from two races (the Southern Dents and Northern Flints), which differ genetically very significantly (Doebley *et al*., 1988), resulted in the Corn Belt Dents encompassing a broad range of genetic diversity. Furthermore, some, perhaps much, of the genetic diversity that was present in the open-pollinated varieties was carried into numerous private and public breeding programmes. This diversity is now sequestered in breeders stocks and is pyramided into new, more productive varieties.

The Challenges Associated with Exotic Germplasm

The approach of using new germplasm, especially exotic germplasm, depends on the current yield level. If this is low, any introduction of exotic germplasm will permit increases in the yield in a more rapid way than if a higher yielding material is currently in use; if the current yield is high it will take a longer time to beat this yield.

Corn breeders working in the US during the 1920s and 1930s tried with extreme patience and hard work to source useful genetics from open-pollinated varieties. However, the relatively poor performance of those open-pollinated varieties, compared with the first cycle inbred lines that were derived from those varieties, forced breeders to concentrate their further efforts upon pedigree breeding and population improvement using inbred lines. Breeders are under pressure to create new varieties with improved performance and to do this they must have useful sources of diversity. Breeders could not devote their time to making slower improvements with landraces or in focusing their efforts to conserve genetic diversity from the landraces. The imperative was to make progress in improving agronomic performance in order to provide farmers with better yields and the nation with a more secure food supply and an improved economy. In order to achieve these objectives, inbred lines that were bred from the landraces became the parents of new breeding populations. In cases where the actual yield level is high, the line derived using exotic germplasm will be used only for breeding crosses, at least in the first cycle, and not as a parental line for a commercial hybrid.

The presence of genetic diversity *per se* is no guarantee that there will be useful genetic diversity for specific traits of interest. Many US maize landraces were heterogeneous but were highly susceptible to insect attack (Holbert *et al.*, 1935; Patch *et al.*, 1941) and rapidly went barren under heat or drought stress (Baker, 1984). Reid (1990) found that several ancient indigenous and pre-Colombian exotic races of maize lack resistance to European corn borer. Teosinte, the presumed wild ancestor of maize, was also found to have low levels of resistance to tunnelling insects. Consequently, germplasm must be thoroughly characterized before potentially useful germplasm can be identified. Once useful germplasm is identified, it still requires many years of pre-breeding or genetic enhancement to recombine those exotic genetics so that they can then be integrated into a productive breeding programme that releases commercially successful varieties for agriculture.

The problems that breeders face in working with exotic germplasm are manyfold and substantial. They include:

- most accessions are not useful;
- most of the landrace germplasm does not have good agronomic characteristics;
- few data exist to select those accessions that might be useful;

- exotic germplasm has linkage groups that are unadapted to other environments; several generations of pre-breeding are required to recombine improved adapted linkages;
- exotic germplasm is photoperiod sensitive and consequently maladapted for evaluation in most agronomically productive temperate regions;
- the improvement of landraces lags behind current elite breeding programmes;
- a long-term persistent effort of 15–25 years or more is required from the initial selection of a landrace and the inclusion of a portion of its germplasm into a commercial variety.

Genetic Resources for Maize Breeding

Increments to food demands and the need to use land, air and water resources more sustainably make it necessary to evaluate germplasm to find new sources that can contribute to those demands. It is a fervent wish that all countries will contribute to this effort so that world hunger may be eliminated.

In order to accomplish this difficult task it will be necessary to obtain accessions with passport data that have enough quantity and quality of seed so the germplasm is evaluated and selected, the selected germplasm is submitted to a process of enhancement and after that the best material may be included in a research programme for breeding and product development. If we only continue to add collections into gene banks and maintain their viability without having even a minimum level of evaluation information on the material, then the collections will, for the majority, continue as unused stocks of seed.

On a global basis, the need is to get, in addition to increased yield, new unique traits that will improve the uses of corn for food. Since there is more demand to improve environmental conditions, some reductions in chemical inputs may be necessary, and this will be only possible if new genes are found that decrease the demand for these products. Also, many soils in the world have aluminium toxicity, so it would be convenient to find some genes that will contribute to tolerance of this stress. We could also find genes for heat and drought tolerance; likewise for cold. Improving kernel quality through increased protein, oil and starch would be beneficial. These are some of the examples in which the maize genetic resources can contribute and be used.

These are neither easy nor rapidly completed tasks. Great amounts of time, effort and patience are required. Decades of regeneration, adaptation, evaluation and pre-breeding are needed to work with just a handful of the many populations that are stored in gene banks or that are utilized in agriculture as landraces or local varieties that are exotic to other regions. However, these efforts are critically important so that germplasm resources can be more effectively and widely available through breeders to the world’s farmers.

Regeneration

This task is very difficult to implement for one institution since it is necessary to have several environmental conditions, land space, personnel, storage facilities, etc., to do so. Success will require the implementation of a well-coordinated plan with partnerships between national and international programmes to enhance the capacity of these programmes to conserve and regenerate vulnerable *ex situ* collections.

The selection of an environment for the regeneration of seed that corresponds to the site at which the collection was obtained is crucial. This practice lessens the possibility of natural and artificial selection and increases the amount of seed. Due to differences in environmental conditions in which maize is grown (especially altitude and latitude) and poor adaptability of accessions when they are planted in locations that are not similar to the original conditions, it is necessary that joint actions be taken in order to ensure that the correct climatic conditions are achieved for regeneration. There are few countries that have all the environmental conditions required for regeneration of accessions. Passport information will help in selecting the best locations for regeneration. It is advisable to perform preliminary adaptation tests, with a few collections representative of the races, in several locations that have been chosen for regeneration.

Phytosanitary regulations make it difficult to exchange germplasm for any purpose. These regulations need to be followed and respected, but it will be necessary to provide flexibility to allow cooperative regeneration projects to occur. The location in which the activity is going to take place can act as a quarantine site that can be visited any time by the inspectors. If any symptoms of disease appear, the plants will be eliminated.

Recognizing that regeneration is one of the most important activities in preserving genetic resources, one seed company, US Department of Agriculture Agricultural Research Service (USDA/ARS), CIMMYT and North Carolina State University are collaborating in projects to regenerate accessions that might otherwise be lost.

Evaluation

Evaluation of maize global genetic resources is critical to determining which germplasm to use in the programme. In order to do this, it is necessary to exchange landrace germplasm freely. It is important to exchange germplasm since there are many examples to demonstrate that foreign germplasm is better than native genetic resources.

Very little effort has been taken in evaluation, yet this is one of the most important activities in the eventual utilization of genetic resources. Lack of knowledge for certain agronomic characteristics has made many accessions practically unusable.

In 1987 Pioneer Hi-Bred International, recognizing that the preservation, documentation, distribution, evaluation and utilization of accessions in the different germplasm banks must be done through coordinated efforts among the different national and international organizations involved, provided $1.5 million to the USDA/ARS to carry out a 5-year maize evaluation project. This effort was named the Latin American Maize Project (LAMP), and was the first coordinated international project to deal with the evaluation of genetic resources of a major world crop species. LAMP was based on the cooperative effort of 12 countries: Argentina, Bolivia, Brazil, Colombia, Chile, Guatemala, Mexico, Paraguay, Peru, the US, Uruguay and Venezuela. The main objective of LAMP was to evaluate the agronomic characteristics of over 14,000 accessions found in Latin American and US germplasm banks so they might then be used in breeding programmes (Salhuana *et al.*, 1991).

LAMP established a five-stage evaluation sequence. The first two stages were for reducing the number of accessions to a feasible number in order to cross them with testers to determine combining ability. In the second stage, 270 accessions were selected as follows: 100 tropical accessions were selected in homologous area 1, 78 temperate accessions in homologous area 5, and 92 in homologous areas 2, 3 and 4. In the third stage, the selected material was interchanged between countries in order to cross with the chosen tester. In stage 4, test-crosses, check hybrids, and varieties were planted in replicated trials in each of the homologous areas and data were recorded for 17 traits including yield (Salhuana and Sevilla, 1995).

As a consequence of LAMP, there now exists a more precise determination of the status of maize stored in germplasm banks in Latin America with respect to: (i) the number of accessions in each gene bank; (ii) the quantity and quality of seed for each accession; (iii) the identification of accessions that need regeneration; (iv) the adaptability of the accessions and races to permit a more thorough and effective exchange of germplasm between regions.

Germplasm Enhancement

Useful principles and methodologies for enhancing germplasm to improve its performance have been outlined by Eberhart *et al.* (1995).

Most of the LAMP germplasm is unadapted to exotic locations and requires enhancement in a long-term approach of conversion and selective adaptation by corn breeders at numerous environments throughout the major corn growing regions of the US. The total process is too large and long-term for public or private institutions to accomplish individually, so it will be more convenient if it is done as a joint effort among several cooperators. Throughout many years of investigations, seed companies have developed inbred lines and hybrids that have demonstrated an increase in maize productivity. Possibly the most productive maize germplasm in the world is now found in these lines and hybrids. For the LAMP material to be more useful it was important for the accessions to be crossed with commercial proprietary inbred lines.

An unprecedented public/private research effort to broaden the genetic diversity of US corn hybrids using enhanced maize germplasm derived from selected LAMP accessions has been initiated as the US Germplasm Enhancement Maize Project (US GEM Project; Salhuana *et al.*, 1994). This is a unique example of collaboration in which 19 public entities and 21 private seed companies are working together with the objective of increasing the productivity and genetic diversity of maize grown in the US.

The companies have made crosses of the LAMP material with their proprietary inbred lines. Their collaboration was incremented by providing in-kind support to allow the necessary replication, nurseries, winter nurseries and environments for selective adaptation. The accessions have been crossed with proprietary inbred lines, and they have been crossed to a second inbred line of another company in order to develop 75% temperate material to give it higher yield potential, improve its agronomic characteristics, and give the added adaptability needed for further breeding. The breeding crosses with 50% and 75% temperate material were crossed to tester inbred lines and placed in yield tests in order to identify the breeding cross from which to start the final selection process.

The stronger disease resistance coming from the exotic germplasm can be maintained and overall agronomic performance can be improved still further by crossing the exotic derived lines once more with temperate germplasm before starting the final selection and breeding process.

Use of Biotechnology in the Activities of Genetic Resource

New capabilities to introduce very exotic genetics are increasingly becoming available from biotechnology. For example, unique flower colours can be created in petunias through genetic engineering (Oud *et al.*, 1995), and insect resistance genes from the bacterium *Bacillus thuringiensis* can be introduced into crop plants. Transformation technologies now make it easier to transfer genes for insect resistance from a bacterium into maize than it is to transfer genes from *Tripsacum* into maize. Transformation technologies also make it much easier to transfer genes into maize from other genera than it is to transfer useful genetics from teosinte, which appears to be the closest wild relative of maize, through crossing and repeated backcrossing. Conventional procedures impose 3–7 years of additional time and effort to segregate and recombine out genes and linkage blocks that would otherwise render the genotype poorly adapted to agriculture. For the same reasons of expediency, transformation, once genes have been cloned, could in the future be preferred for the transfer of certain genes from exotic races of maize into better adapted varieties. Improved knowledge of genotype and its relation to physiology coupled with abilities to alter gene expression could allow breeders capabilities to improve agronomic performance even without the need to source new genetic diversity. For example, Frankel *et al.* (1995) predict that synthetic resistance genes are ‘likely to be developed for a range of pathogens ... [and] will gradually reduce the need for resistance derived from traditional genetic resources'. However, it is critical to realize that most important traits in agriculture are controlled by many genes of individual small effects. For the foreseeable future most useful genetic diversity will be found in the crop species itself. Advances in biotechnology can help to source and utilize this diversity more effectively.

Pioneer Hi-Bred International, in collaboration with other members of private industry (Linkage Genetics and Applied Biosystems), and with the public sector (Brookhaven National Laboratory, and the United States Department of Agriculture Agricultural Research Service at Raleigh, North Carolina, and Griffin, Georgia) have developed a set of primers that will allow amplification of microsatellite or simple sequence repeat (SSR) molecular markers for maize. Primer sequences will be made publicly available to the global community and cost effective assays will be investigated that could, for the first time, make DNA-based codominant molecular marker technology a practical means of characterizing diversity in heterogeneous landraces whether they reside *in situ* or *ex situ*. Characterization of maize landraces using some of these SSRs is now being use at the USDA Plant Introduction Station at Ames, Iowa. These SSRs will also be investigated by researchers at CIMMYT.

Biotechnology can contribute in at least two broad areas in plant breeding. Genetic markers can identify important genes or chromosome regions and genetic transformation can move potentially useful exotic genes into varieties.

Conclusions

Economic Returns from Genetic Resources

The importance of genetic resources will be easier to demonstrate when economic payoffs ensue from safeguarding those resources that are the product of several thousands of years of evolution and human experimentation. This is very difficult to demonstrate, since precise information about the use of genetic resources does not exist. We can cite some examples of the use of maize genetic resources.

Around 20–30 broadly based improved synthetic populations are widely dispersed around the tropics and increasingly contribute to production as varieties or as parents of inbreds (Timothy *et al.*, 1988). Thailand developed a very well distributed population of Suwan-1 (Sriwatanapongse *et al.*, 1992). Colombia formed the widespread ETO synthetic. Other important varieties that are used in the tropics are Tuxpeno, Ecuador 573, and Coastal Tropical Flint and Dent. The economic impact that these varieties have in the different countries has been difficult to measure.

In the US, the effective utilization of new germplasm is more challenging due to existing high levels of yield and the different environmental conditions to which exotic corn is not adapted, especially those due to photoperiod effect. However there are some examples that can be mentioned. Goodman (1993) made excellent progress in adapting tropical maize to grow in the more southerly area of the US. Salhuana (personal communication) developed many inbred lines adapted to the south of the US, and one particularly adapted to Iowa, from one tropical population. These lines are now being using in breeding programmes. In the decade study of Duvick (personal communication), the number of landraces utilized in the five most important inbreds have increased from five in 1930 and 1940 to nine in 1950, 11 in 1960 and 1970, 23 in 1980, and 27 in 1990. There are several examples of utilization of landraces for disease and insect resistance. Also there are good efforts between EMBRAPA (Empresa Brasiliera de Pesquisa Agropecuaria) and CIMMYT to develop maize tolerant to soils containing toxic levels of aluminium.

Biological realities mean that unevaluated and unadapted exotic germplasm will usually have little to no economic worth to a plant breeder or farmer, and that any programmes to source and utilize exotic germplasm will have to compete for resources with other long-term and more basic research programmes. Many breeders will simply not have the resources to devote to such long-term and high risk programmes of research and product development.

Given the long-term and high risk nature of working with exotic germplasm, it is extremely difficult to put economic values upon exotic accessions. However, our long-term survival, together with that of the environment in which we live, is critically dependent upon successfully sourcing and utilizing useful genetic diversity.

Challenges and Future Tasks

The immediate challenges must, therefore, be: (i) to securely conserve genetic diversity; (ii) to characterize genetic diversity; (iii) to evaluate genetic diversity in pre-breeding and enhancement programmes more completely; (iv) to provide resources to accomplish these tasks; (v) to develop and apply new biotechnologies to improve the effectiveness of germplasm conservation, evaluation, and utilization; (vi) to continue to improve the efficiency of agriculture and its degree of harmony with the environment by successful plant breeding.

Perhaps the major challenges will be to accomplish the tasks relating to conservation, evaluation and germplasm enhancement of exotic germplasm in a world where immediate needs for improvement in agricultural production and restraints upon funding are present, and where heated debates are occurring concerning equities and responsibilities among nations in a world that is increasingly globalized, but fractured economically and technologically. To carry out this difficult task it is necessary to have joint efforts to allow more complete evaluation and enhancement of germplasm. Otherwise, the germplasm will languish unused and without prospects of benefits to be derived to anyone, be they breeders, farmers or consumers; and it is to consumers that the most benefits of improved agricultural productivity flow. We must strive by working within the FAO, the Convention on Biological Diversity, within national governments, and within private industry to ensure that funds are provided and programmes can be developed including both the public and private sectors, nationally and internationally, that will enable increased access, evaluation and effective sourcing of a broader base of germplasm. Plant breeding programmes will then be in a better position to serve the needs of agriculture and the environment. There are roles for every participant to play.

Use of Biotechnology in Genetic Resources

Biotechnology can operate at three basic levels of complexity in plant improvement: (i) introduction of a foreign gene that is expressed; (ii) introduction of controlling genes that function at specific stages or times of development; and (iii) more effective transmission of quantitatively inherited genes for agronomically important traits. Currently most practical use is associated with the first of these (e.g. insertion of the *Bt* gene for insect resistance). The latter two applications will have much more practical impact, but they require considerably more basic research to be feasible.

Successful biotechnology must be able to identify, isolate and shift specific genes, as well as ensure their appropriate expression in the target crop. The present knowledge of what specific genes do physiologically and where they are located genetically is still too limited to make it possible to find and move such desirable genes. Also the time and costs of markers-assisted selection are still too great.

The most important agronomic traits are conditioned by several genes, each of small effect. Consequently, these genes are difficult, and perhaps even impossible, to characterize and manipulate using biotechnology. Therefore, for the foreseeable future, most of the genetic base will be found in the gene pools of crop species and their wild relatives. Biotechnology will have an increasingly important role to play in helping plant breeders to better characterize and improve crop productivity. Biotechnology can also increasingly help in the more efficient management and utilization of conserved genetic diversity. Biotechnology can provide tools to help plant breeders more effectively source and manage germplasm. These technologies can help render exotic germplasm more accessible and potentially useful to agriculture. It is imperative that practical success be achieved in sourcing exotic germplasm; otherwise it will be increasingly difficult to find funds to support these programmes.

Global Imperatives and the Role of the Private Industry

Gene banks are established in different countries with limited funds. A great amount of support is dedicated to preserving germplasm without considering evaluation and enhancement. This unsatisfactory condition is true for national and international programmes. The global financial support for conservation and evaluation of genetic resources is insufficient and becoming more restricted each year. It becomes indispensable to work together in the different aspects of genetic resource activities, especially in evaluation and enhancement. To complete these tasks it is necessary to exchange germplasm between countries. We strongly believe that success will come through the cooperation of participating countries.

The success of the LAMP project was founded upon the cooperative efforts of the Principal Investigators who believed that it was necessary to collaborate with strategies focused on success without being daunted by the limitations that would inevitably occur. The results of the LAMP project demonstrated that it is imperative to exchange germplasm among countries without restrictions, since experiences from several countries have shown that the best germplasm is often derived from foreign accessions.

Another more extensive cooperative project is the GEM in which private industry participates in contributing the proprietary inbred lines to crosses with the best LAMP accessions. Private industry also contributes in-kind support helping with nursery rows, yield test plots and isolation rows. Alliances among countries and collaboration with private industry will help to ensure the success of present and future projects in genetic resources, especially in this period when financial resources are scarce and genetic resource activities must compete for funds with other investments that can yield more immediate, but fewer long-term benefits. Collaboration helps to identify additional important traits in exotic germplasm since some cooperators have the facilities and expertise that others lack.

Plant breeders will need to source new germplasm diversity effectively in order to remain competitive within their industry. Strong intellectual property protection has been criticized by some as leading to a reduction in genetic diversity. However, the opposite is more likely to occur. Plant variety protection (PVP) allows other organizations to breed from protected commercially available varieties. Utility patents place protected inbred lines and hybrid varieties into the public domain after 20 years. This period may sound long, but in breeding terms it is not; 20 years represents about two cycles of elite breeding and less than one cycle of breeding using exotic germplasm. Consequently, once protection from patents and utility patents has expired, breeders will be faced with direct competition from germplasm that was once in their proprietary domain. If breeders are not already prepared with new, more productive genetic diversity, they will be heading for a significant loss of demand for their products. For privately funded breeding organizations, the result of being unprepared with new, more productive genotypes would be reduced market share, reduced income, drop in share-value, and loss of jobs, with potential buy out or bankruptcy looming on the horizon. Strong international plant protection (IPP), forces and enables insightful and capable breeding organizations to source new germplasm so that they will be positioned to compete with new seed genetic technology as a key instrument for success in the marketplace.

However, despite the clear needs for successful breeding organizations to maintain a source of useful new genetic diversity, the practical realities of obtaining and allocating funding are liable to result in shortfalls of private investment and effort into basic programmes that otherwise could have helped to deliver useful germplasm for the long term. It is imperative to provide for these shortfalls. The conservation of genetic resources for food and agriculture is an activity that, for the most part, must be funded by government. Private investors will not provide significant funds for conservation of plant germplasm for future plant breeding because the time frame for receiving returns on investment is not only extremely long but also very uncertain.

Private funds are more likely to be forthcoming for enhancement or pre-breeding of germplasm. The GEM Project provides an example of collaborative activities to evaluate useful germplasm. Such activity provides an example where the public and private sectors can join together. Pre-breeding is neither too basic, risky, or long-term for the private sector to engage in, nor does it result in genotypes that are so far along in the process of research toward product development that there is a need for strong intellectual property protection. Consequently, germplasm is evaluated, enhanced and made freely available; and it can even include some component of proprietary germplasm to help to adapt the exotic component. The breeding community should seek to encourage more pre-breeding and enhancement of germplasm including participation by farmer–breeders, national breeding programmes and International Agricultural Research Centers (IARCs) along with input from the private sector.

No single organization, nation or region has the complete range and depth of capacity required to improve its agriculture optimally. No variety has yet been bred that is perfect. Agriculture shows us a legacy of intercontinental exchange of germplasm and mutual interdependence that stems back over several millennia. In the industrialized world during the last three decades, plant breeding has played a significant role enabling the proportion of income that is spent on food to be cut in half. Yet most are unaware of this ‘food dividend’ or simply take the benefits for granted. In order to meet the demands for food and to protect the environment, we must recreate an appreciation of our mutual dependence upon agriculture and provide the investment and support that is due for the support of current and future generations.

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8

Role of International Germplasm Collections in Italian Durum Wheat Breeding Programmes

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Durum breeding in Italy may be considered to have started in the 1920s. At that time, within the thousands of local durum populations, single individuals were selected ('genealogical selection') as starting points of new varieties. This approach went on for three decades, up to the 1950s, and gave origin to a host of improved varieties (Cappelli, Azizia, Dauno, Duro di Puglia, Tripolino, Sardo, Russello, Saragolla, Eiti 6, among others), some of which were destined to remain present on the scene of Italian agriculture for many years to come.

A second period may be considered to have begun in the 1950s, after the Second World War, with the appearance of the products of the first hybridization programmes. The variety Cappelli assumed, *de facto*, a central role in a series of cross combinations, which, however, was essentially confined to partners of the Syrian–Palestinian type, or, more generally, Mediterranean. This second period was marked by the release of numerous varieties. Among these, particularly successful varieties were Garigliano, Capeiti 8, Patrizio 6, Sincape 9, B 52 and Grifoni 235. Further hybridizations among the early products of the period led to the release of Ichnusa, SAS 449, Camar 7, and then Appulo and Trinakria; the latter two are still present today in the fields of many southern farmers.

In the early 1970s, another phase began which was marked by the introduction of bread wheat (*Triticum aestivum*) parents into the hybridization programmes. The idea was to bring from these bread wheat parents a higher spikelet fertility, potentially leading to increased productivity. The environmental hardships of the traditional cultivation areas of durum, however, created insurmountable physiological imbalances for the new high-spike-fertility types during the maturation phase. At the same time, it remained unsolved what

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appeared to be the main obstacle to a rise in productivity in an improved agronomic context: the proneness to lodge.

This latter problem was solved with the first appearance of international, or exotic, durum germplasm in Italy: the CIMMYT dwarfs and semi-dwarfs, derived from crosses with short-culm Japanese bread wheats. They were widely crossed with Cappelli and all the best national releases. The result was two parallel series of varieties, each bred by one of two national institutions: the National Agency for Alternative Energy (ENEA), releasing Creso and others; and the National Institute for Cereal Culture, releasing numerous varieties with names carrying the 'Val' prefix: Valnova, Valselva, Valforte, Valriccardo, and others. Only marginal success was achieved by varieties bred by ENEA itself as a result of a mutagenesis-and-hybridization programme, which, however, could demonstrate the potential of mutagenesis in creating genetic sources of culm shortness other than those characterizing the Japanese wheats.

Resistance to lodging and some level of resistance or tolerance to diseases were the fundamental achievements realized with the two series of new varieties. Even if the 'Val'-series representatives had an appreciable success and are still a meaningful presence in the Italian wheat culture, it was Creso that embodied the most striking breakthrough ever for Italian durum breeding programmes: in 1986, its relative contribution to the total durum production was as high as 42%.

Since the mid-1970s, the genetic bases of the Italian breeding programmes have widened further, with continued contributions from durum international germplasm collections and nurseries of CIMMYT and ICARDA, and revived exchanges at the European level (France, Spain). At present, satisfactory levels of productivity have been attained, presumably as a result of both an increased genetic potentiality and a strengthened lodging resistance, the latter allowing the crop to draw full advantage from improved agrotechnologies.

A future call on exotic germplasm collections shall, therefore, prominently support breeding efforts aimed at achieving better grain and pasta quality. Further stability of production must also be sought by pursuing better levels of resistance or tolerance to diseases and parasites, as well as to environmental stresses.

Durum Wheat Production: the World, European and Italian Realities

Durum wheat is grown worldwide, although its relative economic importance varies from region to region. World production has remained roughly constant over the past 15 years. However, the EU relative contribution to world production has shown a consistent increase: from 17% in the early 1980s to more than 25% in the first half of the 1990s. This increase is largely to be ascribed to Greece and Spain joining the EU. European production today is substantially equivalent to that of the large North American conglomerate (i.e. the US and Canada).

On international markets, EU durum production does not contribute to the formation of global cereal surpluses. Instead, the European transformation industry continues to import, mainly from the US and Canada, sizeable quantities of durum. In this respect, Italy in particular, with its pasta and semolina production, represents the main EU market.

Within the European continent, Italian durum production has always been prominent, both in terms of quantity and quality. During the last 20 years, however, Italy's relative contribution to European global durum production has shown a marked decrease down to about 50–60%. This decline can be attributed not so much to a dwindling of Italian production (which actually increased), as to a larger contribution from other European countries.

Over the same 20-year period, the Italian durum growing area has been fairly constant at about 1.6–1.7 Mha. The increase in durum production is the result of higher productivity of the varieties grown: from 2.1 t ha^{-1} in 1975 to an average of 2.8 in the last 5 years, i.e. an increase of 25%.

The increase in Italian durum productivity observed in recent years may be attributed both to an improvement in cultivation technologies and to the breeding and release of more productive varieties.

Durum Wheat Genetic Variability: Past and Present

The extremely rich presence of durum landraces, especially in southern Italy, helped early breeders to make some progress. The intensive use of such germplasm from the 1920s to the 1970s, first in selection programmes and later in hybridization and selection, could not solve, however, a few fundamental problems impeding improvements in the productivity of the crop.

Most important of all, the attainment of a satisfactory lodging resistance, which permits the application of higher doses of nitrogen fertilizers, together with the incorporation in the species of some level of tolerance to the most dangerous diseases (*Puccinia graminis*, *P. recondita*, *Blumeria graminis*, *Fusarium* spp., *Septoria* spp.), had to wait until germplasm from outside the Mediterranean region was included in the breeding programmes. To be sure, the path most frequently and successfully followed was the hybridization of international germplasm with local types. But the local component, although synergic, was never resolutive.

Genetic erosion against native genetic variability might have taken place. Italy, however, had already started in the 1970s a strong programme of collection and conservation in favour of local durum types, which culminated in the establishment, in Bari, of the Germplasm Institute of the National Research Council. There the institutional goals of conservation, evaluation and characterization of Italian, Mediterranean and other durums have been effectively pursued.

The question remains as to whether or not the introduction and widespread cultivation of new varieties with largely 'exotic' parentage may have dangerously narrowed the genetic basis of the modern Italian cereal culture to the point of posing a threat to the safety of the same. Some evidence tends to point to a reappraisal of such a threat. In fact, the number of varieties grown in Italy over significantly large areas is higher now than it was some decades ago. This is required in part by the fact that the Italian peninsula stretches over more than 1500 km of latitude, with climatic differences not only between north and south but also between east and west regions. Although a few varieties appear to perform equally well anywhere, many others fit only their own area of adaptation ('niche'). This suggests the existence of a multiplicity of varietal genetic backgrounds. The same could be concluded considering the differences among varieties with respect to reaction to diseases and environmental stresses, as well as to grain quality characteristics.

This amplitude of the varietal genetic basis can be traced to the multiplicity and cosmopolitanism of the genetic resources assembled, moulded, and distributed by the major international dispensers of germplasm, e.g. CIMMYT or ICARDA. In addition, intensive germplasm exchanges have taken place among the various European national durum breeding programmes.

Pasta Quality

Although minor quantities are utilized in bread production, Italian durums are mainly destined for pasta production. Good pasta quality is essential in order to win acceptance not only by Italians, but also by many international consumers. Quality is an extremely complex characteristic influenced not only by varietal genotype but also by environmental conditions and by the technological procedures adopted by farmers, millers and pasta factories.

Recent studies by one of the biggest Italian pasta producers have ascertained that the great majority (80%) of national pasta consumers regard the so-called 'resistance to cooking', as the most important qualitative character. Unfortunately, no simple physical or chemical analytical parameter exists, measured on grain, flour or semolina, that is significantly correlated to a good pasta quality and could be used in breeding or preliminary evaluation procedures. Therefore, even today, the best method of quality testing remains the direct appreciation of cooked pasta.

The recent development, however, of a new pasta drying methodology (high-temperature drying) now permits the production of pasta with better 'resistance to cooking', provided the semolina protein content is sufficiently high. A grain protein content as high as 13–14% may result in a good pasta, whereas values of 16–17% may lead to special quality pasta. In turn, effective protein accumulation in the grain is a function of both genetic and environmental (water, nitrogen availability) factors. At the farm level, it determines satisfactory grain volume weights, consistent over years and locations. Therefore, such consistency may be considered as an index of capacity of grain protein synthesis.

Still problematic is a satisfactory analytical determination of protein, or gluten, quality. One of the basic methods still used is the determination of the alveographic parameter, W, while recourse is frequently made to a manual, or empirical examination of the gluten itself for a synthetic evaluation. High values of W are associated with a higher synthesis of glutenins, which results in a stronger gluten tenacity and better cooking quality. In particular, semolinas with W values higher than 180 are considered to possess good rheological quality.

Resistance to Diseases

Several pathogens (e.g. *Puccinia recondita*, *P. graminis*, *Blumeria graminis*, *Septoria* spp. and *Fusarium* spp.) may seriously undermine the stability of durum production in Italy, depending on the occurrence of certain environmental conditions. Parallel to the official network of field evaluation, field epidemiological tests have been performed for many years at a number of locations covering the most important durum cultivation areas. Under field conditions, diseases, if any, were caused by populations of pathogens that probably differed between years and locations.

Several varieties, both native and imported, were found to possess satisfactory levels of resistance to one or more pathogens. Among native materials, a few landraces (Saragolla bianca, Triminia, Nummina, Marzuolo C.) showed resistance or tolerance to brown rust (*P. recondita*), while one variety (Lambro) exhibited a consistent resistance to both brown rust and powdery mildew (*B. graminis*). Among varieties derived from hybridization programmes with exotic material, Grazia and Ofanto showed a good tolerance to powdery mildew, and Creso and Plinio to brown rust. In summary, and with the approximation allowed by field evaluations, the exotic germplasm did not appear to have contributed original sources of resistance.

Conclusions

When, in the late 1960s, the first CIMMYT varieties were received by Italian durum wheat breeders, the latter were engaged in an effort to remould an ancient species into a modern crop which could benefit from the adoption of modern agrotechnologies. The existing varieties were tall, prone to lodging and mostly disease susceptible (although characterized by good grain quality), and could not be grown on good, fertile soils with adequate moisture supply. Cultivation of durum was, therefore, mostly confined to southern and insular regions, with some enclaves in the central regions.

The CIMMYT (and, later, ICARDA) wheats could be utilized as sources of desirable characteristics such as: short culm and lodging resistance, disease resistance, day length insensitivity, and others. To be sure, Italian bread wheat breeders had already, in the 1920s, imported and utilized in their programmes Japanese short straw lines and were able to release short, lodging resistant varieties. However, the transfer of short-straw genes from bread to durum wheats that was attempted in the 1970s was hindered by several problems and was never really successful.

It is difficult to tell whether the gain of 1.4 t ha^{-1} in productivity shown by varieties derived from the utilization of imported germplasm is to be attributed solely to the acquisition of short culm and lodging resistance and the consequent ability to exploit richer agronomic environments. A closer examination, however, reveals that other progressive characteristics were inherited by modern varieties from their exotic ancestors, e.g. short, erect leaves, a better culm structure, a more favourable harvest index, a higher level of disease resistance.

9

An Application of Hedonic Pricing Methods to Value Rice Genetic Resources in India

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Over the period 1965–1986, Indian rice breeders released a total of 306 rice varieties for planting in India. These included varieties that were under development from earlier years. They also included the release of 27 'early green revolution' varieties that were actually developed at IRRI but released in India. The Indian varieties were the result of approximately 20,000 crosses made by Indian breeders since 1950.

A pedigree analysis of each released variety was undertaken. This analysis traced parents, grandparents, etc., back to the original genetic resources in the variety (in most cases, landraces, but in some cases, wild species). Characteristics emphasized in the development of each variety were recorded. This enabled a quantitative description of varieties in terms of year of release, releasing institution, characteristics emphasized, parent and grandparent combinations, number of landraces in the pedigree, generations from landrace materials, and crosses of landrace material.

Table 9.1 reports varietal releases by year. A steadily increasing trend in releases appears to hold from 1965 to 1975, with approximate constancy subsequently. The 27 varieties developed originally at IRRI and the six varieties developed in other foreign breeding programmes have been distributed evenly over time.

Table 9.1 also reports the average number of landraces in each pedigree and the average number of generations since the oldest landraces in each pedigree by year of varietal release.[1] These data show steady growth over time in pedigree complexity. The early green revolution varieties released before 1970 had relatively simple pedigrees. Recent varietal releases are much more complex, with as many as 27 landraces and as many as 12 generations of crosses going back to original landrace material.

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Table 9.1. Summary of varieties by year of release.

Year of release	No. released India	 IRRI	 Other foreign	Average no. of landraces	Average no. of generations
1965	2		1	1	2
1966	2	1		2	1
1967	2			2	1
1968	6			1.5	
1969	6	1		2	0.9
1970	12	1	1	3.8	2.4
1971	8	1		3.6	2.2
1972	17	5		4.2	2.6
1973	14			2.9	
1974	7			4.0	2.7
1975	14	3	1	5.4	3.4
1976	17	2	1	4.1	2.7
1977	12			4.2	2.8
1978	11	4		4.3	2.9
1979	15	1		5.8	3.3
1980	20			4.3	2.7
1981	11	3		6.7	3.9
1982	23	2	1	6.1	4.0
1983	14			4.8	2.9
1984	7		1	5.5	3.6
1985	31	1		6.1	3.9
1986	22	2		8.7	4.6

Table 9.2 summarizes the releases by releasing institution. The Central Variety Release Committee releases varieties where it is deemed that they have broad regional potential. State releases tend to be more location specific. As Table 9.2 indicates, most major state programmes have released ten or more varieties over the period. Even some of the relatively small states have had programmes resulting in released varieties. (Most of these released varieties have been planted on significant acreage.[2])

Table 9.3 summarizes the recorded emphasis on specific characteristics in the breeding and selection of these varieties. Many varieties emphasized more than one characteristic. Disease resistance tends to be the most sought after characteristic, with insect resistance next. Stress tolerance is also emphasized, and some agronomic characteristics are as well. Grain quality also receives emphasis. No single characteristic dominates breeding strategies.

Table 9.4 summarizes parental combinations for the 306 released varieties. It shows that both parents were of Indian origin in only 17% of the crosses (26% if the mutants are considered), and of these, only six were totally of Indian parentage. Of the Indian parentage crosses, most involved a released variety. In

Table 9.2. Varietal release by releasing institution.

Releasing institution	Number released
Central Variety Release Committee	28
Andhra Pradesh	32
Assam	5
Bihar	20
Gujarat	14
Haryana	1
Himachal Pradesh	5
Jammu and Kashmir	5
Karnataka	18
Kerala	17
Madhya Pradesh	13
Maharastra	23
Orissa	29
Pondicherry	3
Punjab	9
Rajastan	3
Sikkim	3
Tamil Nadu	1
Uttar Pradesh	21
West Bengal	10

13% of the cases both parents were foreign and, as with Indian materials, most successful crosses involved a released variety.

The dominant mode of parentage involved one Indian parent and one foreign parent, and the foreign parent was predominantly a released variety. The most frequent combination was a cross of a foreign released variety and a traditional Indian cultivar. The next most frequent was the combination of an Indian released variety with a foreign released variety.

A surprisingly high proportion of crosses involved traditional cultivars, and most of these were Indian. Foreign germplasm has found its way into almost all Indian released varieties, even though India is the repository of a large share of the world's rice genetic resources.[3]

Table 9.5 reports a tabulation of landraces by year of first appearance in a released variety. These data show that the landrace base for Indian varieties has been expanding. (By inference, if breeders had been constrained to work only with the landrace materials being used in breeder collections as of 1970 or so, they would not have produced varieties as valuable as those actually produced.)

For purposes of further analysis, these landrace materials are classified into the six categories (with percentage inclusion in varieties noted) reported in Table 9.6. Pre-1975 and post-1975 landrace categories entered varieties through the building of 'breeders' cores', i.e. of working collections for strategic

Table 9.3. Varietal characteristics: 306 released rice varieties (1968–1986, India).

Characteristic selected	Proportion with characteristic
Disease resistance	
Blast	0.187
Bacterial leaf blight	0.151
Red kernel	0.049
Tungro	0.029
Other	0.059
Insect resistance	
Brown plant hopper	0.059
Gall midge	0.075
Stem borer	0.085
Leafhopper	0.069
Other	0.020
Stress tolerance	
Drought	0.056
Saline soils	0.046
Submergence	0.029
Cold	0.062
Other	0.026
Agronomic qualities	
Photoperiod insensitivity	0.072
Tall	0.046
Early	0.105
High yielding	0.065
Upland production	0.016
Grain quality	
Fine grain	0.056
Scented	0.026
High protein	0.023
General	0.092

crossing purposes. Most breeders maintain a relatively small set of cultivars for crossing purposes. Local breeders typically keep some local landrace materials and a set of advanced materials from national and international sources. They rely on information from national and international trials and from the germplasm collectors to identify promising new materials. National breeders may maintain larger stocks of landraces (and some wild species). They seek to produce new varieties suited to fairly large regions, but they also recognize that they are producing advanced germplasm materials for local (state) breeding

Table 9.4. Parental combinations: 306 released rice varieties (1965–1986, India).

	Second parent						
	Indian			Foreign			
First parent	Traditional cultivar	Advanced line	Released variety	Traditional cultivar	Advanced line	Released variety	Unknown
Indian							
Traditional cultivar	6						
Advanced line	4	7					
Released variety	12	13	11				
Foreign							
Traditional cultivar	3	2	2	7			
Advanced line	7	3	1	5	9		
Released variety	81	16	35	14	8	5	
Unknown	2	3	0	2	0	11	8
Selection mutant	29						

Table 9.5. Appearance of new landraces over time.

	New landraces appearing in pedigrees of released varieties	
Year	No.	Per cent
1965	1	0.6
1966	5	3.0
1967	3	1.8
1968	6	3.6
1969	7	4.2
1970	8	4.8
1971	7	4.2
1972	17	10.1
1973	7	4.2
1974	2	1.2
1975	11	6.5
1976	11	6.5
1977	6	3.6
1978	8	4.8
1979	5	3.0
1980	13	7.7
1981	5	3.0
1982	11	6.5
1983	5	3.0
1984	4	2.4
1985	12	7.1
1986	14	8.3
Total	168	

Table 9.6. Landrace content by origin.

	Proportion of planted area
Indian origin landraces	
Pre-1975	0.62
Post-1975	0.11
Specialized	0.12
Foreign origin landraces	
Pre-1975	0.84
Post-1975	0.07
Specialized	0.03

programmes. Considerable effort is devoted to packaging original materials with specific characteristics to be sent on to local breeders. International breeders concentrate even more on germplasm building and seek to provide national systems with advanced materials. IRRI has had a programme specifically designed to incorporate a broad range of desirable characteristics in advanced lines, which then are used as breeding materials in other countries.[4]

The ‘specialized’ mode for incorporation of original genetic resources into breeders’ cores had its origin in a special problem situation. Several such problem situations have occurred in rice production. The Tungro outbreak in IR8 in 1969 and the grassy stunt virus problem that emerged in 1977 are cases in point. In these situations collection-wide searches for genetic resistance were undertaken.

Hedonic Price Evaluation

Hedonic price evaluation entails a statistical regression relating a measure of varietal improvement in farmers’ fields to factors expected to cause or produce varietal improvement. For India, district-level measurements of rice yields are available. Yields are general productivity indexes and may be influenced by both varietal and non-varietal factors. Accordingly, non-varietal research activities and other yield-increasing investments in rural infrastructure must be considered in hedonic price evaluation.

A two-stage regression analysis was pursued utilizing data for 240 districts. The first stage was designed to estimate the relative contribution that overall varietal improvement made to productivity growth in rice. If it cannot be established that modern high-yielding varieties (HYVs) actually contributed to productivity growth, there is little point in attempting to identify genetic resource effects. Having shown, however, that varietal improvement does affect productivity growth, then one can proceed to the second stage where genetic content variables can be incorporated into the analysis.

The first stage estimates did show that varietal improvement was a significant determinant of rice yields for Indian districts over the 1959–1984 period.

The dependent variable was the rice yield for the district in a given year, relative to the average 1957–1960 rice yield for the district (see Gollin and Evenson, 1990). Independent explanatory variables were:

- The proportion of acreage planted to 'modern' or 'high-yielding' varieties released since 1966. (This was the variable included to test whether varietal improvement actually affected productivity. By 1986, 60% of Indian rice area was planted to HYVs.)
- Indian agricultural research (a stock variable reflecting the contributions of non-varietal public agricultural research).
- Indian private sector R&D relevant to agriculture.
- Agricultural extension services.
- Literacy of farmers.
- Roads (a road density variable).
- Markets (a measure of regulated market infrastructure).
- Irrigation investments.
- IADP programmes (a specialized programme providing additional extension and infrastructure to farmers).

The estimates showed that varietal change contributed more than one-third of the rice productivity gains realized over the post-green revolution period, 1972–1984.

Having shown that rice varietal improvement did contribute to rice productivity, the second stage analysis is justified. In this stage, variables measuring the genetic content of varieties actually planted by farmers were substituted in the analysis for the HYV variable. The analysis was undertaken only for the most recent 5-year period, 1979–1984, because varietal content data for earlier periods were not available. The dependent variable, rice yield, was indexed relative to the 1972–1974 average yield. Thus, the analysis focuses on yield changes in the post-green revolution period. It seeks to determine whether gains in rice yields after the 1972–1974 period have been systematically related to the genetic content of the varieties planted by farmers.

Of the 307 varieties released since 1966, approximately 90 were planted on significant acreage.[5] For each district, genetic content variables were defined for acreage actually planted. These genetic content variables were defined for five clusters of variables as summarized in Table 9.7. For each cluster, the percentage of acreage in that category is reported.

The variables are defined such that for each cluster there is a left-out or reference category. In the breeding source cluster (see Table 9.1), Indian-bred varieties (not mutants) released by the states are the reference group. For the varietal characteristics cluster, the reference group is varieties without special characteristic emphasis (see Table 9.3). For the parental origin cluster, the reference group is the traditional parentage category (see Table 9.4). For the landrace content cluster, it is the pre-1975 Indian national core materials (see Tables 9.1, 9.5 and 9.6). Table 9.7 reports the means for the relevant clusters of the variables.

Table 9.7. Genetic resource content variables: means and estimated impacts.

		Mean	Estimated impact
1. Breeding source			
DIRRI	Per cent of 1984 acreage planted to varieties released by IRRI	0.127	−2.41
DDREL	Per cent of 1984 acreage planted to varieties originating in other foreign countries	0.023	7.94
DMUTSPS	Per cent of 1984 acreage planted to varieties that were mutants	0.013	0.33
DDCVRC	Per cent of 1984 acreage planted to varieties that were released by central variety release committee	0.158	2.23
2. Varietal characteristics			
DRESIST	Per cent of 1984 acreage planted to varieties selected for resistance to disease and insects	0.198	−0.53
DSTRESTL	Per cent of 1984 acreage planted to varieties selected for stress tolerance, drought, cold, heat	0.037	0.53
DAGRON	Per cent of 1984 acreage planted to varieties selected for agronomic characteristics	0.060	0.39
3. Parental origin			
FRADVGR	Per cent of 1984 acreage planted to varieties with foreign advanced GR parents	0.059	−2.29
FIADVGG	Per cent of 1984 acreage planted to varieties with foreign × Indian advanced GR parents	0.079	1.18
4. Pedigree complexity			
DNOLR	1984 acreage weighted average number of landraces in HYVs	2.00	0.42
PCTFLR	1984 acreage weighted per cent of foreign origin landraces	0.80	−0.11
DGENS	1984 acreage weighted average number of generations from landraces in HYVs	1.29	0.81
5. Landrace content			
DOINTCRE	1984 acreage weighted landrace proportion from pre-1975 international core	0.411	2.00
DNNATCRE	1984 acreage weighted landrace proportion from post-1975 national core	0.033	1.24
DNINTCRE	1984 acreage weighted landrace proportion from post-1975 international core	0.018	−35.0
DNNATFRN	1984 acreage weighted landrace proportion from specialized national search	0.009	14.9
DNINTFRN	1984 acreage weighted landrace proportion from specialized international search	0.015	34.1

Five separate regression analyses, one for each cluster, were undertaken. All explanatory variables for rice productivity from the first stage were included in each regression. In addition, the content variables in each cluster (and their interactions with the public research variable) were included. Table 9.7 reports the estimated impact elasticity of the genetic content variables.

The estimated impact elasticities are evaluated at the mean of the data set and are interpretable as the percentage change in yield from a one-unit change in the genetic content variable. It is best to think of these as the percentage change in yield from a 1% change in the area planted to varieties containing the indicated genetic content. Note that these are relative to the left-out group.

Consider the breeding source variables. They indicate that the varieties released by the central variety release committee (DDCVRC) have had a higher impact than other releases (the left-out group). Foreign-origin varieties not released directly by IRRI (DDREL) are also associated with higher productivity. Direct IRRI-released varieties have lower productivity impacts than the reference group varieties. Many of these varieties are the early green revolution varieties, and some may be recent releases suited to problem situations.

The varietal characteristics variables indicate that varieties stressing grain quality are also high-yielding. The stress on agronomic characteristics and stress tolerance also produces higher yields than the reference group (varieties with no selection strategy for characteristics). Varieties with resistance to disease and insects appear to have lower yields than the reference group, but it should be noted that the incidence of pest and disease problems is not measured in the data set. This result may be reflecting pest and disease incidence.

The parental origin estimates are particularly complex. The value of cultivars where both parents are foreign advanced cultivars is lower than when varieties have mixed foreign and Indian parentage.

The pedigree complexity variables indicate that varieties with higher landrace content and more generations from landraces have higher yields. These findings provide support for the contention that genetic resources are valuable.

The final set of estimates for landrace content are of most interest, however, because they speak directly to the implicit value of genetic resources. The reference group in this case is material based exclusively on ‘old’ (i.e. pre-1975) national core landraces (see Table 9.6). The coefficients in the analysis indicate the contribution relative to the reference material. (Note: this is a small part of the total landrace content.)

The fact that old international genetic resources still have yield-increasing value in the early 1980s is not surprising. This essentially reflects the yield-increasing power of the genetic resource combinations that created the green revolution.

The fact that new (i.e. entering pedigrees after 1975) national landrace material contributes to varietal value is important because it shows that systematic and strategic incorporation of more landrace materials into the breeders’ core has a payoff. It is not entirely clear why post-1975 international core materials do not have the same effect. This may be due to the disease and pest incidence problem discussed in the varietal characteristics analysis. It is also consistent with the negative IRRI effect in the breeding sources analysis.

The estimated impacts of the special search materials turn out to be quite large. This has considerable relevance to genetic resource management, because these special search materials are found in the fringes of the collection. They are typically found in materials where only one trait is valuable. The probability of discovering such material is very low, because such traits are extremely rare. The probability of discovering such traits in the conventional part of collections where cultivars have multiple trait value is lower than it is in the wild species and 'unusual' materials. Since the probability of discovering such traits is greater the larger the collection of such materials, evidence of their value indicates that the collection, preservation and maintenance of such materials has value.

Economic Interpretation of the Results

The estimated impact elasticities provide the percentage increase in yields from a 1% increase in the area planted to varieties containing the indicated genetic content. Consider the variable DOINTCRE. Forty-one per cent of Indian rice acreage in 1984 was planted to varieties containing pre-1975 international core materials. These are effectively the original green revolution genetic resources. The elasticity of 2.00 tells us that if a 1% expansion in old international core were to occur at the expense of the reference group (i.e. from 0.411 to 0.421), average rice yields in India would increase by 2%.

The more pertinent calculation is to ask what the post-1975 materials have contributed to yields. This can be done by multiplying the 1984 levels for DNNACRE, etc., by their respective elasticities. This calculation should include the negative DNINTCRE coefficient. This calculation yields:

$$0.033 \times 1.24 - 0.018 \times 35.0 + 0.009 \times 14.9 + 0.015 \times 34.1 = 0.0562.$$

Thus, by this estimate, yields were higher for all of India by 5.62% than they would have been had no new genetic resources beyond the original green revolution resources been available to breeders. Since the total HYV contribution to the period was 13.4%, one can infer that reworking the original genetic materials would have contributed 7.78% to yields (see Gollin and Evenson, 1990).

It is readily obvious that most of the yield gains from new materials are due to the specialized search materials. Rather than attempt, however, to make a separate calculation for these materials, it is perhaps best to treat the 5.62% yield increase as a conservative estimate of the contribution to yields made by the size as well as the maintenance of the genetic resource stock. This calculation is made holding breeding effort and all other research, extension, irrigation and market contributions constant (i.e. correcting for them).

The 5.62% realized up to 1984 is likely to continue to increase as area planted to the newer varieties expands. If the 5.62% is conservatively treated as having been realized at a 0.5% rate over the 11 years leading up to 1984, a cost–benefit or rate of return analysis can be undertaken (under the conservative assumption that no further gains after 1989 will be realized). To do this, an estimate of the time lag between the incurrence of costs and the realization of the yield gain benefits is required. With that time lag, the present value of the stock of genetic resources can be computed given a discount rate.

If a 20 year average time lag between the incurrence of costs and the realization of benefits is supposed, and a 10% real discount rate is utilized, the present value of a 0.5% yield increase 20 years hence is 0.061 at a 10% discount rate (0.027 at a 15% discount rate). This number can then be multiplied by the value of India's rice crop (approximately $10 billion) to obtain the annual (discounted) flow of value from the genetic resource stock.

The value of the 0.5% contribution at the time it was realized in India was $50 million. The present value of the $50 million 20 years prior to realization is $6.1 million at a 10% discount rate ($2.7 million dollars at a 15% discount rate).

These values can now be compared with the costs of maintaining and operating the genetic resource collections. They can also be compared with the costs associated with developing a larger collection. The costs of maintaining the larger collection of rice material at IRRI are roughly $0.7 million annually (see Chang, 1989). The costs of maintaining the Indian collections are probably $0.3 million or so. Thus it is quite clear that the economic value of genetic resources in India exceeds the costs of maintaining them. If India were to invest say $20 million over a 10-year period to expand its collection further, this would add to the annual costs of maintaining the collections. Even if this raised annual costs by $3 million per year, the value produced by such additional resources would more than justify the expenditures. Indeed, since much of the estimated value of new materials emanates from the fringe materials, the value of a 'nearly complete' collection relative to its cost is probably higher than the value of the present collection relative to its costs.

Of course, as this chapter has shown, germplasm collections are international and are exchanged internationally. Collections at IRRI and in other countries have contributed to productivity gains in India. Conversely, Indian germplasm has contributed to productivity growth in other countries. A global calculation for irrigated rice using the Indian estimates would show that a 0.5% increase in output per unit input 20 years from now would be valued at approximately $600 million, and its present value would be $74 million at a 10% discount rate ($32 million at a 15% discount rate). These values may be compared with the current costs of germplasm collection maintenance of perhaps $10 million per year. If the current collections were brought to 'near-complete' status over the next 10 years at a cost of $5 million per year, this would, when amortized and adjusted for the larger size of collections, possibly raise the annual costs of collection maintenance, etc., to $20 million per year. This is well below the estimated present value of the contribution each year. Even if the

Indian estimates overstate the impact of new genetic resources by a factor of two or three, the economics of moving to a 'near-complete' collection justifies doing so.[6]

Notes

1. The number of generations is a useful index of genetic complexity.
2. Approximately 100 of the 306 varieties released since 1966 were planted in 1984. Of these 306 varieties, 118 were released after 1980. Thus, a high proportion of released varieties were actually important varieties.
3. IRRI has been the major source of the foreign germplasm.
4. The genetic evaluation unit at IRRI has sought to combine multiple traits in advanced lines and varieties.
5. Ninety were planted in the 250 districts analysed. Approximately 100 were planted in all districts.
6. Very high costs associated with collecting the 'last few' plants would probably not be justified.

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10

Varietal Trait Values for Rice in India

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From 1967 to 1991 rice production in India grew by 2.82% per year. Area planted to rice grew by 0.58% per year and rice yields grew by 2.28% per year. Yield increases were the result of increased input use (including irrigation) and the adoption of modern rice varieties. The classification of 'modern varieties' has not been constant over time as rice breeders have incorporated new traits into modern rice varieties. In this chapter we report estimates of the economic value of several of these traits using data from farms in India.

In earlier work, Gollin and Evenson (Chapter 9) applied hedonic evaluation methods to district production data where estimates of the genetic resource content of rice varieties were available. An alternative and more direct procedure for evaluating trait values is to utilize data on actual varietal yields in the field. The ideal data set would be produced by a controlled experiment where natural factors including disease and insect susceptibility were held constant. Such data do not exist but can be approximated in the two data sets that are used in this study.

The first data set is compiled by ICAR for selected districts and years. ICAR reports yields for the three 'highest yielding' varieties in farmers' yield trials in each district–year combination for irrigated and unirrigated, kharif and rabi season rice. Fertilizer use is controlled and yields are reported for a sample of farms in the district. Each variety can be given trait characteristics and hence yields can be related to these characteristics. This data set is available for the years 1977–1989, covering some 45 districts in India. The weakness of these data is that the sample size of three is not large enough to provide an adequate control group. Furthermore, it is a highly selected reference group. It is plausible that the district average yield for the year in question and other district-level variables might represent a control group. Thus if poor weather affects the district

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average, it should affect the top three varieties as well, or if pest incidences were severe it could have affected all varieties. But it is also possible that the ICAR sample was representative of the district.

The second varietal data set is more promising. These state-level data are reported by state departments of agriculture and by the state Directorate of Economics and Statistics for different years. For each state–year combination, all important varieties planted are included in the data set. Yields from crop-cutting experiments carried out on farmers' fields are reported in this data set. The data set covers the five states of Punjab, Haryana, Andhra Pradesh, Tamil Nadu and Karnataka. For these data, one can use the yields of other varieties in the state as a reference group. Thus for a given year the yield of varieties with a particular trait can be compared with the yields of all varieties in the state. Weather, insect and disease problems, etc., can be considered to have influenced all varieties equally.

Means and Definitions of Variables

Table 10.1 contains the variable definitions and means of the independent and trait variables. Independent variables are defined only in the case of the first data set. We have the definitions as well as means of trait variables for both data sets, and can characterize the independent variables contained in the first data set. They indicate that 86% of observations belonged to kharif season and 88% of them were under irrigated conditions. The average length of varietal use after their release was 7.2 years. In the districts in question, 45% of the farmers were literate. In these districts, the road length index increased from 1 in 1955–1959 to 2.29 in the period 1977–1989, and they had 44% of the cropped area under irrigation. The variable means of extension workers per farm, index of rice area and index of rice yield are reported in logarithmic form. For these districts, the average research stock variable was computed to be 4.76.

The means of the trait variables presented for both the data sets are more relevant for the present study. They indicate the degree of disease and pest resistance embedded into the varieties in use in the 45 districts of the first data set and the five states of the second data set. In the first data set, the rice varieties under use have the following disease and pest resistance traits. On average, 11% of them are resistant to blast, 10% to bacterial leaf blight, 3% to bacterial leaf stripe, 24% to rice tungro virus and 1% to sheath blight. Similarly, 13% of them are resistant to brown plant hopper, 7% to gall midge and 8% to stem borers. The second data set reports a different set of trait values for disease and pest resistance in the states under consideration. The varieties in vogue in the sample contain, on average, the following degrees of disease and pest resistance: 19% to rice blast; 12% to bacterial leaf blight; 13% to rice tungro virus; and 2% to sheath blight. They also contain resistance to the insect pests to the extent of 12% to brown plant hopper, 11% to green leaf hopper, 4% to white-backed plant hopper, 16% to gall midge, and 6% to stem borer.

Table 10.1. Variable definitions (means), Indian district and state variety data sets.

Dependent: ln(variety yield) − ln(district average yield, all varieties)	District mean	State mean
Independent		
KARIF: dummy = 1 if kharif trial	0.86	
IRRI: dummy = 1 if irrigated trial	0.88	
VARAGE: years since release of variety	7.2	
LEXF: ln(extension staff per farm)	2.46	
LITERACY: per cent literate	0.45	
NINCA: net irrigated area (not cropped area)		
IROADS: index of road length = 1 in 1955–1959		
LIARICE: index of rice area = 1 in 1955–1959		
LVIARICE: index of rice yield = 1 in 1955–1959	0.66	
RAINFALL: annual rainfall	4.00	
RESEARCH: research stock (Evenson *et al.*, 1996)	4.76	
Trait variables		
BL: dummy variable = 1 if resistant to blast	0.11	0.19
BLB: dummy variable = 1 if resistant to bacterial leaf blight	0.10	
BLS: dummy variable = 1 if resistant to bacterial leaf stripe	0.03	0.00
RTV: dummy variable = 1 if resistant to rice tungro virus	0.24	0.13
SHBL: dummy variable = 1 if resistant to sheath blight	0.01	0.02
BPH: dummy variable = 1 if resistant to brown plant hopper	0.13	0.12
GLH: dummy variable = 1 if resistant to green leaf hopper	0.07	0.11
WBPH: dummy variable = 1 if resistant to white-backed plant hopper	0.02	0.04
GM: dummy variable = 1 if resistant to gall midge	0.17	0.16
SB: dummy variable = 1 if resistant to stem borers	0.08	0.06

An attempt is made to estimate the contribution of the above trait values to rice yield by regressing the yield by variety on the trait values of different varieties. For the district data set, a number of district variables are specified as control variables. In addition, dummy variables for agroclimatic zones are included in the district regressions. For the state data set, state × year dummy variables are included for all state × year combinations. This effectively means that variety yields are compared with the state–year mean yields.

Estimates

The coefficients and significance levels for trait variable coefficients are reported in Table 10.2 for both data sets. Two specifications are reported for the district data. In the first, all trait variables are included. In this specification three trait coefficients had marginally significant negative coefficients, possibly reflecting susceptibility. In the second specification, these three variables are dropped. In the state regressions, no varieties with resistance to bacterial leaf stripe are included in the data set.

The estimates actually tend to be reinforcing. In the case of the first data set,

Table 10.2. Trait value estimates.

Trait	District 1	District 2	State
Blast	−0.134*		0.184**
Bacterial leaf blight	−0.077	−0.069	−0.134**
Bacterial leaf stripe	−0.065	0.173	
Rice tungro virus	−0.146*		0.068
Sheath blight	1.48**	1.49**	0.108
Brown plant hopper	−0.151*		0.033
Green leaf hopper	0.037	0.052	0.123**
White-backed plant hopper	0.309**	0.309**	0.377**
Gall midge	0.091	0.102*	0.174**
Stem borer	0.155*	0.029	0.141*

* *r* between 1.5 and 2.0; ** *r* greater than 2.0.

sheath blight resistance and white-backed plant hopper resistance contributed positively to yield increases in both the specifications. Stem borer resistance contributed positively to yield in the first specification, and gall midge resistance had positive effects on yield in the second specification. In the state data set, bacterial leaf blight resistance depressed rice yield, contrary to normal expectations. Resistance to blast contributed positively to yield. Resistance to other diseases did not yield any significant impacts. Resistance to insect pests such as green leaf hopper, white-backed plant hopper, gall midge, and stem borer yielded significant and positive impacts on yield. Only the resistance to brown plant hopper did not yield a significant effect.

To sum up the results, varieties with insect resistance show better performance in the field in both data sets, although neither showed that resistance to brown plant hopper is important. The estimates for disease resistance, on the other hand, are much weaker. Both data sets show yield effects for sheath blight resistance and the state data set shows a blast resistance effect and a positive but non-significant rice tungro virus effect.

Economic Implications

The estimates reported in Table 10.2 are important to economic interpretation subject to two conditions. First, the trait value is confined to achievements where there is real insect or disease stress. Thus traits are not valuable over all rice acreage. Second, trait values are ‘additive’ in that a variety may incorporate more than one trait and each trait will contribute to yields.

Perhaps the simplest calculation utilizing both of these conditions is to compute the value of traits in India by multiplying mean values (from Table 10.1) by trait values (from Table 10.2), dropping negative trait values. This is an estimate of the specific values of these traits actually realized in India by the mid-

1980s or so. They are underestimates of the full value of these traits because of incomplete adoption and incomplete breeding processes.

These calculations for the district data show only a 2% yield gain for disease resistance and 3% yield gain for insect resistance. The state varietal estimate, on the other hand, shows a 4.5% yield gain from disease resistance and a 6.9% yield gain from insect resistance.

The nature of the data suggests that the state estimate is a more reasonable one than that computed from the district data. Adoption of varieties incorporating these traits is quite low (Table 10.1) with only a few traits covering 20% of the area at the mean of the data set. By 1992 these adoption levels are higher by a factor of 1.5–2.

We would thus consider it a reasonable (and conservative) estimate that conventional breeding for disease resistance has produced a 2–5% yield gain in India. Conventional breeding for insect resistance has produced a 3–7% yield gain in India. Further, conventional breeding efforts are likely to increase these levels further – perhaps doubling them in another 20 years.

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11

Modern Varieties, Traits, Commodity Supply and Factor Demand in Indian Agriculture

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The characterization of varieties of rice (and of other crops as well) as ‘modern’ or ‘high yielding’ (as opposed to traditional) has been quite important for policy analysis. Many countries collect and report data on the share of area planted to modern varieties (MVs) by region and period. Different rates of change in MV area are often taken to be indicators of policy success (especially of research policies) and of resource–technology interactions.

It is important to note, however, that the class of MVs has not been static through time. The original MVs of rice made available to farmers in the late 1960s (IR8–IR20 and related varieties) were largely replaced during the 1970s by a second generation of MVs that incorporated several new ‘traits’, especially brown plant hopper (BPH) resistance and Tungro resistance. That generation of MVs, in turn, has now been replaced by further generations of MVs with added traits for resistance to insect pests and diseases, for tolerance to ecological stresses (heat, cold, drought, floods) and for agronomic traits (especially grain quality).

These traits have become important features of research policy and design. Rice breeders seek both ‘quantitative’ genetic objectives and specialized trait-based genetic objectives. The ‘IRRI plant-type’ as exemplified by IR8 represented a major advance in quantitative genetic traits which are complex and controlled by many genes. The incorporation of specialized traits, which are controlled by a single (or few) genes, has been the objective of most rice breeding work since the development of the IRRI plant type. The Genetic Evaluation and Utilization (GEU) programme at IRRI, for example, was directed toward incorporating a number of specialized traits into rice varieties. (IRRI has also recently started work on a second plant type.)

Specialized traits are also likely to be the objectives of rice biotechnology

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research. The tools of biotechnology allow breeders to search for 'alien gene' sources of traits. It is thus important that estimates of the economic value of these traits be made.

It is possible to use 'hedonic' regression methods to infer trait values. These methods require a measure of value of the item in which traits are embedded – in this case in rice cultivars. As noted above, traits have two means by which they contribute values. First, they may result in higher rice yields, because of reduced losses from pests and disease (or they may result in higher value). But, second, they also contribute value if they enable high-yielding quantitative plant types to be produced in rice ecologies or environments where they were previously unsuited.

In light of this dual nature of trait values (i.e. affecting both yield and MV adoption), a model of MV adoption, supply and factor demands is suited to trait value analysis and to supply analysis. Such a model is specified in the following section of this chapter. The subsequent section summarizes data from India suited to estimation of the model, and the final section reports estimates for a region of north India.

Trait Values in a Model of Crop Supply and Factor Demand

Supply analysis has traditionally ignored technology as a major determinant of supply. Consider the traditional 'Nerlovian' supply response model as represented by equations (1)–(3):

$$A_t^* = A\left(P_t, Z_t\right). \tag{1}$$

Desired acreage planted to crop *i* in period *t* is specified to be a function of relative prices of crop *i*, P_t, and other infrastructural variables, Z_t, in equation (1).

$$A_t - A_{t-1} = \beta\left(A_t^* - A_{t-1}\right). \tag{2}$$

Costs of adjustment, however, prevent farmers from fully moving from last period's acreage to desired acreage in year *t*. Equation (2) states that the fraction β of the change will be made in each period.

If equation (1) is a linear function:

$$A_t^* = a + bP_t + cZ_t \,,$$

then

$$\begin{aligned} A_t - A_{t-1} &= \beta\left[\left(a + bP_t + cZ_t\right) - A_{t-1}\right] \\ A_t - A_{t-1} &= \beta a + \beta bP_t + \beta cZ_t - \beta A_{t-1} \\ A_t &= \beta a + \beta bP_t + \beta cZ_t + \left(1 - \beta\right)A_{t-1}. \end{aligned} \tag{3}$$

Equation (3) is typically estimated with some kind of error specification to account for the lagged dependent variable specification. Technology variables could be incorporated in Z_t provided they were exogenous. Adoption of MVs is typically a choice variable and thus endogenous, although some features of MVs, e.g. the availability of traits, may be considered the product of research programmes and thus not a choice variable to farmers.

In the older supply response literature a yield equation is sometimes estimated to achieve a full supply model.

The older duality-based supply model has also typically ignored technology, and the adjustment cost dynamics have typically also been ignored in earlier works. Equations (4)–(6) set out the fundamentals of the standard duality model.

Equation (4) describes a multiple output transformation function where two products (Y_1, Y_2) are produced using variable inputs (X_1, X_2, X_3), fixed factors, F, infrastructure, I, and technology, T:

$$G\left(Y_1, Y_2, X_1, X_2, X_3, F, I, T\right) = 0. \tag{4}$$

Variable profits are defined as:

$$\Pi = P_1Y_1 + P_2Y_2 - R_1X_1 - R_2X_2 - R_3X_3. \tag{5}$$

Maximized variable profits are defined as:

$$\Pi^* = P_1Y_1^* + P_2Y_2^* - R_1X_1^* - R_2X_2^* - R_3X_3^* \tag{6}$$

where Y_1^* and Y_2^* are profit-maximizing levels determined by maximizing equation (5) subject to equation (4). Since these levels are functions of output prices, input prices, F, I and T, the maximized profits function can be written as:

$$\Pi^* = \Pi\left(P_1, P_2, R_1, R_2, R_3, F, I, T\right). \tag{7}$$

The Shephard–Hotelling Lemma applied to Equations (6) and (7) yields a system of output supply and factor demand equations:

$$\begin{aligned}
\partial\Pi^*/\partial P_1 &= Y_1 = Y_1\left(P_1, P_2, R_1, R_2, R_3, F, I, T\right)\\
\partial\Pi^*/\partial P_2 &= Y_2 = Y_2\left(P_1, P_2, R_1, R_2, R_3, F, I, T\right)\\
\partial\Pi^*/\partial R_1 &= X_1 = X_1\left(P_1, P_2, R_1, R_2, R_3, F, I, T\right)\\
\partial\Pi^*/\partial R_2 &= X_2 = X_2\left(P_1, P_2, R_1, R_2, R_3, F, I, T\right)\\
\partial\Pi^*/\partial R_3 &= X_3 = X_3\left(P_1, P_2, R_1, R_2, R_3, F, I, T\right).
\end{aligned} \tag{8}$$

Equation system (8) has been applied to a number of agricultural data sets (Huffman and Evenson 1993; Evenson *et al.*, 1996) and technology variables have been incorporated into these systems. The 'shadow prices' (i.e. $\partial\Pi^*/\partial T$) of technology variables can be computed and evaluated. Some of these systems have utilized MV variables as technology variables, although the exogeneity of such variables is in question. (Evenson *et al.*, (1996) treat these as exogenous when computed for all crops.)

Equation system (8) does not utilize measures of crop acreage on the grounds that acreage allocation is implied by the supply decision and variable factor demand decisions. Of course it is true that the quantity supplied is simply acreage times yield, and we could justify replacing the supply equations in (8) with acreage equations and yield equations on these grounds. This would, by itself, be insufficient grounds for doing so, but there are at least four solid justifications. These are:

1. Acreage and yield decisions have a true sequential nature (Antle, 1983).
2. Error terms, especially weather errors, affect yields, but not acreage.
3. MV specifications can be endogenized.
4. Dynamic adjustment specifications can be more easily justified.

The sequential decision argument runs as follows. Farmers make their crop acreage decision based on information available prior to planting time. They make provisional input decisions at the same time. Once planting begins they cannot alter their acreage choice, but they can alter other input choices in response to changes in prices and weather events. Weather events may thus affect both factor use and yields.

Adjustment costs may impinge on the use of variable inputs as well as on acreage although one would expect acreage adjustment costs to reflect these variable input costs as well. (Family labour use may be a quasi-fixed factor with high adjustment costs, for example.)

Farmers respond to changes in technology as well as to changes in prices. Their ultimate objective is net revenue or net profits. They will compare net revenues from one crop with net revenues from another crop, then formulate expectations by observing MV availability and adoption as well as prices. The profits function model implies cross-equation restrictions on net revenues. Hence both MV or technology terms and prices will have these restrictions.

MV adoption itself should be treated as an endogenous choice variable. The logic of the traits discussion suggests that profitability and the *availability* of traits, along with farmer characteristics and extension, will govern MV adoption. One of the concerns in this specification is to measure trait availability so as to achieve 'exogeneity' for trait availability while allowing for endogeneity of the MV adoption itself.

In this study this is accomplished as follows:

1. MV profitability for rice is proxied by state acreage ratios of MV rice yields to traditional (unirrigated) rice yields. Dummy variables for districts are interacted with this variable to allow for proportional district differences. This variable reflects trait values to some extent.

2. For India, data have been collected for ‘leading’ rice varieties over the 1978–1992 period. In selected districts, farmers’ yield traits for the three leading rice varieties were collected. The set of such varieties for each major agro-climatic region then constitutes a collection of ultimately successful varieties. For this set of varieties, it is possible through geneology analysis and breeders’ ratings to compute acreage traits in the set of such varieties and to date them according to the date of release of the ultimately successful varieties. These ‘availability’ data are exogenous to farmers in that they represent breeders’ success.

The model suggested by these considerations is shown as equation system (9):

$$\begin{array}{cl}
\begin{array}{c}\text{Modern}\\ \text{variety}\\ \text{adoption}\end{array} & \begin{cases} MV1: Y_1^*, I, TR_1^*, T_1 \\ \\ MV2: Y_2^*, I, TR_1^*, T_2 \end{cases} \\
\begin{array}{c}\text{Acreage}\\ \text{decision}\end{array} & \begin{cases} A1: MV1, MV2, P_1, P_2, R_1, R_2, R_3, T_1, T_2, I, F, A_{1t-1} \\ A2: MV1, MV2, P_1, P_2, R_1, R_2, R_3, T_1, T_2, I, F, A_{2t-1} \end{cases} \\
\begin{array}{c}\text{Demand}\\ \text{for}\\ \text{factors}\end{array} & \begin{cases} X_1: MV1, MV2, P_1, P_2, R_1, R_2, R_3, T_1, T_2, I, F \\ X_2: MV1, MV2, P_1, P_2, R_1, R_2, R_3, T_1, T_2, I, F \\ X_3: MV1, MV2, P_1, P_2, R_1, R_2, R_3, T_1, T_2, I, F \end{cases} \\
\begin{array}{c}\text{Yield}\\ \text{outcomes}\end{array} & \begin{cases} Y1: A1, MV1, T_1, P_1, R_1, R_2, R_3, I, W, TR, F \\ Y2: A2, MV2, T_2, P_2, R_1, R_2, R_3, I, F. \end{cases}
\end{array} \tag{9}$$

System (9) has four blocks. The first is a set of two equations determining MV adoption. State yield ratios, Y_1^*, etc., and technology (research), T_1^*, variables are determinants of adoption. The infrastructure and skill variables, *I*, are included in this (and other blocks) as well. The rice trait availability data (TR_1^*)are also included.

The second block is the acreage price response block. Each equation in this block includes all (endogenous) MV variables, all prices and all research variables (*T*) as well as *I* and *F* variables. Cross equation restrictions hold for the MV variable (e.g. $\partial A1/\partial MV2 = \partial A2/\partial MV1$), for the price variables, and for the research variables. Acreage decisions are treated as subject to Nerlovian cost adjustment (A_{t-1}).

The third block includes the variable input demand equations.

The fourth block includes the yield equations. These include only the ‘own’ areas, MV, price and research variables. They also include the *I* variables and weather variables *W*. For rice the trait values are also included.

This system then constitutes a complete supply-factor demand system based on profit maximization in MV adoption decisions, acreage decisions and yield (supply) outcomes. One can compute the implicit shadow prices for the policy variables, *I*, *T*, *F* and *TR* (traits). These are evaluated as impacts on farm revenue.

Application to Indian Data: the North India Wheat Region

For the north India wheat region, a two-commodity, four-input system was developed. The relevant variables are briefly defined and summarized in Table 11.1.

The system was estimated for alternative sets of traits. Table 11.2 reports the full set of estimates for trait set 1 utilizing 3SLS in the seemingly unrelated regression system. Cross-equation restrictions were applied where relevant. All equations included district dummy variables so this is a ‘fixed effects’ estimation.

Since this is a ‘structural’ model, the coefficients do not show the full effects of the independent variables. For example, extension affects MV adoption and has additional effects on yields and demand for factors.

Consider first the two MV adoption equations:

- Expected revenues as reflected in state yields times prices have the expected effects for both rice and wheat. An increase in traditional rice revenues stimulates MV adoption in wheat.
- Extension stimulates rice MV adoption, but not wheat MV adoption.
- Literacy stimulates MV adoption.
- Road infrastructure stimulates MV adoption.
- Irrigation investment stimulates MV adoption.
- The availability of new traits and the increased complexity of rice MVs stimulates rice MV adoption.

Next consider the area equations:

- Expansion of rice MV adoption has small negative impacts on wheat area, but wheat MV adoption has a positive impact on both wheat and rice areas. It appears that the higher yielding rice varieties tend to lead farmers to reduce acreage planted to rice, and shift to other summer crops. There is little substitution of other crops for wheat.
- Higher wheat revenues stimulate more area in both wheat and rice.
- Factor prices have few effects on area – except for wages for wheat, where higher wages stimulate more wheat area. (Note, there may be some endogeneity here.)
- Research, given MV adoption, tends to encourage substitution of other crops for rice and wheat.
- Extension stimulates more area in both crops.
- Literacy has little effect on area planted.
- Road infrastructure stimulates more area in both crops.
- Irrigation investment stimulates more area in both crops.
- Lagged area effects show significant adjustment costs.

Table 11.1. Variable definitions: north India wheat region.

Variable	Definition	Mean
1. Endogenous		
PHYVRICE	Per cent of area planted to mod rice	0.28
PHYVWHT	Per cent of area planted to mod wheat	0.39
ARICE	Area planted to rice (kha)	64.6
AWHEAT	Area planted to wheat (kha)	169.9
QBullock	Quantity (bullock power)	150,489
QTractor	Quantity (tractor use)	2,879
QLabour	Quantity (labour)	65.941
QFert	Quantity (fertilizer)	2,709
YRICE	Yield (rice)	1.502
YWHEAT	Yield (wheat)	1.631
2. Exogenous		
Prices (revenues)		
MR2	Ratio: expected revenue trad rice/mod rice	0.89
MR3	Ratio: expected revenue wheat/mod rice	1.21
MR4	Ratio: expected revenue mod wheat/mod rice	1.14
MW1	Ratio: expected revenue trad rice/mod wheat	0.84
MW2	Ratio: expected revenue mod rice/mod wheat	0.74
MW4	Ratio: expected revenue trad wheat/mod wheat	0.94
WAGEOUT	Wage/P output	2.27
TRACOUT	Price of tractors/P output	3,352
FERTOUT	Price of fertilizer/P output	1,084
BULLOUT	Price of bullocks/P output	281
Technology		
LGCRICE5	Rice research stock (Evenson *et al*., 1996)	19.75
LGCWHT5	Wheat research stock (Evenson *et al*., 1996)	7.37
EXT	Extension staff/farm	7.80
LITERACY	Per cent literate farmers	0.300
Infrastructure		
IROADS	Index of change in roads	1.813
NIANCA	Net irrigated acreage/net cropped area	0.44
Weather		
YEARRAIN	Rainfall (year)	782
JUNERAIN	Rainfall (June)	90
JUARAIN	Rainfall (July, August)	436
Rice traits		
AGRQUAL	Leading varieties with improved agronomic quality	1.25
ABIOSTRESS	Leading varieties with ecology stress tolerance	2.85
DISINS	Leading varieties host plant disease, insect resistance	7.47
NLR	Number of landraces in leading varieties	3.05

mod, modern; trad, traditional.

Table 11.2. Two-commodity system north India wheat region, 1956–1987

	Endogenous independent variables									
	Per cent HYV		Area planted		Yield		Demand for factors			
	Rice	Wheat	Rice	Wheat	Rice	Wheat	QBullock	QTractor	QLabour	QFert
1. Endogenous										
PHYVRICE			−8.18 (1.35)	−27.6 (2.16)	0.988 (9.59)		35,740 (1.87)	2,943 (3.36)	6,425 (1.00)	22,172 (3.51)
PHYVWHT			10.74 (2.26)	39.39 (4.07)		0.502 (8.23)	−44,884 (2.99)	−1,218 (2.09)	−12,053 (2.38)	−4,992 (1.01)
ARICE × lagged PHYVRICE			0.865 (50.37)		0.001 (1.78)					
AWHT × lagged PHYVWHT				0.804 (37.7)		0.001 (1.52)				
2. Exogenous										
MR2	−1.09 (13.8)									
MR3	0.121 (1.40)									
MR4	−0.128 (1.43)	0.841 (8.97)	5.03 (1.85)	1.73 (0.32)			16,472 (1.91)	865 (2.60)	5,841 (2.01)	4,522 (1.56)
MW1		0.809 (8.89)								
MW4		−1.42 (11.82)								
WAGEOUT			−0.65 (0.60)	7.52 (3.25)			−27,401 (7.91)	847 (6.29)	−7,101 (6.08)	3,984 (3.48)
TRACOUT			−0.001 (0.41)	−0.002 (0.59)			4.54 (0.71)	−71.4 (2.88)	0.97 (0.45)	0.93 (0.44)
FERTOUT			−0.002 (0.64)	0.002 (0.27)			19.88 (1.69)	0.610 (1.34)	3.21 (0.81)	−6.68 (1.73)
BULLOUT			−0.008 (0.54)	−0.075 (2.81)			38.1 (0.91)	−2.31 (1.42)	24.9 (1.77)	−17.6 (1.23)

LGCRICE5			−61.21 (4.08)	−30.15 (0.99)	0.637 (0.11)		80,399 (1.68)	−7,084 (3.81)	−25,873 (1.60)	−71,088 (4.50)
LGCWHT5			−732.40 (6.80)	−168.7 (4.31)		−0.977 (2.76)	83,859 (1.37)	6,743 (2.82)	70,172 (3.39)	−91.977 (4.53)
EXT	0.021 (6.54)	−0.015 (5.71)	1.99 (3.32)	1.36 (1.92)	0.023 (8.18)	0.065 (10.16)	−1,987 (1.81)	134 (3.14)	−281 (0.76)	4,513 (12.47)
LITERACY	0.191 (1.20)	0.413 (2.64)	−50.07 (3.96)	6.40 (0.24)	−0.581 (1.86)	0.225 (0.89)	−160,064 (4.10)	−10,018 (6.60)	−112,465 (8.53)	−110,622 (8.57)
IROADS	0.074 (6.91)	0.012 (1.77)	3.04 (3.11)	0.63 (0.32)	0.282 (12.6)	0.049 (2.78)	−6,886 (2.73)	1,428 (11.89)	−3,067 (2.94)	3,482 (3.41)
NIANCA	0.128 (2.70)	0.208 (4.13)	0.529 (0.13)	22.62 (2.39)	0.822 (8.75)	0.556 (6.05)	−28,104 (2.24)	4,809 (9.81)	29,922 (7.04)	41,630 (9.99)
YEARRAIN					0.0002 (8.10)	−0.000 (1.27)				
JUNERAIN					0.000 (0.35)	−0.000 (2.69)				
JUARAIN					0.000 (0.47)	0.000 (1.26)				
AGRQUAL	0.006 (3.05)				0.005 (5.37)					
ABIOSTRESS	0.016 (1.81)				0.025 (1.13)					
DISINS	0.037 (6.26)				0.015 (1.11)					
NLR	0.033 (4.43)				−0.044 (2.56)					
YEAR	−0.023 (7.48)	0.026 (14.9)	13.80 (7.19)	14.61 (3.80)	−0.022 (0.83)	0.064 (2.45)	−7,896 (1.31)	−77.6 (0.33)	−7.84 (1.31)	10,862 (5.45)

Next consider the yield effects:

- MV effects are high in both crops, but higher in rice.
- Area effects are small but positive. Expansion of area does not lead to lower yields.
- Research, given MV adoption, has little effect (research produced the MVs and this is its main contribution).
- Extension positively affects yields.
- Literacy has little effect.
- Road infrastructure positively affects yields.
- Irrigation investment increases yields.
- Rice traits have mixed effects. Varietal complexity (number of landraces) results in lower yield (but stimulated MV adoption). Insect resistance traits lead to higher yields (and higher adoption). Disease resistance effects are smaller.

Finally, consider the factor demand equations:

- Rice MV adoption stimulates more demand for all factors, especially for tractors and fertilizer.
- Wheat MV has input savings effects, especially for labour and bullocks.
- Revenue effects for wheat outweigh those for rice and have positive effects on factor demand.
- Factor prices have expected own price effects (except for bullocks). Labour and tractors are substitutes.
- Rice research holding MVs constant saves factors. Wheat research stimulates factor use.
- Literacy saves factors.
- Road infrastructure saves labour and bullocks and stimulates tractor and fertilizer demand.
- Irrigation investment stimulates tractor, labour and fertilizer demand and reduces bullocks demand.

Economic Effects

One can compute the implicit shadow prices for the policy variables, *I*, *T*, *F* and *TR* (traits). These are evaluated as impacts on farm revenue.

The PHYVRICE equation clearly shows that traits affect the adoption of modern rice varieties and that they drive MV expansion beyond the original first generation levels. The three variables AGRQUAL, ABIOSTRESS and DISINS increased PHYVRICE by 27% over first generation levels. An increase in NLR of 2 also increased PHYVRICE by 6–7%. Thus we can conclude that the addition of these traits probably expanded PHYVRICE by roughly one-third, i.e. from 40% of area to 60% of area by 1984. By 1995 this has increased further to 75%.

The effects of traits on average yields is negligible when the negative NLR coefficient is considered.

Thus, we can approximate the value of third and fourth generation traits as an expansion of modern rice area of 15–20% times the yield effect of PHYVRICE. This indicates a yield increase of roughly one ton per hectare (a 65% increase).

MVs also increased input use per hectare by about 10%, so the net productivity increase was probably in the order of 50%. The trait values associated with third and fourth generation breeding then added 8–10% to national agricultural income. This estimate is roughly double the Gollin–Evenson estimate based on yield effects only (Chapter 9).

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12

Crop-loss Data and Trait Value Estimates for Rice in Indonesia

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Plant breeders make a distinction between ‘quantitative’ characteristics of rice cultivars and specific traits. Quantitative characteristics or traits describe the biological performance of the cultivar and are governed by a number of genes. The semi-dwarf plant type as typified by the first generation of modern rice varieties (e.g. IR8) is a quantitative characteristic. Specific traits are usually controlled by a single gene (or very few genes) and are typically found in plants (usually in landraces or wild species) that do not themselves have valuable quantitative characteristics. Through backcrossing and other methods, breeders can incorporate these specific traits into modern cultivars with valuable quantitative characteristics.

Important qualitative traits include the following: (i) resistance to insect damage; (ii) resistance (tolerance) to disease damage; (iii) tolerance of ecological stresses (cold, heat, flood, drought); and (iv) grain quality and agroeconomic features (e.g. ease of harvesting).

The first two categories are directly related to crop-loss evidence. Crop-loss data showing estimates of farm losses from specific insect pests and diseases are now available for several countries. Some of these loss data cover losses due to ecological stress as well. Crop-loss data can then at least potentially be linked with varietal trait data in a ‘hedonic’ type regression to estimate the value of varietal traits.

This chapter reports hedonic value estimates based on crop-loss data from Indonesia. A short review of crop-loss evidence for rice is first presented. Then rice productivity and varietal change data in Indonesia are reviewed. A short methodology section discusses the hedonic methods both for crop-loss and productivity specification. Estimates for Indonesia are presented and discussed. The

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final section discusses the limitations and promise of crop-loss data for trait value estimation.

Crop-loss Data

There are at least three conceptual problems with crop-loss estimates. The first is the distinction between *actual* losses by farmers given that certain loss reduction practices (e.g. pesticide application, crop rotation, etc.) were used and *potential* losses if such practices were not used. This distinction is important because the incorporation of resistance typically will produce both lower actual losses and reduced pesticide use. The reduction in actual losses will not be a full measure of trait values. Potential losses may be a better measure, although pesticide use data should ideally be used.

The second conceptual problem is that crop losses may not be 'additive'. That is, total losses from two or more insect pests may be greater or less than the losses attributed individually to each pest (and similarly for diseases). Crop-loss data are typically attributed to individual pests.

The third conceptual issue is that the incorporation of insect or disease resistance into modern varieties (MVs) may result in the adoption of the higher yielding cultivar in locations where the pests are endemic. Crop losses may not actually be reduced, but yields will have been increased.

A related issue that requires consideration in actual estimates is that the natural incidence of pest and disease pressure varies by location and over time. Variation by location creates a 'left-out' variable problem. Locations with high natural incidence may have high losses even though resistance to pests and diseases is quite valuable. Variation over time means that pest and disease resistance may be of little or no value in some periods and of high value in others.

A recent study of rice crop loss reports loss measures for Indonesia, China and India (Evenson *et al.*, 1996). The Chinese data show actual losses, given existing protection, and potential losses without protection.

This study showed that actual loss levels were relatively low. For disease losses, they were less than 1% in Indonesia (in 1986). They were between 1 and 2% in China. Insect losses were higher in Indonesia and India but not in China, generally being less than 2% (although they were 4.25% in Indonesia before MVs were introduced). Potential losses in China were in the 5–7% range. (The Nepal estimates were in the 15% range.)

In Indonesia, crop losses from insects were higher prior to 1980 when first generation (see below) modern rice varieties were replaced with second and third generation MVs.

Method: Hedonic Trait Valuation

Hedonic trait valuation methods can be described as follows:

$$V_{ij} = F\,(T_{1ij}, T_{2ij}, \ldots, T_{nij}, Z_{ij}) \tag{1}$$

where: V_{ij} is some measure of the economic value of a variety i (or a set of varieties) in location j; $T_{1ij}, T_{2ij}, \ldots, T_{nij}$ is an index of the possession of traits 1, 2, ... , n (e.g. resistance to gall midge) of the variety or set of varieties in location j; Z_{ij} is a vector of economic and ecological factors. The function itself may be linear or non-linear.

Crop-loss data are typically available for a location and time period. In Indonesia, losses by type (insect and disease) are measured by province and year. A matching set of trait indexes is required. This requires data on varieties planted and trait ratings by variety. For Indonesia it was possible to compute the percentage of area planted in each region and period with specific traits.

Equation (1) does not explicitly deal with several econometric problems. The first, as noted above, is that there is a natural incidence factor for pests and diseases. And this may vary by both location and time period. If a good measure of this factor were included in Z_{ij}, equation (1) could be regarded as a ‘technical’ relationship between losses and traits. The fact that the traits, i.e. the adoption of varieties with the traits, may be endogenous (e.g. it may respond to the Z_{ij} vector and to economic factors) can be set aside if the Z_{ij} vector is complete and controls for differences in natural incidence. But if natural incidence is not well measured, endogeneity cannot be set aside.

A related problem lies behind this specification; reduced crop losses (as measured by per cent of the crop actually lost) may be a poor measure of the value of a trait. Ideally one would like a measure of average variable cost. Pesticides, herbicides, etc., as well as farm practices, can be and are used to reduce crop losses. The incorporation of traits may reduce the costs of these chemicals and practices. As noted earlier, these traits may also have the effect of enabling the adoption of modern high-yielding varieties (i.e. with high-yielding quantitative traits) to be adopted in locations where they otherwise would not be adopted (the ecological stress tolerance traits would be particularly likely to have this effect).

In this study, the problem of endogeneity of traits will not be addressed directly (see Evenson, 1994, for a treatment of this problem). However, three measures of this will be utilized: crop losses, pesticide use and TFP (which is an index of changes in average variable cost).

Productivity and Modern Rice Varieties in Indonesia

For Indonesia, sufficient data exist on inputs by crop to enable the calculation of total factor productivity indexes (TFP) that take into account the use of conventionally measured inputs. These indexes show that after considering all inputs, Indonesia has achieved impressive growth in TFP in rice.

Rice varieties in Indonesia have undergone considerable change within the MV class. Dwidjono (1993) has defined the following ‘generations’ of rice varieties.

- Generation 1. This generation includes IR5, IR8, IR20 and C463. These are the first semi-dwarf varieties developed in the Philippines (IR5 and IR8 at IRRI, C463 at the University of the Philippines). It also includes Pelita 1/1 and Pelita 1/2, the first Indonesian-bred varieties. These varieties were generally subject to brown plant hopper (BPH) and tungro virus attacks.
- Generation 2. This generation includes varieties developed at IRRI and in Indonesia that incorporated BPH resistance and tungro resistance. These include IR22, IR34 (from IRRI) and several varieties from Indonesian programmes. These varieties were developed in response to the incidence of insect and disease problems afflicting the first generation of MVs.
- Generation 3. This generation includes both IRRI (IR32–38) and Indonesian varieties that incorporate multiple resistance and tolerance traits. The IRRI varieties were the result of its Genetic Evaluation and Utilization (GEU) programme in the 1970s.
- Generation 4. This generation includes other MVs incorporating more location-specific and related traits. These varieties were released in the 1980s and include mostly Indonesian varieties.

Each of these MVs was rated by plant breeders for resistance to three diseases (bacterial leaf blight, tungro virus and grassy stunt virus) and two insect pests (BPH and gall midge (GM)).

Variables

For Indonesia it was possible to construct a full variable set for eight regions for the 1971–1990 period. Table 12.1 provides a definition of each variable used in the analysis. Variables are identified as endogenous or exogenous.

The endogenous variables include each of the five crop loss variables, pesticide use, and a cumulated index of rice total factor productivity. The pesticide variable is treated as an independent determining variable. Thus a simultaneous equations estimation procedure is required. The procedure utilized is two-stage least squares (2SLS).

Estimates

Table 12.2 reports 2SLS coefficients and asymptotic ‘t’ ratios for each of the five crop-loss equations (Table 12.3 reports the sixth equation predicting the pesticide use variable which was estimated). Three specifications are estimated. In

Table 12.1. Variables: Indonesia study.

I. Dependent variables	
Crop-loss variables (per cent of crop)	
Brown plant hopper	0.0072
Gall midge	0.0014
Bacterial leaf blight	0.0016
Grassy stunt virus	0.00016
Rice tungro virus	0.000478
Pesticide costs (rupiahs ha^{-1})	0.5585
Rice TFP (index)	1.432
II. Independent variables	
Pesticide costs (rupiahs ha^{-1}), treated as an exogenous variable	
Rice inputs index	1.150
Intensification programme (per cent coverage)	0.67
Farm size (ha)	1.224
Roads (proportion of villages with 2 km of all-weather roads)	59.10
Research stock (see Evenson, 1994)	5.53
Extension (staff per farm)	0.00016
Varietal resistance (per cent of area)	
Brown plant hopper	0.56
Gall midge	0.30
Bacterial leaf blight	0.55
Grassy stunt virus	0.05
Rice tungro virus	0.07
Modern varietal generations (per cent of area)	
Generation 1	0.097
Generation 2	0.083
Generation 3	0.357
Generation 4	0.154

the first, varietal resistance variables are included but generation variables are excluded. In the second, both resistance and generational variables are included. In the third, only generational variables are included.

The *a priori* expectations are that increased areas planted to varieties with resistance to the insect or disease problem should reduce crop losses. It is also generally expected that pesticide use will reduce crop losses. Research on rice, holding varietal characteristics constant, is a measure of non-varietal research findings, and this too is expected to be crop-loss reducing.

Examination of the estimates indicates that there probably is a problem with the fact that the natural susceptibility of each region to crop losses varies by region and year. A region with high natural susceptibility will likely have more resistant varieties, more pesticide use, and more losses. This will create a positive bias in the trait coefficients, offsetting the expected negative resistance

Table 12.2. Crop-loss determinants.

	Specification	Farm size	Rice research	Pesticide use	Varietal resistance	Breeding generation				
						1	2	3	4	R^2
Brown plant hopper	(1)	−0.0692 (2.26)	−0.0078 (1.51)	0.72 (0.90)	−0.0213 (2.11)					(0.45)
	(2)	−0.0273 (0.86)	−0.0023 (0.68)	−0.89 (0.83)	0.010 (0.27)	0.038 (2.07)	0.022 (0.01)	−0.0150 (0.40)	0.001 (0.03)	(0.52)
	(3)	−0.0189 (0.57)	−0.0074 (0.12)	−1.92 (1.26)		0.036 (1.97)	0.030 (1.76)	−0.010 (0.70)	−0.019 (1.01)	(0.52)
Gall midge	(1)	0.0076 (0.36)	0.0033 (1.07)	−0.82 (1.24)	−0.0193 (3.28)					(0.22)
	(2)	0.0045 (0.20)	0.0025 (0.64)	−1.08 (1.42)	0.0054 (0.33)	−0.005 (0.38)	0.006 (0.57)	−0.022 (1.24)	0.05 (1.17)	(0.24)
	(3)	0.0028 (0.12)	0.0021 (0.52)	−0.76 (0.72)		−0.003 (0.26)	0.007 (0.58)	−0.16 (1.61)	0.003 (0.22)	(0.23)
Bacterial leaf blight	(1)	−0.0012 (1.78)	−0.0002 (2.09)	0.40 (2.35)	0.0002 (1.11)					(0.21)
	(2)	−0.0016 (2.18)	−0.0003 (2.18)	0.07 (0.90)	0.0001 (0.09)	−0.0004 (0.94)	−0.0007 (1.61)	−0.0002 (0.27)	0.0002 (0.36)	(0.25)
	(3)	−0.0014 (1.95)	−0.0002 (0.93)	0.10 (0.29)		−0.0004 (1.05)	−0.0007 (0.74)	−0.0002 (0.67)	0.0003 (0.87)	(0.25)
Grassy stunt virus	(1)	−0.0016 (1.45)	−0.00024 (1.74)	0.008 (0.15)	−0.0001 (0.09)					(0.20)
	(2)	−0.0017 (1.35)	−0.0003 (1.08)	−0.05 (0.90)	0.0001 (0.12)	−0.0019 (2.67)	−0.0003 (0.43)	−0.0010 (1.79)	0.0001 (0.19)	(0.37)
	(3)	−0.0009 (0.62)	−0.0001 (0.43)	−0.15 (2.30)		−0.0022 (2.83)	−0.0003 (0.38)	−0.0014 (2.27)	0.0008 (0.95)	(0.27)
Rice Tungro virus	(1)	0.0042 (1.19)	0.0004 (0.90)	−0.010 (1.10)	−0.0033 (1.19)					(0.25)
	(2)	0.0072 (1.68)	0.0010 (1.35)	0.035 (0.19)	−0.0007 (0.18)	0.0004 (0.18)	0.0025 (1.07)	0.0003 (0.15)	−0.0044 (1.34)	(0.27)
	(3)	0.0068 (1.59)	0.0010 (1.29)	0.069 (0.35)		0.0005 (0.20)	0.0024 (1.07)	0.0064 (0.20)	−0.0044 (1.74)	(0.30)

and pesticide use impacts. All equations included dummy variables for regions, but this has not fully controlled this problem.

The coefficients for pesticide use are marginally significant and negative only in the insect loss cases. They do not show strong effects for disease losses (except for grassy stunt virus). Varietal resistance traits are also not consistently significant in their effects on losses. There is some evidence for insect loss reduction.

When generational variables are included along with trait variables (version 2), trait coefficients are effectively reduced to zero. These generations are expected to have different effects by generation. We do not expect generation 1 to have strong effects. We find strong impacts only for grassy stunt virus losses. We expect stronger negative impacts from generation 2, and we find these for bacterial leaf blight. The strongest impacts should show up for generation 3, and we do find negative impacts in all but the rice tungro case where we find them in generation 4. In other cases, generation 4 varieties do not reduce losses (given that generation 3 has already reduced them to some degree).

Interestingly, non-varietal research appears to have loss-reducing impacts for BPH, bacterial leaf blight and grassy stunt virus. There is also some evidence that larger farms have lower per acre crop losses for these same pests and diseases.

Table 12.3 reports the pesticide use and rice TFP index equations. Pesticide use, holding all natural factors constant, should be reduced by expanded varietal resistance planted. This is not the case for most estimates reported in Table 12.3 where some positive effects are found, suggesting a bias due to unmeasured natural susceptibility. The inclusion of the generation variables (version 2) suggests some generation 3 impacts on pesticide use holding specific resistances constant (enough to cut pesticide use by half). Non-varietal research and extension did not appear to reduce pesticide use.

The TFP equation included crop inputs (including pesticide use) as an independent variable to provide some control for mismeasured factor shares. This variable, along with the intensification, farm size and roads variables, contributed little to explaining TFP growth. The chief variable determining TFP growth in rice is the research stock variable. It has high statistical significance in all specifications.

There is additional explanation to be had from the traits and generational variables, however. When the traits are included, three of the five appear to be significantly positive and the sum of the five coefficients is positive (and approximately equal to one, indicating that a 1% expansion in every trait would produce a 1% expansion in TFP).

When generational variables are added, four of the five trait variables become negative and the sum of coefficients becomes negative (-0.12). The generational variables are positive and quite high. They suggest that full generation 4 expansion may contribute to a doubling of TFP (yields) relative to the traditional varieties. However, when the resistance variables are dropped from the equation, the generational coefficients fall (to about 30% of their level in specification 2).

Table 12.3. Pesticide use and rice TFP determinants.

	Pesticide use ha^{-1}			Rice TFP index		
Specification	(1)	(2)	(3)	(1)	(2)	(3)
Rice research	1355	1300	1629	0.2787	0.2654	0.2678
	(1.28)	(1.26)	(1.31)	(6.44)	(6.48)	(5.40)
Rice inputs						
Extension	865	349	888			
	(1.05)	(0.38)	(0.88)			
Intensification programme	−32	−23	−69	−0.0014	−0.0017	−0.0021
	(1.49)	(1.09)	(2.95)	(1.35)	(1.87)	(2.02)
Farm size	4630	4226	5318	0.152	0.054	0.223
	(1.36)	(1.27)	(1.48)	(0.98)	(0.36)	(1.24)
Roads	62	64	51	0.0032	−0.0004	0.0011
	(2.41)	(2.49)	(1.68)	(0.27)	(0.33)	(0.84)
Varietal resistance						
BPH	2048	5896		−0.127	−0.507	
	(1.20)	(1.30)		(1.37)	(2.60)	
GM	−4342	627		0.591	0.619	
	(2.71)	(0.26)		(8.03)	(5.74)	
BLB	1257	6290		−0.184	−0.672	
	(0.59)	(1.67)		(1.89)	(4.23)	
GSV	10,622	7550		0.543	0.482	
	(4.96)	(3.22)		(5.48)	(4.61)	
RTV	−5015	−6985		0.172	−0.048	
	(1.87)	(2.35)		(1.39)	(0.37)	
Breeding generation						
1		326	−0.247		0.067	0.128
		(0.17)	(0.12)		(0.81)	(1.31)
2		−2571	4136		0.406	−0.105
		(0.55)	(1.93)		(2.06)	(1.16)
3		−12,324	−1248		0.812	0.254
		(1.84)	(0.78)		(2.87)	(3.46)
4		−5081	8303		0.986	0.125
		(0.71)	(4.37)		(3.25)	(1.45)
R^2	0.90	0.98	0.87	0.94	0.96	0.94

These results, then, appear to be an indication that the trait variables are subject to some natural susceptibility bias, and the negative coefficients in specification 2 suggest that acreage planted to varieties resistant to these diseases is responding to natural susceptibility and thus to some extent controlling for it, allowing for stronger generational impacts to be measured. Dropping these control variables reduces the size of the generational effect.

Economic Implications of the Estimates

It is relevant to note two conditions affecting the economic interpretation of the estimates. The first is that the values of traits are confined to those environments where disease and insect pressure is greatest. The second is that the trait values included in this study are incomplete. A new variety may have several traits and each has value. Since this study only covered two insect resistance and three disease resistance traits, it probably underestimates the full value of all traits.

Consider first the evidence regarding loss reduction. Specification (1) indicates that if all varieties had BPH resistance, losses from this pest would be reduced by 2%. Approximately the same can be said for GM resistance. In actuality only 60% of the varieties have BPH resistance and roughly 40% have GM resistance.

Thus by these estimates actual losses are only about 1% lower because of these two traits. But if we consider other insect pests and a further expansion of trait area, we could conclude that conventional plant breeding has reduced crop losses by 3–5% (considering these two insect pests to represent 25–33% of insect problems). There appears to be future potential for another 3–5% reduction if biotechnology methods enable a more complete incorporation of insect resistance traits.

For disease resistance traits, the evidence is less clear. Only rice Tungro resistance shows indication of loss reduction, and that is only by 0.3%. Even with some expansion to other diseases, it is difficult to say that disease resistance has contributed much more than 1% to crop-loss reduction to date.

The pesticide use estimates from specification 1 in Table 12.3 indicate that the total set of traits reduces pesticide use by 20% (the sum of coefficients is 4570, which is 80% of mean pesticide use). This amounts to roughly 1% of crop value.

Finally, the TFP equation can be utilized to calculate trait values. If we leave in the negative value for BPH, we obtain a coefficient of 0.46 for insect resistance and a combined coefficient of 0.53 for disease resistance. Multiplying these coefficients by adoption levels, these estimates imply that TFP indexes (yields) are higher (average costs are lower) by roughly 11% because of insect resistance and by 3% or so because of disease resistance traits.

The TFP-based estimates are higher than the combined crop-loss and pesticide estimates. With an expansion factor to cover other diseases and insects, the TFP evidence suggests that 15% of current TFP levels is due to these five traits. The generation 3 evidence (specification 3) indicates a 25% generation 3 gain. This is more than double the contributions suggested by the crop-loss and pesticide reduction estimates.

These estimates, however, can be reconsidered by noting that TFP (yields) may incorporate a synergistic effect, i.e. the sum is greater than the parts – in this case greater than the crop-loss parts.

It may thus be reasonable to conclude that, to date, rice yields in Indonesia are roughly 15% higher because of these traits, and that with synergism they may be 25% higher. It should be noted that this synergism is really due to quantitative trait improvement. Conventional plant breeding methods have allowed considerable gains to be realized in Indonesia and more are in the offing. This chapter has not directly considered ecological stress traits, although these may be captured in the TFP estimates, nor have grain quality traits been considered. Further research is required to more adequately address these issues.

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13

Breeding Values of Rice Genetic Resources

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Since 1960, the International Rice Research Institute (IRRI), located in the Philippines, has played a key role in worldwide efforts to develop improved varieties of rice. IRRI has a number of programmes to facilitate rice genetic improvement. IRRI's own plant breeding programme (IRPB) produces improved cultivars, both in the form of 'varieties' that are ready for use in farmers' fields and in the form of 'advanced lines' suited for use as parent material in national plant breeding programmes. IRRI maintains an international collection of rice genetic resources, the International Rice Germplasm Collection (IRGC) designed to preserve germplasm and to provide it freely to the international scientific community, including national germplasm collections. In addition, IRRI maintains and coordinates a system of international nurseries, the International Network for the Genetic Evaluation of Rice (INGER), through which advanced genetic materials are exchanged and evaluated.

In this chapter we analyse the economic role of IRRI's three international programmes (IRPB, IRGC and INGER) and estimate their economic contributions as embodied in improved rice cultivars. We conduct a genealogical analysis of released rice varieties from national rice breeding programmes and IRRI since 1965, when the first modern high-yielding rice varieties were released, and we trace the 'routes' by which rice germplasm is incorporated into improved varieties. An econometric analysis is undertaken to estimate the impacts of the IRPB, IRGC and INGER programmes on the number of improved varieties developed over the 1965–1990 period. Calculations based on these estimates provide estimates of economic value.[1]

For this study we have compiled a database of 1709 modern rice varieties released since the early 1960s.[2] For each of these released varieties, a complete genealogy was assembled, which included the date and origin of the cross on

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which the variety was based, as well as the date and origin of all parents, grandparents and other ancestors. Thus ancestry was traced back to original ancestors, in most cases, landraces or wild species.[3] In addition we were able to determine whether the cross or any ancestors appeared in IRRI's international testing programmes (INGER nurseries) and whether they were selected from these nurseries for crossing.[4]

Of the 1709 modern varieties and elite (advanced) lines, 33 were released prior to 1965 (and thus prior to the release of any IRRI materials).[5] Table 13.1 gives the frequency of release by country and by time period. Where release dates were not available, approximate dates were estimated based on available information.

The data set includes materials from numerous countries, but it is relatively more complete for rice-producing countries of South and Southeast Asia than for those from other regions. India, in particular, is represented in the data set at a level that appears to be disproportionately large, with 643 varieties. Although India's breeding programmes have a long and productive history, the data set probably reflects a bias towards India based on the extensive and available data.[6] For a number of reasons, Japanese varieties were not included in this analysis.[7] The data indicate that numbers of released varieties rose steadily during the 1970s but have stabilized over the past 15 years. In some countries and regions, however, such as Latin America, varietal release totals have climbed markedly in the most recent period.

Table 13.1. Numbers of varieties included in the data set, by country of release and by time period of release.

Country/region	Pre 1965	1966–70	1971–75	1976–80	1981–85	1986–91	Total
Africa	3	7	6	17	26	42	101
Bangladesh	1	7	8	11	4	3	34
Burma	0	4	6	21	37	8	76
China	0	1	8	30	31	12	82
India	10	67	136	139	125	166	643
Indonesia	1	2	5	21	10	9	48
Korea	0	5	11	35	40	15	106
Latin America	7	9	48	32	43	100	239
Nepal	0	0	1	10	4	2	17
Oceania	0	1	4	1	0	0	6
Pakistan	0	4	2	3	3	0	12
The Philippines	3	4	13	23	8	2	53
Sri Lanka	3	14	4	8	21	3	53
Taiwan	0	3	0	3	0	0	6
Thailand	1	2	4	8	5	3	23
USA	2	5	18	17	3	6	51
Vietnam	0	16	6	16	16	5	59
Other SE Asia	2	1	8	7	6	5	29
Other	0	7	15	15	15	19	71
Total	33	159	305	417	397	400	1709

International Flows of Genetic Resources

Table 13.2 reports measures of international flows of genetic resources associated with the released varieties and the parents of the released varieties. Of the 1709 released varieties, 390 (24%) were the result of a cross made outside the releasing country. IRRI was the source for 294 of these varieties. Other national programmes were the source for 96 releases. (Appendix Table 13.A1 provides country details for varieties.)

After IRRI, India was the next largest exporter of varieties, with 28 Indian varieties released elsewhere. India was also a large importer of varieties; 70 of its 643 varieties originated elsewhere, with 53 from IRRI. Sri Lankan varieties were released 11 times in other countries. Twelve Thai varieties were released in Myanmar; Myanmar was one of the largest importers of rice varieties; 43 of its 76 releases were imported varieties, including varieties from Bangladesh, China, India, Indonesia, IRRI, the Philippines, Sri Lanka, Thailand and Vietnam.

In addition to IRRI's direct role as a source of exported varieties, it has served as a conduit through which elite lines have moved from country to country. Even before the establishment of INGER in 1975, IRRI scientists helped to test and disseminate elite lines of rice around the world. This function was formalized with the inauguration of INGER. Through INGER's activities, elite lines and released varieties from national research programmes have been made available for international testing and evaluation. Participating countries have gained access to promising varieties, and in some cases, they have been able to import them directly from the INGER nurseries.

INGER itself keeps a complete and accurate set of data on varietal importing that has occurred through its programmes. INGER has documented more than 300 instances of varieties imported after appearing in INGER trials.[8] Our study lacks complete data on varietal releases in participant countries, especially in Africa and Latin America. Nonetheless, for a limited set of countries, this study

Table 13.2. International genetic resource flows by time period.

	Pre-1965	1966–1970	1971–1975	1976–1980	1981–1985	1986–1991	Total
I. Released varieties, per cent based on							
IRRI cross	3	25	19	22	18	12	17
Other NAR cross	16	7	6	6	6	5	6
Own NAR cross	81	68	75	72	76	83	77
II. Parents of released varieties, per cent with one or more parents							
IRRI cross	0	24	29	33	23	19	24
Other NAR cross	27	25	21	15	18	20	18
Own NAR cross	73	51	50	52	59	61	58

was able to identify nearly 200 instances in which varieties could have been imported through INGER.[9] In particular, INGER has played a significant role in disseminating IRRI lines. For varieties developed at IRRI and released by national programmes, INGER was the apparent conduit in half of the cases, all of them in the period, 1976–1991.

Since 1976, INGER has also become the primary channel through which nationally developed varieties have been transferred from one country to another. Since 1976, 37 national programme varieties have been imported through INGER. During the same period, the number of national programme varieties imported through other avenues has diminished from 13 in 1976–1980 to six in 1986–1991. INGER has played an important role in facilitating the transfer of varieties across geographic zones; for instance, both of two Sri Lankan varieties released in Africa came through INGER, and both of two Indian varieties released in Latin America came through INGER.

Perhaps more remarkable than the direct international flows of varieties has been the international flows of parents of the varieties. Nearly three-quarters of the varieties in the data set (1263) have at least one imported parent. Including imported varieties, 810 releases (47%) have at least one parent from IRRI, and 619 (36%) have at least one parent from another national programme (Table 13.2). Excluding imported varieties, more than 500 varieties have at least one parent from IRRI. Excluding both imported varieties and those with IRRI parents, more than 350 released varieties have at least one parent from another national programme. This indicates that the importation of parent materials is taking place across national programmes on a large scale. (Appendix Table 13.A2 reports country details for parents.)[10]

The extent of international exchange – both of varieties and of parents – implies that a large majority of the varieties in the data set were developed using breeding lines from outside the country of release. In fact, only 145 varieties out of 1709 (8.5%) were developed entirely from own-country parents, grandparents and other ancestors. Most of these were simple varieties with fewer than four ancestors in their pedigree. The extent of this international flow of germplasm is extraordinary: no country in the data set has failed to take advantage of unimproved or improved germplasm from other countries.

National rice improvement programmes have depended to differing extents on IRRI lines as sources of genetic materials (Appendix Tables 13.A1 and 13.A2). Some countries have borrowed many of their released varieties or parent lines from IRRI, while others have used IRRI materials in conjunction with local varieties or other internationally available breeding lines. For example, Vietnam and Pakistan have based their modern varieties almost completely on IRRI lines, but Sri Lanka used a large pool of other breeding lines as sources of germplasm.

Routes (Pathways) from Origin to Release

In order to analyse more formally the impacts of IRGC, IRPB and INGER, it is useful to trace the routes by which varieties were released. Table 13.3 provides a tabular summary of released varieties by pathway or route. These routes are defined to be mutually exclusive categories, so that each variety in the data set falls into exactly one of the following categories:

- Borrowed varieties.
  R1. IRRI line, borrowed through INGER (IRRI/INGER).
  R2. IRRI line, borrowed independently of INGER (IRRI/NO INGER).
  R3. Variety from another national programme, borrowed through INGER (OTHER NATL/INGER).
  R4. Variety from another national programme, borrowed independently of INGER (OTHER NATL/NO INGER).
- Nationally developed varieties, borrowed parents.
  R5. At least one parent from IRRI, borrowed through INGER (IRRI PARENT/INGER).
  R6. At least one parent from IRRI, borrowed independently of INGER (IRRI PARENT/NO INGER).
  R7. No IRRI parents, but at least one parent borrowed from another national programme via INGER (OTHER NATL PARENT/INGER).
  R8. No IRRI parents, but a least one parent borrowed from another national programme independently of INGER (OTHER NATL PARENT/NO INGER).
- Nationally developed varieties and parents, borrowed grandparents.
  R9. At least one grandparent from IRRI, borrowed through INGER (IRRI/GPARENT/INGER).

Table 13.3. Number of varieties released by route, by date.

	Pre-1965	1966–1970	1971–1975	1976–1980	1981–1985	1986–1991	Total
IRRI/INGER	0	0	5	50	52	39	146
IRRI/NO INGER	1	37	50	38	16	6	148
OTHER NATIONAL/INGER	0	0	0	10	15	12	37
OTHER NATIONAL/NO INGER	5	10	16	13	9	6	59
IRRI PARENT/INGER	0	0	0	46	89	79	214
IRRI PARENT/NO INGER	0	52	110	117	15	19	313
OTHER NATIONAL PARENT/INGER	3	2	15	34	69	85	208
OTHER NATIONAL PARENT/ NO INGER	9	30	50	22	13	27	151
OTHER	7	10	33	63	90	85	288
PURE NATIONAL	8	18	24	24	29	42	145
Total	33	159	303	417	397	400	1709

See text for definitions of categories.

R10. At least one grandparent from IRRI, borrowed independently of INGER (IRRI/GPARENT/NO INGER).
R11. No IRRI grandparent, but at least one grandparent borrowed from another national programme via INGER (OTHER GPARENT/INGER).
R12. No IRRI grandparents, but at least one grandparent borrowed from another national programme independently of INGER (OTHER GPARENT/NO INGER).

- Nationally developed varieties, parents, grandparents.

R13. All parents and grandparents from country of release (PURE NATIONAL).

In practice, virtually no varieties fell into categories 9 or 11, since INGER has not been in existence long enough to provide many grandparent materials. Moreover, many varieties with borrowed grandparents also have borrowed parents, or are even borrowed varieties. Thus, in some of the tables that follow, routes 9–12 are collapsed into a single category labelled ‘OTHER’.

International genetic exchange has been enormously important. Since 1970, only 7.8% of new varieties have been of ‘pure’ national development. The most significant channels of release have been the use of IRRI parents. Before 1975, IRRI parents were obviously not channelled through INGER, but in recent years, the largest single pathway for developing new varieties has been to use IRRI parents taken from INGER.

The importance of INGER can be seen by looking at the time trends on borrowing through INGER. Since 1981, more than half of released varieties (440 out of 797) have either been borrowed through INGER or were bred from parents borrowed through INGER.[11]

Table 13.4 reports numbers of ancestors and proportions of rare traits by route and by region. This table shows that IRRI material has been the conveyor of high landrace content and high rare trait content. In other words, IRRI materials have provided multiple single-gene traits packaged into readily usable breeding lines. IRRI has not, however, been the primary source of new ancestral material; most of the influx of landraces and other ancestral material has occurred through national and local breeding programmes. In these programmes, breeders are combining modern varieties with popular local and traditional varieties.

IRGC, IRPB and INGER Impacts on Numbers of Released Varieties

The data for routes suggest a substantial impact for IRRI programmes. A considerable number of borrowed varieties, parents, grandparents and ancestors from IRRI attests to the impact of the IRRI plant breeding programme, though not to its recent contribution. Flows through INGER also attest to its impact, although at least some of the INGER flows are substitutes for other flows. IRRI’s germplasm collection has contributed to the flows by supplying genetic material

Table 13.4. Routes of varietal release: descriptive statistics.

Route	No. of varieties	Per cent of varieties	Total area	Per cent of area	Average no. of landraces		Average no. of landraces independent of IRRI		Average no. of landraces with rare trait index >5.0
					Pre-1976	Post-1976	Pre-1976	Post-1976	
IRRI/INGER	146	8.5	5177	13.3	n.a.	13.2	n.a.	0.0	12.55
IRRI/NO INGER	148	8.7	3959	10.2	5.4	12.4	0.0	0.0	7.66
OTHER/INGER	37	2.2	411	1.1	n.a.	4.2	n.a.	2.1	3.35
OTHER/NO INGER	59	3.5	2954	7.6	4.4	5.2	2.5	1.6	4.14
IRRI PARENT/INGER	214	12.5	6570	16.9	n.a.	10.4	n.a.	1.2	9.55
IRRI PARENT/NO INGER	313	18.3	5589	14.4	5.6	9.5	1.7	1.4	6.53
OTHER PARENT/INGER	208	12.2	4283	11.0	n.a.	2.9	n.a.	2.5	1.52
OTHER PARENT/NO INGER	151	8.8	3228	8.3	3.4	4.8	3.4	3.8	2.68
IRRI GPARENT/INGER	14	0.8	670	1.7	0.0	7.2	0.0	3.0	6.00
IRRI GPARENT/NO INGER	94	5.5	1436	3.7	7.4	10.7	4.6	3.6	8.93
OTHER GPARENT/INGER	0	0.0	0	0.0	0.0	0.0	0.0	0.0	0.00
OTHER GPARENT/NO INGER	180	10.5	1482	3.8	4.4	4.1	4.3	3.8	2.04
PURE NATIONAL	145	8.5	3121	8.0	3.2	2.6	2.7	2.2	1.10

to plant breeders at IRRI and in national programmes. Some of this material flows through INGER as well.

In order to address the question of impact in a statistically sound manner, a model that takes national choices into account is required. Variables measuring the impacts on investments in IRGC, IRPB and INGER are required.

Table 13.5 provides a summary of the variables defined for this analysis. These are defined for 15 countries (or groups of countries) for the 1965–1990 period. The key endogenous variables to be 'explained' are R1–R9, the annual varietal releases by route. This set of varieties by route is 'jointly' determined by a set of explanatory variables. In addition, the number of landraces and the number of international and national rare trait materials are also endogenous variables.

The explanatory variables include variables measuring IRGC, IRPB and INGER activities, national demand and national plant breeding activities. Of these, the most complicated is the measure of INGER activities, NING, the number of nurseries in a country. Since this is chosen by the country, it cannot be treated as an exogenous or predetermined variable. It must be modeled as simultaneously determined along with the other endogenous variables. The variables measuring IRGC and IRPB, on the other hand, can be considered to be predetermined and thus exogenous to the national level variables. IRGC, the cumulated number of catalogued IRGC accessions (with passport data), can be

Table 13.5. Variables: IRGC, IRPB, INGER impacts on flows of genetic resources.

I. Endogenous variables measured at the national level	
NING	The number of INGER nurseries in the country in each year
R1–R8, R13	Flows of released varieties by year by route
II. Predetermined variables: IRRI	
POOLR	Size of total landrace pool
POOLRI	Size of IRRI origin landrace pool
ENTRIES	The number of IRRI materials placed in INGER
III. Predetermined variables: national level	
CNLR	Cumulated landraces of national origin in released varieties
CILR	Cumulated landraces of IRRI origin in released varieties by year
IV. Exogenous variables: international level	
IRGC	Cumulated number of IRGC occasions catalogued with identifiers by year
V. Exogenous variables: national level	
OING	Number of INGER nurseries in other countries
AREA	Land area planted to rice
Country dummy variables	
Time dummies	(1975–1980), (1981–1985), (1986–1990)

considered to be a determinant of the number of INGER nurseries undertaken in a participant country. IRGC also should have some effect on the rare trait contents. It can also be considered to contribute to the index of IRPB activities, which is measured by the cumulative size of the internationally contributed landrace pool, POOLRI, and to the size of the total landrace pool, POOLR.

Other exogenous variables include the cumulated landraces, both international and national, which are measures of national plant breeding activity. In addition the area planted to rice in a country should be governing genetic resource flows because it reflects demand.

Table 13.6 reports coefficient estimates and '*t*' values from the third stage of a three-stage least squares (3SLS) estimate of the system of ten equations. The intercept and country dummy and time dummy variables coefficients are not reported since they do not generally enter into the policy implications of the results.

The first equation is the equation determining the number of INGER nurseries that the host country chooses. The nurseries have expanded over time and the time dummies reflect this expansion. The rice area variable also explains why countries add more INGER nurseries. We also find that countries respond positively to their neighbours' decisions to conduct INGER nurseries and, most important, that as the catalogued accessions in IRGC expands, the number of INGER nurseries expands. INGER nurseries do not respond to the number of materials placed in trials by IRRI and have actually declined as the total landrace pool has expanded, given the response to IRGC. Thus we find a number of factors influencing the number of INGER nurseries placed in different countries. The 3SLS model treats this number as endogenously determined in the nine route or pathway equations.

As noted earlier, the 'model' underlying the Table 13.6 estimates is one in which the 'flow' of varietal releases through each route or pathway responds to four governing variables in addition to rice area, country and time effects. Two of these variables measure international plant breeding activities (CILR and POOLRI), one measures national plant breeding activities (CNLR), and the fourth, NING, is the outcome of both international (IRGC) and national activities. We expect each of these activities to have different impacts on each flow. In particular, the introduction of INGER is expected to increase the likelihood that a released variety has passed through INGER. We are, however, interested in the total impact, i.e. the sum of the flow impacts, because this tells us whether the activity caused an expansion in the total number of varieties released.

We note first that the AREA variable, while a strong determinant of the number of INGER trials in a country, is not a significant determinant of flows. This is consistent with the interpretation that plant breeding activities (not simply the sizes of countries) govern releases.

Now consider the impact of the variables indexing national and international plant breeding activities. The effort of national plant breeding programmes is indexed by the cumulated stock of landraces and ancestral material embodied in varietal releases by each national programme (CNLR). This

Table 13.6. Estimates of INGER, IRGC, IRPB and NPB impacts 3SLS estimates of ten equation system.

	Independent variables								
Dependent variable	OING	IRGC	ENTRIES	POOLR	NING	CNLR	CILR	POOLRI	AREA
NING	0.0588	0.000875	−0.00007	−0.0999					0.0319
	(7.85)	(2.17)	(0.04)	(2.60)					(16.59)
R1					0.00037	−0.0034	0.0021	0.00013	0.0001
IRRI/INGER					(.16)	(2.57)	(4.42)	(0.05)	(1.09)
R2					−0.0078	0.0013	−0.0008	0.00628	0.0002
IRRI/NO INGER					(3.16)	(1.00)	(1.70)	(2.38)	(2.38)
R3					0.0010	0.0002	0.0006	0.00036	−0.00003
OTHER/INGER					(0.74)	(0.30)	(0.57)	(0.24)	(0.93)
R4					−0.0002	−0.0001	0.0001	0.00389	−0.00007
OTHER/NO INGER					(0.13)	(0.09)	(0.20)	(2.89)	(1.44)
R5					0.0036	0.0054	0.0010	−0.00416	−0.00004
IRRI PARENT/INGER					(1.05)	(2.89)	(1.47)	(1.10)	(0.58)
R6					0.0053	0.0036	−0.0032	0.0254	−0.00000
IRRI PARENT/NO INGER					(0.89)	(1.13)	(2.69)	(3.86)	(0.00)
R7					0.0087	0.0040	−0.0002	0.00062	−0.0004
OTHER PARENT/INGER					(1.72)	(1.43)	(0.22)	(0.11)	(1.82)
R8					0.0121	−0.00068	−0.0005	0.0124	−0.00051
OTHER PARENT/NO INGER					(3.56)	(0.35)	(0.92)	(3.42)	(3.86)
R13					0.0065	0.0068	0.0010	0.00015	−0.00006
NATIONAL					(1.25)	(2.38)	(1.00)	(0.03)	(2.21)
Sum of coefficients					0.0295	0.0173	−0.0003	0.0451	
F test on sum					4.75	5.26	0.014	8.35	
Prob. > F					0.037	0.021	0.903	0.004	
System $R^2 = 0.54$									

variable has generally positive impacts on most routes and a positive and statistically significant total impact. Not surprisingly, successful national breeding programmes cause more varietal releases.

The two variables measuring the IRRI plant breeding programme, CILR and POOLRI, clearly indicate that it is the size of the IRRI origin landrace pool that is important and not the cumulative stock. In other words, what seems to be important is the introduction of new landrace material into the pool, not the replication of those landraces which are largely the contribution of national programmes. Each landrace added to the pool by IRRI contributes 0.045 varieties annually in each country as indicated by the statistically significant sum of the coefficients.

Now consider the INGER impact. The expansion of INGER diverted varietal flows away from NO INGER routes (R2 and R4) to INGER routes (though this diversion was not highly significant). For parental materials, INGER has a positive impact on all routes including stimulus of NO INGER routes (R6 and R8). This suggests that the INGER nurseries stimulated more international search for genetic resources. It also reflects the fact that INGER nurseries actually include parent and grandparent cultivars that were not initially introduced through INGER.

F tests tell us that NING has a significant positive impact on the total flow of released varieties. The coefficient 0.0295 indicates that one additional INGER nursery is associated with 0.0295 additional released varieties. Thus the addition of 34 nurseries (a nursery is counted in each location in each year) adds one released variety. The implication for ending the INGER programme (i.e. stopping the 900–1000 nurseries each year in recent years) is that this would reduce the recent annual flow of released varieties from 80 per year to around 60 per year. This indicates that INGER has added to the production of released varieties by roughly 25%. This is a large impact.

Each landrace added from IRRI sources causes approximately 0.68 added varieties to be released in each future year. (This coefficient is based on replication in 15 countries.)

IRGC also has an impact on released varieties because it induces added INGER nurseries. The addition of one accession to IRGC causes $(0.000875 \times 15) = 0.0013$ INGER nurseries. This, in turn, means that $(0.0295 \times 0.0013 \times 15) = 0.0058$ more varieties are produced. Thus adding 1000 accessions to IRGC causes 5.8 added released varieties in each future year.

Economic Implications

The economic implications of these estimates are quite important. We estimate that IRGC, IRPB and the INGER programmes of germplasm exchange have caused a larger number of varietal releases than would otherwise have occurred. We show that the varieties produced in this expansion are probably not qualitatively different in terms of characteristics from all other varieties (see

Evenson and Gollin, 1991). In order to develop estimates of the value of these varieties, we require an estimate of the average value of modern rice varieties in farmers' fields.

Evenson and David (1993) report estimates of modern variety impacts for India, Pakistan, Bangladesh, the Philippines, Thailand, Indonesia and Brazil. These range from a relatively high value for India to lower values for the other countries. The approximate value of modern varieties in 1990 in indica rice regions was US$3.5 billion. If we consider this to be the cumulated contribution of the first 1400 modern varieties, we obtain an average value of a released variety of US$2.5 million per year, and this annual value continues into perpetuity because we assume varietal improvements to be additive.

Using simple arithmetic, this allows us to estimate the economic effects of various IRRI activities. First, consider the consequences of ending the INGER programme. We estimate that this would reduce the flow of released varieties by 20 varieties per year. There is a time lag between appearance in INGER and production: suppose this to be 5 years, then further suppose that the INGER effect lasted only 10 years (i.e. INGER chiefly speeded up the release of varieties that would have been released an average of 10 years later). The present value of the 20 varieties over the 6th–15th years discounted at 10% is US$1.9 billion. This is an estimate of the loss if INGER nurseries were to be eliminated.[12]

We can also compute the value of adding 1000 catalogued accessions to IRGC. According to our estimate, this will generate 5.8 added released varieties. This will generate an annual US$145 million income stream with a delay of, say, 10 years. The present value of this stream at a 10% discount rate is US$325 million.[13]

The value of an added landrace introduced by IRRI is also high. (This is a landrace not previously used in a released variety that is incorporated into a new released variety through IRRI's efforts. Think, for example, of IRRI's introduction of a gene from a wild species.) Our results indicate that after an IRRI landrace is added, varietal releases expand by 0.68 varieties in the first year, 2 × 0.68 in the second year, etc. Assuming that this process begins after 5 years and then continues for 10 more years, we can compute the present value of an IRRI-added landrace to be US$50 million discounted at 10%.[14]

There is thus little question that the continued operation of INGER, the operations of IRGC and the completion of accessions to IRGC are economically justified. These are high payoff activities. In addition, the expansion of the landrace pool by IRRI has a high payoff.

Notes

1. The genealogy of a released rice variety contains a wealth of information about the process of rice breeding and about the dissemination and flow of rice genetic materials. The usefulness of rice genealogies as a tool for analysing research programmes was first noted by Hargrove (1978, 1979), Hargrove and Cabanilla (1979) and Hargrove *et al.*,

(1980, 1985). The first attempt to use genealogical analysis in the economic evaluation of agricultural research and in the setting of agricultural research priorities was by Gollin and Evenson (1991) and Evenson and Gollin (1991). Much of the material in this chapter is included in Evenson and Gollin (1997).

2. The study drew heavily on a number of data sets available through IRRI. The first of these was a list of elite lines and released varieties from more than 40 countries. This data set, collected by V.L. Cabanilla and T.R. Hargrove for the International Rice Genealogy Database, provides information on the parentage and release dates of most indica rice varieties since 1968. An accompanying data set, containing more than 6500 entries, contains breeding records that make it possible to trace complete or partial genealogies for all the elite lines and released varieties in the first data set. This data set is also based on work by Cabanilla and Hargrove, although much expansion and modification was carried out for this study. These alterations transformed the two data sets into a united, self-contained, self-referencing data set.

3. Formally, a landrace is a farmer-developed variety selected over time in response to a specific physical environment and to specific social and economic constraints. In this paper, however, we occasionally depart from this usage to include other varieties of rice that have been in common use by farmers for long periods of time and that pre-date modern breeding efforts.

4. It was also possible to combine the varietal data with additional data sets from INGER. Two INGER data sets, from IRRI, were used. The first was a list of entries in INGER since its inception; the second was a list of the nurseries in which these entries were used. By matching the names of varieties to the list of INGER entries, it was possible to infer the inclusion of varieties and ancestors in INGER.

5. These 33 varieties were generally regarded to be early ‘modern’ varieties.

6. It is reasonable to assume that most released varieties have been planted on significant acreage. Although some varieties are adopted widely, while others are planted in specific agroecological zones or geographic regions, most varietal releases are in fact used by farmers.

7. In particular, we had incomplete data on Japanese rice varieties and suspected that there has been relatively little recent flow of germplasm between Japan and the other countries in our study.

8. D.V. Seshu, personal communication, 1992. At the time, Dr Seshu served as director of INGER.

9. The criterion used was whether varieties developed in one country were released in another country 2 or more years following their appearance in INGER. (Given the omission in our data set of many countries in Africa and Latin America, which have imported actively from INGER, the figures appear to be consistent with the data maintained by INGER.) Since typography and nomenclature also make it difficult to match named varieties with INGER entries, it is likely that imports through INGER have been undercounted, rather than overcounted, in our study.

10. As many as 422 of the varieties based on internationally exchanged parents may have been developed from materials chosen out of INGER, in the sense that the parent first appeared in INGER trials 4 years or more prior to the release of the variety. About half of the INGER parents were IRRI materials, and half were varieties from national programmes other than the one of eventual release. Parents chosen out of INGER have steadily grown to account for larger proportions of borrowing. By 1986–1991, as much as 80% of parental selection may have taken place via INGER.

11. Note that grandparent varieties will have had a shorter period to have been influenced by INGER because of the time lag between appearance in INGER and their ultimate appearance as a grandparent. INGER, however, may have had a large impact on these flows, even if there were NO INGER flows because it stimulated more international searching for genetic resources. Similarly the IRRI landrace pool may also stimulate these flows by inducing national programme efforts to complement IRRI materials (see Evenson and Gollin, 1991).
12. If a 5% discount rate is used, this value is US$6 billion.
13. At 5%, it is US$1450 million.
14. At 5%, it is US$158 million.

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Appendix Table 13.A1. Matrix of varietal borrowing (numbers in parentheses represent borrowings through INGER).

	Other	Latin America	Oceania	Bangladesh	Africa	Burma	USA	China	India	Indonesia	IRRI	Korea	SE Asia	Nepal	Pakistan	The Philippines	Sri Lanka	Taiwan	Thailand	Vietnam	Total
Other	9	7	0	0	0	1	0	5 (2)	16	3 (2)	18 (9)	6	5	0	0	0	0	1	0	0	71 (13)
Latin America	3 (1)	185 (2)	0	0	1 (1)	0	5	0	2 (2)	0	39 (15)	1	0	0	0	2	1 (1)	0	0	0	239 (22)
Oceania	0	0	1	0	0	0	0	0	0	0	5	0	0	0	0	0	0	0	0	0	6 (0)
Bangladesh	0	0	0	17	0	0	0	1	4 (1)	0	11 (3)	0	1	0	0	0	0	0	0	0	34 (4)
Africa	1	1 (1)	0	0	69 (1)	0	0	0	1 (1)	0	26 (12)	0	0	0	0	1	2 (2)	0	0	0	101 (17)
Burma	2	0	0	1 (1)	0	33	0	1 (1)	1	1 (1)	18 (5)	0	2 (1)	0	0	1	2 (2)	0	12 (6)	2 (2)	76 (19)
USA	0	1	0	0	0	0	48	0	0	0	2 (2)	0	0	0	0	0	0	0	0	0	51 (2)
China	0	0	0	0	0	0	0	66	1	0	13 (8)	1	0	0	0	0	1 (1)	0	0	0	82 (9)
India	5	0	0	0	1	0	0	0	573	0	53 (33)	0	1	0	1	1	4 (3)	2	1 (1)	1	643 (37)
Indonesia	0	0	0	0	0	0	0	0	0	29	18 (13)	0	0	0	0	1	0	0	0	0	48 (13)
SE Asia	0	0	0	0	0	0	0	0	1	0	7 (2)	0	21	0	0	0	0	0	0	0	29 (2)
Korea	0	0	0	0	0	0	0	0	0	0	1	105	0	0	0	0	0	0	0	0	106 (0)
Nepal	0	0	0	0	0	0	0	0	0	0	5 (2)	0	1	8	0	0	1 (1)	0	0	0	17 (3)
Pakistan	0	0	0	0	0	0	0	0	0	0	7	0	0	0	5	0	0	0	0	0	12 (0)
The Philippines	0	0	0	0	0	0	0	0	0	0	25 (15)	0	0	0	0	26	0	0	0	1	53 (15)
Sri Lanka	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	51	0	0	0	53 (0)
Taiwan	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0	6 (0)
Thailand	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	23	0	23 (0)
Vietnam	0	0	0	0	0	0	0	0	0	0	44 (27)	0	0	0	0	0	0	0	0	15	59 (27)
Total	20 (1)	194 (3)	1 (0)	18 (1)	71 (2)	34 (0)	53 (0)	73 (3)	601 (4)	34 (3)	294 (146)	113 (0)	31 (1)	8 (0)	6 (0)	32 (0)	62 (10)	9 (0)	36 (7)	19 (2)	1709 (183)

Appendix Table 13.A2. Matrix of parental borrowing (numbers in parentheses represent borrowings through INGER).

	Other	Latin America	Oceania	Bangladesh	Africa	Burma	USA	China	India	Indonesia	IRRI	Korea	SE Asia	Nepal	Pakistan	The Philippines	Sri Lanka	Taiwan	Thailand	Vietnam	Total
Other	28 (2)	2	0	0	0	1	1	0	42 (23)	4	48 (13)	1	7	0	0	4 (3)	0	2 (1)	2	0	142 (42)
Latin America	116 (26)	73 (20)	0	0	4 (3)	0	22 (3)	0	62 (58)	3 (5)	161 (68)	4	0	0	0	8	6 (3)	5 (2)	10 (3)	4 (3)	478 (198)
Oceania	0	0	0	0	2	0	2	0	5	0	0	0	0	0	0	0	0	1	2	0	0 (0)
Bangladesh	4 (1)	0	0	1 (1)	0	0	2	1	18 (11)	2	34 (9)	0	2	0	0	2	0	1 (1)	0	1 (1)	68 (24)
Africa	33 (20)	3 (2)	0	0	34 (13)	0	0	2 (2)	57 (51)	6 (4)	42 (24)	0	6 (3)	0	0	3	3 (3)	5 (1)	5	3 (3)	202 (126)
Burma	26 (15)	0	0	0	0	1	0	1	68 (68)	5 (1)	38 (29)	0	1	0	0	7 (5)	0	2	0	3 (4)	152 (122)
USA	28	2	0	0	0	0	47 (1)	0	15 (15)	0	6 (4)	0	0	0	0	0	1	1	2 (4)	0	102 (24)
China	42 (13)	0	0	0	0	0	0	20 (7)	27 (29)	1 (2)	72 (52)	0	0	0	0	0	1	1	0	0	164 (103)
India	150 (32)	1	0	3 (2)	4 (4)	0	2 (1)	10 (3)	637 (101)	14 (7)	351 (174)	0	23 (13)	0	0	15 (6)	10 (4)	57 (14)	7 (4)	0	1284 (365)
Indonesia	11 (3)	0	0	0	0	0	0	1	22 (12)	22 (1)	35 (14)	0	1	0	0	2	0	0	2	0	96 (32)
SE Asia	0	0	0	0	0	0	0	1	9 (5)	3	17 (7)	0	9 (1)	0	0	3 (2)	0	2	2	0	58 (20)
Korea	0	0	0	0	0	0	0	0	3 (3)	0	49 (15)	74 (8)	0	0	0	0	0	0	0	0	201 (29)
Nepal	9	0	0	1	1	0	0	0	7 (4)	1	10 (4)	0	2	0	0	1	2 (2)	0	0	0	34 (14)
Pakistan	1	0	0	0	0	0	0	2	6 (3)	0	12 (4)	0	0	0	0	1	0	0	2	0	24 (8)
The Philippines	20	0	0	0	0	0	4	0	11 (2)	5 (1)	45 (13)	0	2	0	0	18 (2)	0	0	0	0	105 (18)
Sri Lanka	24 (3)	0	0	0	0	0	1 (1)	1 (1)	4 (3)	3 (1)	22 (4)	0	0	0	0	0	50 (5)	1	0	0	106 (18)
Taiwan	2	0	0	0	0	0	0	0	3 (2)	0	5	0	0	0	0	0	0	2	0	0	12 (2)
Thailand	12 (5)	0	0	0	0	0	0	0	12 (11)	2	7 (5)	0	0	0	0	1	0	1	11 (1)	0	46 (22)
Vietnam	11 (1)	0	0	0	0	0	0	3	34 (22)	3	63 (23)	0	1	0	0	1	0	0	0	2	118 (46)
Total	517 (121)	81 (22)	0	5 (5)	43 (20)	2	81 (6)	43 (13)	1039 (423)	74 (22)	1022 (462)	79 (8)	54 (17)	0	0	66 (22)	72 (17)	81 (19)	45 (14)	13 (11)	3404 (000)

Part IV
Property Rights

14

Creating Linkages Between Valuation, Conservation and Sustainable Development of Genetic Resources

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Very substantial gains have been realized in yields of most major crops over the past several decades (Echeverria, 1991; Osten-Sacken, 1992). Some of these increases are due to improved farming techniques, irrigation, and the use of commercial fertilizers and pesticides. However, a substantial portion can be attributed to the introduction of improved crop varieties. Unfortunately, the success of modern crop breeding programmes could be undermining the basis for continued progress. Expanded use of improved varieties has led to the abandonment and *in situ* extinction of many traditional varieties or landraces, which historically have provided much of the genetic diversity available to crop breeders (Vaughan and Chang, 1992). Conversion of natural ecosystems to agricultural and urban uses and the introduction of non-native species are also endangering some wild relatives of major crop species. Concern over the erosion of crop genetic resources led to the creation in 1974 of the International Board for Plant Genetic Resources (IBPGR) which is charged with promoting an international network of genetic resource centres. Over the past 20 years, there has been a continued increase in the number of gene banks around the world and a corresponding increase in the number of samples stored (Marshall, 1990).

Public funding for crop research and genetic resource conservation has generally been linked with a policy of universal access to the fruits of that research and a commitment to the concept of open access to genetic resources worldwide. In the past, national agricultural research systems (NARS) and international agricultural research centres (IARCs) have collected, transferred and exchanged germplasm without compensation. In return, new varieties have generally been made available without charge. As part of the Undertaking on Plant Genetic Resources, delegates to FAO’s biennial conference in 1983

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approved an expansion of this basic framework to include universal access to new varieties developed by private firms. The unrestricted use and reproduction of privately developed crop varieties has proved unacceptable to most developed countries, and they have responded by providing crop breeders with patent-like protection in the form of plant breeders' rights. However, there has been no complementary movement to require breeders to provide compensation for access to genetic resources.

A policy of open access to genetic resources and the products of scientific research involving those resources provides little direct incentive to protect genetic diversity and scant incentives for private sector research. Still, if combined with sufficient public funding for genetic resource conservation and development, this policy can be justified on the basis of the important social benefits derived from new crop varieties. However, recent concerns over the financial health of the system of crop research centres comprising the Consultative Group on International Agricultural Research (CGIAR) raises the question of the level of global commitment to publicly funded agricultural research over the long term.

The only realistic alternative to the existing system of dual open access is one that recognizes property rights over biological resources as well as intellectual property rights (IPRs) over the products of crop research activities. This is the policy approach that is embodied in the Convention on Biological Diversity (CBD).

The CBD signed at the Rio Earth Summit in 1992 represents a first step away from a system of open access to genetic resources. The Convention repeatedly affirms sovereign rights to genetic resources and calls for the sharing of the benefits arising from commercial and other utilization of genetic resources with the source country. While the Convention's rather vague requirements for technology transfer have caused some concern in developed countries, particularly the USA, the language on transfer of technology is immediately followed by an explicit recognition of intellectual property rights. 'In the case of technology subject to patents and other intellectual property rights, such access and transfer shall be provided on terms which recognize and are consistent with the adequate and effective protection of intellectual property rights' (CBD, article 16).

The objectives of the Convention as stated in Article I include conservation and sustainable use of genetic resources which are defined in Article 2 as any material of plant, animal, microbial or other origin containing functional units of heredity and having actual or potential value. Nevertheless, the degree to which the CBD will or should affect use of genetic resources for crop research is a matter of some debate. One interpretation of the Convention is that germplasm collected and stored in international gene banks prior to the Convention entering into force would not be subjected to the requirements of the Convention (Witmeyer, 1993). Even if this interpretation is universally accepted, the question still arises whether future uses of previously collected material stored in international gene banks and/or future accessions should be governed by the Convention or similar rules.

My focus in this chapter is to contribute to the ongoing discussion of the combination of economic information, institutional arrangements and economic incentives that are needed for efficient conservation and utilization of crop genetic resources. The following section examines several genetic resource valuation models and suggests conceptual extensions of the models as well as empirical research needs. The final section of the chapter sketches the outline of a system of compensation for access to genetic resources and licensing of research products. Potential advantages and obstacles to implementation of such a system are also discussed.

Valuing Genetic Resources

Economic valuation of genetic resources can contribute to policy and management decisions in several ways. First, estimates of the total economic value of landraces, wild relatives of crop species, and biodiversity in general can help to guide allocations of resources between biodiversity conservation and other socially valuable endeavours. In addition, economic valuation and decision models can be used to guide resource allocation between various types of genetic resource conservation, research and development. These latter policy decisions would include issues such as whether to devote additional resources to evaluation of existing genetic stocks or to the collection of new germplasm, or whether to preserve resources *in situ* or *ex situ*. Estimates of the economic value of genetic resources to society and the most efficient means of conserving and utilizing these resources are particularly important in a policy setting that is heavily reliant on public and non-profit funding for support of genetic resource conservation and crop breeding programmes. Genetic resource valuation models can also assist in designing economic incentives and institutional arrangements that will lead to economically efficient conservation and development decisions.

There are a number of characteristics of genetic resources that must be considered in any valuation model that is intended to be used for policy analysis. These include problems in defining and protecting property rights, significant positive externalities from agricultural research, increasing demand for agricultural products due to population and income growth, rapid technological change, imperfect information and the irreversibility of extinction. Added to these considerations are the potential for declining benefits of existing varieties due to evolution of insect and disease organisms, climate change, more stringent environmental controls and changing consumer preferences. While the introduction of improved crop varieties and farming techniques has increased *per capita* agricultural production in most parts of the world, continuation of this trend is by no means assured, particularly if there is continued erosion in crop genetic resources. This implies that valuation models should also incorporate some degree of risk aversion.

An early, elegant, and quite flexible model of the research and development process that was illustrated in relation to crop research was developed by Evenson and Kislev (1976). This model has several interesting features that, with further elaboration and development, could make it particularly useful for estimating the value of genetic resource conservation. Evenson and Kislev model crop breeding as a process of sampling (i.e. developing new varieties) from a statistical distribution defining the yields of all potential new varieties that can be derived from a given stock of genetic resources with existing technologies. Trials which exceed the yield of the existing crop variety are considered successful and this creates a new higher standard for success in subsequent trials. Unless a new distribution with a higher mean and/or greater variance can be sampled, the Evenson and Kislev model indicates diminishing returns to crop research and diminishing returns to saving another crop variety for future research. However, Evenson and Kislev (1976) distinguish between this type of applied research and basic research activities which can either raise the mean of the distribution or allow new distributions to be searched. New crop breeding techniques that facilitated crosses with more distantly related species and recombinant DNA technologies are examples of the results of basic research that allow sampling from new, more genetically diverse 'distributions'.

In the Evenson and Kislev model, if there is continued progress in basic research, then there need not be declining returns to applied crop research. Evenson and Kislev (1976) also recognize that advances in basic research create an allocation problem across different applied research technologies. This can be illustrated in terms of the levels of funding that should be devoted to traditional crop breeding techniques using close relatives of commercial varieties, evaluation of wild relatives of these crops, and transgenic breeding using genetic material from a much wider range of species. In the Evenson and Kislev model this resource allocation decision is characterized in terms of how many samples to draw from each of these genetic distributions given declining expected returns per sample. An advance in basic research which creates the possibility or reduces the cost of sampling from a more diverse distribution (e.g. wild relatives of major crops) can have the result of reducing the efficient level of applied research from the old distribution (e.g. landraces).

Several policy implications could be drawn from Evenson and Kislev's basic model. First, genetic material from increasingly distant relatives of crop varieties combined with continued advances in basic genetic research will be needed to allow for continued increases in crop yields. However, over time, the exhaustion of economic returns from breeding programmes using close genetic relatives may decrease the importance of conserving these stocks and increase the value of more diverse genetic material. On the other hand, the very large number of species that can be sampled when cost-competitive transgenic breeding techniques are available tends to minimize the incentive for conservation of any single species.

Extension of the Evenson and Kislev model to include several other factors described above could modify these policy implications. For example, the Evenson and Kislev model does not include the potential for declining yields of existing varieties due to evolution of crop diseases and pest species. The model also does not explicitly incorporate a growing global demand for food. The first of these factors would tend to reduce the rate of declining returns from sampling within any given genetic distribution and could revive the economic value of distributions that were no longer economically productive. A genetic trait that was of no value in previous trials may suddenly become extremely valuable due to evolution of new crop pests. In addition, rising demand for new and improved agricultural products would increase the expected value of any randomly selected genetic sample. The marginal value of conserving an additional species or subspecies will depend on the magnitude of these two value-increasing factors relative to the discount rate and the declining marginal value of sampling for any particular trait.

Another model of the genetic value of biodiversity developed by Brown and Goldstein (1984) incorporates a probability of failure for each of *k* different traits of the currently preferred crop variety. As might be expected, the value of conserving substitute varieties increases as the probability of failure increases. Brown and Goldstein also developed a model where the probability of failure is a function of the number of acres planted. If the number of substitute varieties increases the expected value of the best substitute but at a declining rate, then the optimum number of substitute varieties to maintain increases if the discount rate declines, if the crop has higher value, if the chance of failure is increased or if the cost of preserving substitute varieties is reduced. Although Brown and Goldstein (1984) also consider the marginal value of additional genetic resources in developing new crop varieties, their analysis of this issue is based on a static model that is essentially a simplified version of Evenson and Kislev's model of applied research.

It would be worthwhile to combine aspects of the Evenson and Kislev and Brown and Goldstein models and to extend them in several ways. The resulting dynamic model would include declining yield increases from research with existing technologies on a given genetic distribution, a decay function for crop yields, changing consumer preferences, increasing demand for agricultural products, and creation of new genetic stocks to sample or alterations in the economic characteristics of existing stocks due to advances in basic research. This model could allow for a more detailed analysis of the value of preserving genetic resources by defining a three-dimensional matrix of possible genetic sampling distributions. Major food crops would be one axis of this matrix. Landraces, modern varieties, close wild relatives, and more distant components of biodiversity would form the second axis. Valuable traits such as resistance to specific insect pests or diseases as well as drought or salinity tolerance would be the third variable defining each sampling distribution. In theory there could be a unique set of parameters for the crop breeding distribution associated with each cell of the matrix. The expected value of preserving genetic resources (whether *in situ* or *ex situ*) in any given category would be a function of the opportunity cost of preservation, the rate of yield declines in existing varieties, the rate of growth in demand for agricultural products, potential changes in consumer preferences, the discount rate, and the distribution shifting effects of basic research.

Another element listed above that must be taken into account in a valuation model of genetic resources is the economic implication of imperfect information given the irreversibility of extinction. Fisher and Hanemann (1986) have shown how these factors give rise to a set of non-negative option values. To incorporate the option value of genetic resource conservation into the valuation model outlined above, the question of whether or not to preserve a particular species or subspecies for agricultural research would need to be conducted in terms of a sequential decision analysis (Crabbe, 1987; Artuso, 1996). Preservation of genetic material in any time period allows for a new choice in the following time period that includes the option to benefit from new information about the expected value of the preserved genetic resources. Since the value of genetic conservation is a stochastic variable affected by crop yields, demand and technological change, it may be economically justifiable to make a decision to conserve genetic material for a defined period even if the opportunity costs of long-term preservation exceed the expected benefits. A model of the economic value of genetic resources that incorporates option value must be structured in the form of a stochastic dynamic programming problem.

The concept of option value also has applications in the analysis of the evolutionary potential of *in situ* collections. It is often asserted that *in situ* conservation can complement *ex situ* preservation by permitting continued coevolutionary development of the crop species in relation to natural pests and diseases (Vaughan and Chang, 1992). Extinction of landraces or wild relatives of crop species in the wild eliminates the option to benefit from these evolutionary changes.

Incorporating option value into the model also highlights the importance of incorporating risk aversion. Preserving genetic material keeps all options alive and therefore would tend to minimize the frequency and duration of major crop failures or food shortages. To the degree that the social costs of crop failures and food shortages increase rapidly with shortfalls in yield, this would increase the option value of genetic resource conservation.

To this point I have discussed possible extensions of several valuation models in purely conceptual terms. While I believe that the development of improved conceptual models will contribute to policy formulation, equally important is the need for empirical estimation of critical parameters. How rapidly have yields increased due to prior crop breeding efforts? How rapidly does the rate of yield increases from specific crop breeding technologies decline given different levels of diversity in the breeding stock? What has been the rate of increase in losses of new crop varieties over time due to pests and disease organisms? How are new biotechnological developments affecting the costs and probabilities of developing higher yielding transgenic varieties? To what degree are these technologies also reducing the cost or increasing the potential yield gains from breeding programmes using more closely related genetic material? Results of empirical studies and the survey of crop researchers discussed in

Chapter 19 of this volume indicate that a good deal of data and expert assessment are available, at least for rice. These data could provide a base for development and estimation of more comprehensive valuation models. As more data become available, a Bayesian approach could be used to update critical parameter estimates in the model.

To incorporate option value fully into the model as described above, more detailed information is also needed on the opportunity costs of *in situ* conservation of endangered habitats with potentially valuable genetic resources. Some priority setting will be needed here. An initial focus might include threatened areas with remaining *in situ* stocks of landraces or habitats with wild crop relatives. Opportunity costs of preserving other rare, threatened and biologically rich habitats might also be evaluated in relation to their potential contribution to transgenic breeding programmes.

Market Mechanisms and Economic Incentives

Economic valuation of genetic resources is not an end in itself. The ultimate objective is the efficient allocation of resources to preservation and utilization of genetic resources. As conceptual models, benefit estimation techniques and empirical data for economic valuation improve, valuation studies can be used to guide genetic resource conservation, research and development activities. But while we are working on developing and estimating the perfect model, we should also be experimenting with systems for translating international social values into efficient incentives for genetic resource managers and breeders. Indeed, implementation of certain types of market mechanisms and economic incentives could help to speed the development of improved valuation models by increasing both the supply of empirical data and the demand for valuation results.

Before discussing possible incentive systems and institutional arrangements, it is important to clarify what groups would be the focus of incentive programmes. To the degree that *in situ* conservation is determined to be of value for certain types of genetic resources, then the focus of conservation incentives would be farmers as well as planners and managers of protected natural areas. Where *ex situ* conservation is deemed to be the most cost-effective strategy, then the focus shifts to incentive systems and institutional arrangements that will encourage efficient collection, storage, maintenance and evaluation of genetic resources *ex situ*.

As described earlier, the treatment of genetic resources as the common heritage of humanity provides insufficient incentives for farmers or nations to preserve these resources *in situ* or to collect them for *ex situ* conservation. Without departing drastically from existing institutional arrangements, greater *in situ* conservation could be encouraged by a system of genetic call options. For genetic resources where the international benefits of *in situ* conservation exceed opportunity costs, farmers and other landowners could be paid to maintain these genetic resources *in situ*. In return, the purchasers of these genetic options contracts would be granted the right to obtain samples of the genetic material over some specified period of time. As described below, the contract might include further compensation if and when samples were actually collected. To avoid the potential moral hazard of the landowner selling genetic resource options and then destroying these resources by converting the land to a different use, the option payments could be made on an annual basis subject to verification that the resource has been preserved.

If political or financial considerations make it difficult to maintain all potentially valuable germplasm at IARCs, then a similar system of genetic options could be established to encourage efficient levels of *ex situ* conservation at NARS. The IARCs or other potential users of crop genetic resources would provide annual payments to national germplasm centres contingent on the results of annual inspections to verify that proper storage and maintenance procedures are being followed. These payments would ensure the right to access particular types of germplasm for the duration of the agreement. The option agreement could also include a predefined level of compensation if and when samples were actually requested.

Additional incentives for *in situ* and *ex situ* conservation could be provided by taking another step away from the common heritage concept governing international agricultural research. In addition to purchasing genetic call options, agricultural research centres could be encouraged to license the new varieties they develop. The structure of the license agreement and the level of compensation might depend on the type of purchaser (e.g. NARS, private firm, IARC) and purpose (e.g. research, subsidized public distribution, profit-oriented commercialization). While licensing agreements could inhibit dissemination of new varieties once they have been developed, it would also create additional incentives and sources of funding for increasing the number of new varieties available. With the exception of hybrid varieties, creating a market for new varieties developed by NARS and IARCs would depend on reaching a broader international agreement over plant breeders' rights at least for varieties developed by IARCs and NARS.

Combining a licensing system for new crop varieties with a set of genetic call options would begin to provide a market structure that translates demand for new crop varieties into incentives for conservation of genetic material. To complete the linkage, however, would require the negotiation of broader compensation arrangements with suppliers of genetic resources. Since the announcement of the contract between Merck and Costa Rica's Instituto Nacional de Biodiversidad (INBio) and the signing of the CBD, compensation arrangements for access to genetic resources have become increasingly common in relation to natural product research in the pharmaceutical industry (Reid *et al*., 1993; Artuso, 1996). These contracts generally include a small advance payment, mostly to cover collection costs, some technical assistance and training, and varying levels of contingent compensation, usually in the form of royalty rights.

Arguments against a system of compensation for suppliers of genetic material for purposes of crop breeding usually emphasize the difficulty of determining the relative contributions of different sources of genetic material to a new crop variety. To the degree that genealogies of modern varieties and records of the sources of germplasm contributions are available, this problem can be handled by providing compensation to each source on a purely proportional basis. An alternative is to deal with the issue prospectively and incrementally. Compensation arrangements would be negotiated for any new additions to genetic resource centres or newly collected samples used in future research. When a new variety is developed, compensation would not be made for germplasm contributions from previously collected samples stored at IARCs.

The advantage of the universal, proportional approach is a certain degree of equity, although this may be purchased at a cost of substantial accounting and administrative difficulties. The purely prospective approach avoids some of these book-keeping problems, but could be viewed as unfairly penalizing those contributors who in the past had been particularly cooperative in contributing germplasm to IARCs. A combined approach might, therefore, be most appropriate. Contingent compensation agreements (e.g. royalties) would be made for any new accessions to IARCs and included in the genetic call options described above. In addition, a portion of any revenues generated from licensing agreements for new IARC varieties would be passed on to NARS in proportion to each country's contribution to the overall germplasm held in IARCs.

The economic incentives and market structures outlined above can also be applied to genetic collections and crop research conducted by NARS and the private sector. If the CGIAR centres moved toward a system of licensing and compensation, it would quickly become a standard for exchange of genetic material and release of new crop varieties This would put the responsibility on the NARS to coordinate national *ex situ* and *in situ* conservation programmes. Purchasers of genetic resource access rights or option contracts would negotiate with the NARS or some other organization designated by the central government, and this organization would be responsible for structuring effective and equitable *in situ* conservation incentives at the local level.

The system of international crop research has been quite successful in conserving valuable germplasm and developing new crop varieties. Altering the principle of free exchange that has governed this system since its inception involves significant risks and obstacles. But there are also substantial risks in continued adherence to the common heritage concept. With continued advances in transgenic breeding programmes, there will be an increasing tension between the sovereign rights and equitable compensation requirements of the CBD and the common heritage concept which currently guides the international agricultural research system. There is already a growing conflict between the principle of free access to genetic resources and the pressure to expand plant breeders' rights in countries with advanced agricultural research sectors. It is also likely that the funding requirements of agricultural research programmes will become increasingly difficult to maintain from public and charitable sources. A system of compensation for access to genetic resources and licensing of research products has the potential to increase both *in situ* and *ex situ* conservation incentives, provide new sources of funding for national and international crop breeding programmes, create stronger linkages between the value of research products and funding sources, and create a more favourable environment for private sector crop research. Given the significant positive externalities associated with agricultural research and conservation of genetic resources, market mechanisms and economic incentives should not be expected to eliminate the need for public funding. However, most developed and some developing countries are already moving towards a mixed system of public and private agricultural research. Technological, economic and political factors are now creating an opportunity to promote this transition at an international level.

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15

Farmers' Rights

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Plant genetic resources (PGRs) for food and agriculture are as essential to human life on earth as air and water, and, therefore, have an enormous value as the basis for agricultural production and food security. PGRs are both the building blocks of living matter and the raw material for the fast-growing plant breeding and biotechnology industries. They are and will remain the principal source of genes and gene sequences for conventional and biotechnology-based plant improvement in the foreseeable future. However, there has been a growing concern over recent decades that many of these resources might now be lost at a rapidly increasing rate, as fewer homogenous modern varieties are adopted.

The existing portfolio of PGRs was developed throughout the world, over thousands of years of agriculture, by selection and adaptation to differing and changing conditions. This diversity is one of humanity's greatest capital resources for sustainably increasing food production, adapting to changing agro-ecological conditions and meeting future market demands. However, while the *use value* of these resources is clear (as the main basis for food production gains in the present century), the failure of markets to attribute sufficient *exchange value* to them is one of the major factors behind their accelerating loss. Although these resources are a capital asset for both present and future generations, their price is fixed only as a function of the demand of the present generation. To maintain an optimal portfolio of these resources over the longer term, the challenge is to find means to internalize conservation costs within the production costs.

The raw material of the plant breeder originally comes from the fields of the small farmer. Much of the plant genetic diversity still actively used is maintained and continuously selected by small farmers, co-evolving with pathogen complexes and adapting to changing environmental conditions and human needs.

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Their landraces may not be as productive, under optimal conditions, as the modern homogenous varieties of formal plant breeders, but they are, and will continue to be, the very basis of future productivity gains. PGRs are now subject to sovereign rights. The Convention on Biological Diversity (CBD) reconfirmed this and specified that they are under the sovereignty of the government of the state in which they 'developed their distinctive properties'.

The future extension of intellectual property rights (IPR) regimes, without an equitable sharing of the benefits with the donors of germplasm, could result in the erection of formidable barriers to access to genetic resources. Restrictions on access, as a result of the failure to provide adequate value-appropriation and redistribution regimes, could have the perverse effect of reducing the overall flow of innovation and improvement in agriculture.

While in some countries plant breeders appropriate value through plant breeders' rights or patents on plant varieties, there is no parallel appropriation mechanism to act as an incentive for the providers of germplasm to continue to maintain and make available these resources. Many countries have questioned the fairness and equity of providing for legal proprietary rights over modern plant varieties while not providing any rights to the holders of the resources from which they are developed. Moreover, unless a share of the benefits reaches farmers and national institutions maintaining (whether *in situ* or *ex situ*) and developing landraces, they will have no incentive to continue to maintain and develop them.

Farmers' Rights

Farmers' rights were negotiated through the Commission on Plant Genetic Resources[1] and unanimously adopted by countries in the FAO Conference in order to offer a pragmatic concept by which the issues of access and benefit-sharing could be addressed in a systematic and fair manner.

The concept is intended to form the basis of a formal recognition and reward system to encourage and enhance the continued role of farmers and rural communities in the conservation and use of plant genetic resources. It aims at reconciling the view of the 'technology-rich ' and the 'gene-rich' countries in order to ensure access to PGRs within a fair and equitable system.

Farmers' rights also provide some counterbalance to 'formal' IPRs, which compensate for the latest innovation, without acknowledging that, in many cases, these innovations are only the last step in cumulative inventions carried out over many human generations in different parts of the world.

International Agreements on Farmers' Rights

The concept of farmers' rights arose from debates, which started in 1979 in the FAO, concerning the fact that while modern breeding may generate returns through plant breeders' rights or other IPR legislation, no system of compensation or incentives existed for the providers of germplasm. During these debates, even the principle that germplasm should be available for scientific and breeding proposes was questioned, unless there was the recognition of the rights of germplasm donors to be compensated for their contribution.

The debates finally led to a negotiated compromise: the simultaneous and parallel international recognition of plant breeders' and farmers' rights. This recognition is embodied in FAO Conference Resolutions 4/89, 5/89 and 3/91. These three resolutions were negotiated by the Commission on Plant Genetic Resources, and unanimously adopted by more than 160 countries in 1989 and 1991.

Resolution 5/89 defines farmers' rights as 'rights arising from the past, present and future contribution of farmers in conserving, improving and making available plant genetic resources, particularly those in the centers of origin/diversity. These rights are vested in the international community, as trustees for present and future generations of farmers, for the purpose of ensuring full benefits of farmers and supporting the continuation of their contributions'.

The same resolution further defines these objectives, as being to:

- 'ensure that the need for conservation is globally recognized and that sufficient funds for these purposes will be available';
- 'assist farmers and farming communities, in all regions of the world, but especially in the areas of origin/diversity of plant genetic resources, in the protection and conservation of their plant genetic resources, and of the natural biosphere';
- 'allow farmers, their communities, and countries in all regions, to participate fully in the benefits derived, at present and in the future, from the improved use of plant genetic resources, through plant breeding and other scientific methods'.

Resolution 3/91 dealt with financial and institutional aspects of the implementation of Farmers' Rights and agreed:

- 'that Farmers' Rights will be implemented through an international fund on plant genetic resources which will support plant genetic conservation and utilization programs, particularly, but not exclusively, in the developing countries';
- 'that the effective conservation and sustainable utilization of plant genetic resources is a pressing and permanent need and therefore the resources for the international fund as well as for other funding mechanisms should be substantial, sustainable and based on the principles of equity and transparency';
- 'that, through the Commission on Plant Genetic Resources, the donors of genetic resources, funds and technology will determine and oversee the policies, programs and priorities of the fund and other funding mechanisms, with the advice of the appropriate bodies'.

Various estimates have been made of the magnitude of the resources required, at global level, for the international fund that will contribute to the implementation of farmers' rights.

The UN Conference on Environment and Development's (UNCED) Agenda 21 in the programme area, 'Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Sustainable Agriculture', called, *inter alia*, for further steps to be taken to realize farmers' rights. Agenda 21 estimated the average total annual cost of implementing the activities of this programme area at about $600 million, including about $300 million from the international community on grant or concessional terms.

The discussions and consensus reached by the participants at the Keystone International Dialogue on Plant Genetic Resources are significant since the participants, although attending in their personal capacities, reflected all the interests concerned, including governments, industry, non-governmental and intergovernmental organizations. The meetings were followed by a consultation organized in Stockholm, in January 1992, by the Swedish Agency for Research Cooperation with Developing Countries (SAREC) that involved government experts from Asia, Africa, Europe and the Americas, as well as participants from international bodies. At these meetings the concept of farmers' rights and its implementation through an international fund was supported. Estimates of the size of the fund required, ranging from US$300 million to US$500 million per annum,[2] and some proposals for its governance were made.

The Fifth Session of the Commission on Plant Genetic Resources noted that 'the nature of contributions to the fund, and the other funding mechanisms referred to in Resolution 3/91, had been extensively discussed, but that no agreement had yet been reached.' However, it noted that the technical and financial needs to ensure conservation and to promote the sustainable use of the world's PGRs had to be determined and quantified. The Commission agreed that this should be done through a country-driven process, whereby the first Report on the State of the World's Plant Genetic Resources and the Global Plan of Action on Plant Genetic Resources would be developed, as part of the participatory process for the Fourth International Technical Conference on Plant Genetic Resources. It agreed that the Global Plan of Action would identify the activities, projects and programmes needed to overcome present constraints, in line with the relevant parts of Agenda 21. By financing the Global Plan of Action, through the International Fund, and other funding mechanisms, as foreseen in Resolution 3/91, the international community would contribute to the realization of farmers' rights.

The Global Plan of Action has been prepared through a country-driven process whereby nearly 156 countries have submitted country reports, and 11 regional and sub-regional meetings, involving 143 countries, have been held. The Global Plan of Action was endorsed at the Fourth International Technical Conference on Plant Genetic Resources convened by the FAO in Leipzig, Germany, in June 1996.

Follow-up to the CBD: Current Negotiations for the Realization of Farmers' Rights, in the Context of the Revision of the International Undertaking

The Conference for the Adoption of the Agreed Text of the CBD also adopted complementary Resolution 3 that identified farmers' rights as an outstanding issue not addressed by the Convention, and recognized that solutions should be sought within the FAO Global System.

Following the entry into force of the Convention, countries, through the FAO Conference, adopted Resolution 7/93 for the negotiation of the revision of the International Undertaking in harmony with the Convention, including *inter alia*, the realization of farmers' rights. These negotiations are being carried out through regular and extraordinary negotiating sessions of the Commission. (For more detailed information on the revision of the International Undertaking, see Appendix 15.1.) Relevant international organizations also participate as observers in sessions of the Commission. In order to facilitate the negotiations, a number of documents and analytical studies have been prepared by the secretariat for the consideration of the Commission.[3]

The following paragraphs summarize the discussions relevant to farmers' rights in the 1995 session of the Commission's working group. Since these discussions are on-going in the Commission, the considerations of the working group do not necessarily reflect the definitive views of countries.

During the meeting it was recognized that, while farmers' rights were not incorporated into the CBD, Resolution 3 of the Nairobi Final Act had requested FAO to develop them within the FAO Global System on Plant Genetic Resources. The importance of this concept, the pioneering work performed by FAO and its Commission on Plant Genetic Resources, and the need to make the concept operational within the framework of the International Undertaking and in the context of sustainable agriculture were acknowledged.

Countries noted that it was difficult to exercise these rights in the absence of legislation, and that they required a legal framework, perhaps beginning at the level of 'international law'. Many countries considered that farmers' rights should be developed on an equal footing with plant breeders' rights.

The question of whether collective or individual rights were at issue has been raised, and it was considered that these concepts were compatible and that a collective compensation system should facilitate the fair and equitable distribution of the commercial benefits accruing as a result of the use of the material, which would encourage farmers to continue their work of conserving and developing PGRs.

The concept of 'added value' inherent in farmers' rights was emphasized, which justified their collective character, as was the difficulty of likening them to the concept of plant breeders' rights. Farmers could be considered beneficiaries of the work performed by plant breeders, and farmers' rights should be considered as being complementary, and not opposed, to plant breeders' rights.

There was agreement on the need to develop an International Fund on Plant Genetic Resources, agreed upon in Resolution 3/91, in order to make farmers' rights effective.

Some countries considered that the implementation of farmers' rights should not be limited to the fund but should also include aspects such as the following:

- the traditional rights of farmers and their communities to keep, use, exchange, share and market their seeds and plant reproductive material, including the right to re-use farm-saved seed known as the 'farmer's privilege';
- access by farmers to new technologies and other research achievements;
- protecting local technologies, traditional cropping practices and other informal innovative systems; and
- the rights of communities as custodians of indigenous knowledge and of their own PGRs.

Many countries considered that farmers' rights should be developed through a *sui generis* system (whether or not based on IPR) at the national and international levels.

On the subject of funding sources, several countries felt that the fund for implementing farmers' rights should be replenished through 'fixed contributions' regulated under international agreements. It was also felt that the resources of the fund could come from both public sector and private sector sources. It was also suggested that it did not necessarily have to be a completely new fund, but could be an autonomous 'window' of existing funding mechanisms.

It was pointed out that the concept of farmers' rights had several operational dimensions, and in order to avoid confusion these dimensions should be dealt with separately, perhaps in separate articles of the revised Undertaking. Three articles were suggested dealing with the following points:

1. Restating and balancing the concept of farmers' rights against the concept of plant breeders' rights; including the acknowledgement of the right to 'the farmer's privilege', namely the right to continue the traditional practice of re-using, on their own holdings, the seeds they harvest themselves.
2. Linking farmers' rights to the funding mechanism, which would not only make it possible to compensate and provide incentives for farmers to contribute towards the conservation and development of PGRs, but would also lay the foundations for just and equitable sharing of the benefits deriving from PGRs, with a possible reference to the Global Plan of Action.
3. Establishing the rights of traditional farmers and communities in the national context as custodians of indigenous knowledge and PGRs (in line with Article 8(j) of the CBD).

It was noted that the revised Undertaking could become a protocol to the Convention. Nevertheless, it was considered premature to decide on whether the Undertaking should be a protocol to the CBD.

With this background, the Sixth Session of the Commission (19–30 June 1995) reviewed a negotiating draft of the revised Undertaking, which incorporates into a single text the original Undertaking and the resolutions incorporating the agreed interpretation and the recognition of farmers' rights. The Sixth Session of the Commission recommended that two further sessions be held in 1996.

Concluding Remarks

The last few years have seen a dramatic increase in public awareness and of political debates on the subject of PGRs. These resources (within the contexts of biodiversity and biotechnologies) have become the focus of many international negotiations (including TRIPS/WTO, the CBD, UNCED's Agenda 21, the CGIAR restructuring), as well as a bridge between environment and development.

The concept of farmers' rights is even more important and more urgent following the TRIPS (Trade-related Aspects of Intellectual Property Rights, Including Trade in Counterfeit Goods) Agreement outcome of the GATT Uruguay Round, which will oblige parties to it (nearly all countries, developing as well as developed) to protect the rights of commercial breeders and biotechnologists and their companies.

Some developing countries are considering the inclusion of a mechanism for farmers' rights as part of the development of *sui generis* legislation, following the TRIPS Agreement. Proposed legislation in India envisages returning a share of the royalties on seed sales to a fund for strengthening farmers' PGR activities. This is an interesting proposal that deserves careful consideration.

However, to be truly meaningful, the implementation of farmers' rights requires international action and international resources because, in every country, most of the germplasm used in agriculture comes from other countries. There is great interdependence among countries for PGRs for food and agriculture. At the regional level for instance, and for major crops, the average interdependency has been estimated to be more than 70%, and at a national level it may be estimated that, for its major crops, every country depends more than 90% on genetic resources that originated in other countries.

Without the implementation of farmers' rights at the international level the present inequities will increase, and the present forces driving genetic erosion are also likely to be magnified.

Farmers' rights may not be in themselves, strictly speaking, an IPR mechanism. However, nothing prevents new *sui generis* IPR legislation incorporating the concept as in the proposed Indian legislation.

The implementation of farmers' rights should:

1. Ensure that farmers, farming communities and their countries receive a *just share of the benefits* derived from PGRs, which they have developed, maintained and made available, and thereby.

2. *Provide incentives and means for the conservation and further development* of these resources through cooperation between farmers, breeders and the national and international research services. Farmers' rights are not just a question of justice and equity, but also of ensuring that the genetic resources on which we all depend are conserved and continue to be made available.

This will require financial mechanisms and legal instruments.

Notes

1. The FAO Commission on Plant Genetic Resources, established in 1983 (and which in 1995 became the Commission on Genetic Resources for Food and Agriculture), is an intergovernmental forum which develops international agreements and consensus on access and benefit-sharing in relation to plant genetic resources for food and agriculture. Member countries have been involved in negotiations on these matters since the Commission was established. Agreements on farmers' rights, reached through these negotiations, have been embodied in the International Undertaking on Plant Genetic Resources, which was the first international agreement on PGRs. The Undertaking seeks to 'ensure that plant genetic resources of economic and/or social interest, particularly for agriculture, will be explored, evaluated and made available for plant breeding and scientific purposes'.

2. The Second Session of the Keystone International Dialogue, Madras, 1990, agreed to propose that 'the best way of recognizing Farmers' Rights would be a mandatory fund', and that 'there should be a compulsory funding mechanism'. It also stated that for an International Fund for Plant Genetic Resources, a 'conservative estimate indicates that at least US$500 million per annum should be available to begin to meet these urgent needs'. The Third and Final Session of the International Dialogue, in Oslo in 1991, proposed a 'Global Initiative for the Security and Sustainable Use of Plant Genetic Resources', including a fund for plant genetic resources. The financial estimates previously made were reviewed, and it was concluded that 'a minimum of $1.5 billion of additional funds [would] be needed during 1993–2000'. The dialogue report emphasized that the fund 'should be established on a sustainable basis', and that 'it should not be taken from existing development assistance budgets and not be subject to erratic or unreasonable fluctuations'. The international consultation of experts from governments, intergovernmental organizations, non-governmental organizations and private industry was convened by the government of Sweden through SAREC to follow up the Keystone recommendations and make specific proposals for the UNCED process. This consultation reiterated the need for a fund for the conservation and utilization of PGRs to complement existing activities and to be based on an agreed global plan of action. If the fund were established under the CBD, it was proposed that for PGR, as for other components of biodiversity, the fund should be operationally separate and managed by an international agency with competence in the relevant area. The FAO Commission on Plant Genetic Resources was identified as an appropriate body for decision-making on global policy issues, programmes and priorities with regard to the conservation and utilization of PGRs.

3. Document CPGR-6/95/8, *Revision of the International Undertaking on Plant Genetic Resources. Issues for Consideration in Stage II: Access to Plant Genetic Resources, and Farmers'*

Rights (especially paras 14 and 24–55) provided details on the current status of negotiations related to the establishment of the Fund and identified questions to be resolved. These include the nature of the funding (voluntary or mandatory); the question of linkage between the financial responsibilities and the benefits derived from the use of PGRs, and the question of who should bear financial responsibilities (countries, users or consumers). They also include how the relative needs and entitlements of beneficiaries, especially developing countries, are to be estimated and how farmers and local communities may benefit from the funding. Document CPGR-6/95/8 Supp., *Revision of the International Undertaking on Plant Genetic Resources. Analysis of Some Technical, Economic and Legal Aspects for Consideration in Stage II* (especially paras 7–18 and 24–32, as well as Appendices I and III), and a number of background study papers provided the Commission with technical information on, and analysis of, the economic and legal aspects, including possible options, as the basis for negotiations towards resolution of the pending issues related to the establishment and operation of the Fund. The institutional and legal aspects of the Fund are discussed in document CPGR-6/95/9, *Revision of the International Undertaking on Plant Genetic Resources. Stage III – Legal and Institutional Matters* (especially in paras 23–25).

Appendix 15.1. The International Undertaking on Plant Genetic Resources and the Development of Farmers' Rights

The International Undertaking was adopted by FAO Conference Resolution 8/83. It was the first comprehensive international agreement concerning PGRs. With the Commission on Genetic Resources for Food and Agriculture as a forum where countries can discuss and negotiate on matters related to genetic resources and agriculture, it is one of the foundations of the FAO Global System for the Conservation and Sustainable Utilization of Plant Genetic Resources.

The Undertaking seeks to 'ensure that plant genetic resources of economic and/or social interest, particularly for agriculture, will be explored, evaluated and made available for plant breeding and scientific purposes'.

As originally negotiated, the Undertaking was based on the 'universally accepted principle that plant genetic resources are a heritage of mankind and consequently should be available without restriction'. By the definition of PGRs in the Undertaking (Article 2), this concept applies to both the new products of biotechnology (commercial varieties and breeding lines), and to farmers' varieties and wild materials. However, this concept of unrestricted access is qualified. The Undertaking gives a number of possible ways by which samples of genetic resources could be made available: free of charge, on the basis of mutual exchange, or on mutually agreed terms.

In order to overcome reservations by certain countries to the Undertaking, it was qualified and interpreted by three complementary resolutions, adopted by the FAO Conference, which recognized that: Plant Breeders' Rights, as provided for by the Union for the Protection of New Varieties of Plants (UPOV) Convention of 1978, were not inconsistent with the Undertaking, and simultaneously recognized Farmers' Rights (4/89) and Plant Breeder's Rights (5/89); reaffirmed that the concept of the heritage of mankind is subject to the sovereign rights of nations over their genetic resources; and agreed that farmers' rights will be implemented through an international fund for PGRs (3/91).

The agreement embodied in these resolutions led to new qualifications on the principle of 'unrestricted access' in a number of ways:

1. It affirmed the sovereign rights of countries over their PGRs.
2. It clarified the fact that free access does not necessarily mean access free of charge by, on the one hand, recognizing that plant breeders' rights are not incompatible with the Undertaking, and, on the other, by recognizing farmers' rights, both of which allow for some form of compensation.
3. It limited the benefits of the Undertaking, including access to genetic resources, to those countries adhering to the Undertaking.
4. It limited the scope of the free access provision such that breeders' lines and farmers' breeding material were excluded.

The process of developing the Undertaking through agreed interpretations, in line with the aims of the original text, sought to establish and maintain a balance between access to the new products of biotechnology (commercial varieties and breeders' lines) on the one hand, and farmers' varieties and wild material on the other, and the interests of developed and developing countries, by balancing the rights of breeders (formal innovators) and farmers (informal innovators).

Agenda 21, adopted by the United Nations Conference on Environment and Development (UNCED), called for the strengthening of the FAO Global System on Plant Genetic Resources and its adjustment in line with the outcome of negotiations on the CBD, as well as for the realization of farmers' rights. The Conference for the Adoption of the Agreed Text of the Convention on Biological Diversity also adopted complementary Resolution 3, identified access to existing *ex situ* collections and farmers' rights as outstanding issues not addressed by the Convention, and recognized that solutions should be sought within the FAO Global System.

In following up on these matters, the FAO Conference, in November 1993, welcomed this resolution and unanimously adopted Resolution 7/93, 'Revision of the International Undertaking on Plant Genetic Resources', which requested the Director-General to provide a forum for negotiations among governments for:

1. The adaptation of the International Undertaking on Plant Genetic Resources, in harmony with the CBD.
2. Consideration of the issue of access on mutually agreed terms to PGRs, including *ex situ* collections not addressed by the Convention.
3. The issue of the realization of farmers' rights.

In the resolution, the Conference urged that the process be carried out through the Commission on Plant Genetic Resources (since 1995, the Commission on Genetic Resources for Food and Agriculture) with the help of its working group, in close collaboration with the governing body of the CBD. FAO has reported regularly to the governing bodies of the Convention on progress in the revision of the negotiations. The Second Conference of the Parties to the Convention (6–17 November 1995), by Decision 8, 'declared its support for the process engaged in the FAO Commission on Plant Genetic Resources', including 'the implementation of FAO Conference Resolution 7/93 for the adaptation of the International Undertaking on Plant Genetic Resources, in harmony with the Convention', and called for the process to be carried out as soon as possible.

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Intellectual Property and Farmers' Rights*

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Over the first few decades of the next century, world food production will have to continue its current historically rapid rate of advance if expanding populations are to be properly fed. Expanded cultivation and irrigation will account for very little of the growth in supply. The world must rely instead on continued high rates of yield increases to prevent food shortages and famines in the near future. These in turn depend on continued success in breeding more productive varieties ('cultivars') of major crops. Access of breeders to the necessary breeding materials is obviously essential for success.

Thus germplasm, the 'material that controls heredity' (Witt, 1985, p. 8), has become an essential international resource. Most agricultural germplasm originates in the 'South', and is used by the 'North' without compensation to its providers. But the rules of exchange are now changing, and the new regime is the subject of intense discussion in several international fora. Many articulate, interesting and informative studies have addressed this general issue, but they do not deal explicitly with the balance of interests at stake. They may well leave their readers asking: Have the countries of the South been frittering away their national patrimony by allowing free access to their agricultural germplasm? Will germplasm in the next decade become, like oil in the 1970s, the basis for a sudden surge in wealth for countries of the South?

At a time when the implications of the Convention on Biological Diversity (CBD) are being worked out, the implementation of Agenda 21 is under discussion, and the TRIPS provisions included in the last GATT round have committed countries of the South to extend intellectual property protection to genetic

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materials including plants, it might be useful to address the order of magnitude of the prospective gains from exploitation of these rights for agricultural applications, as well as their distributional potential. Methods currently under discussion for capturing these gains on behalf of 'Farmers' Rights' to their germplasm threaten to impose new costs on the international agricultural system. Are the prospective gains sufficient to justify these costs?

Compensation for Germplasm Resources: Northern and Southern Approaches

Discussions of intellectual property rights issues relating to plant breeding have been vigorous and extensive over the last few decades. The legal protection of new plant material has expanded quite rapidly in the North over this period, especially in the United States. The latter insisted on the recent GATT negotiations on the Agreement on 'Trade-related Aspects of Intellectual Property Rights, Including Trade in Counterfeit Goods' (TRIPS), which calls for protection of plant varieties worldwide. Article 27, 3(b) includes the provision that 'Members shall provide for the protection of plant varieties either by patents or by an effective *sui generis* system or by any combination thereof'. There is a novelty requirement in Article 27, 1. The force of these provisions with respect to agriculture may well depend on legal interpretation of exclusions in Article 27, 2, which include those necessary to protect 'human, animal or plant life or health or to avoid serious prejudice to the environment ... ' (Contracting Parties to the General Agreement on Tariffs and Trade, Uruguay Round (including GATT, 1994)).

Concerns about establishment of germplasm rights had already been evolving in less developed countries, but the trend was in the opposite direction, towards freer access to currently proprietary resources rather than toward reinforcement of private property rights. The less developed countries were understandably dissatisfied with the great asymmetry between the free access to landraces and wild and weedy varieties, mostly from the South, by plant breeders, mostly in the North or in the North-sponsored CGIAR system, and the assertion of property rights by private breeders over the descendants of this germplasm. Their concerns materialized in the 22nd Food and Agriculture Organization of the United Nations (FAO) conference in 1983 as the 'International Undertaking on Plant Genetic Resources' and in the subsequent 1992 CBD which states that each Contracting Party shall:

> Subject to its national legislation, respect, preserve and maintain knowledge, innovations and practices of indigenous and local communities embodying traditional lifestyles relevant for the conservation and sustainable use of biological diversity and promote their wider application with the approval and involvement of the holders of such knowledge, innovations and practices and encourage the equitable sharing of benefits arising from the utilization of such knowledge, innovations and practices (United Nations Environment Program (UNEP) 1992 Article 8(j)).

Taken together, the CBD and TRIPS appear implicitly to imply compensation for the community providers of indigenous knowledge. The absence of demands for free access to enhanced germplasm and breeders' proprietary cultivars leaves room for recognition of the legitimacy of private markets in the latter. There is, potentially, something for everyone in a regime in compliance with the CBD.

Means of Enforcement of Farmers' Rights under TRIPS

Patents

If TRIPS means patents in their present form, it will offer little to farmers who provide *in situ* conservation beyond, at best, defence of their continued right to free access to the genetic material in the seeds they use. Standards of patentability include novelty, provide for compensation only for individuals as distinct from communities, and exclude disembodied knowledge.

How would less developed countries fare under TRIPS? Farmers' rights to their germplasm and knowledge could not be effectively protected by a conventional patent system. Patents have never applied to pure knowledge of techniques or processes, nor to intellectual property acquired from other parties. The notion of an Amazonian tribe obtaining a patent for their traditional communal knowledge of the insecticidal benefits of a jungle plant is unrealistic.

Alternatives to Patent Protection

Several modes of compensation for development of intellectual property compensation are worth considering in cases for which patents are unavailable. These include protecting local knowledge as a 'trade secret' that can be marketed under the protection of trade secrecy law (Vogel, 1994). Farmers can also be compensated individually or as a collective group for innovation as well as conservation via transfers to them directly, or to their government as in the Merck–Inbio agreement and in debt-for-nature swaps, which apply to other aspects of biodiversity conservation.

Development of effective means of compensating farmers for their germplasm and related knowledge is an unsolved problem. Here we concentrate on a separate but related issue: What could such protection be worth to farmers? Assuming full compensation is feasible, what could less developed countries expect from full remuneration for the value of their germplasm? As a preliminary, we delineate some important distinctions in the next section.

Farmers' Rights: North versus South?

The relationship between modern agriculture and its genetic resources is frequently cast as a North–South issue.[1] But this turns out to be an example of the fallacy of composition. It is true that most of the world's agricultural genetic resources hail from the South. But most of the countries of the South are poor in agricultural genetic resources and rely on germplasm originating elsewhere. The ultimate source of agricultural germplasm is often ambiguous or obscure, as crops evolve in the process of cultivation.

Most crop germplasm is the product of the evolution of its ancestors *in situ*, predominantly in farmers' gardens and fields and their weedy margins, in geographic centres of diversity which are predominantly located in the South. Crops grown in these centres of diversity may derive from ancestors that grew elsewhere, as is the case for Ethiopian wheat. Centres of diversity are not necessarily places of origin.

In contrast, most major crop production takes place far removed from centres of diversity, in relatively gene-poor ecosystems. The exception that proves the rule that gene-poor areas are centres of production is the major rice species *Oryza sativa* L., which is still predominantly grown near its centres of origin in Asia. But within Asia, major areas of irrigated cultivation have environments quite different from the gene-rich natural habitats from which the species evolved.

Wheat production is dominated by production regions in China, the ex-Soviet countries, India, France, the USA, Canada, Argentina and Australia, distant from one of wheat's centres of diversity in Ethiopia, and bread wheat's major centre of domestication in the Syrian–Mesopotamian plains (Harlan, 1970, p. 21). Corn production in the United States, China, Europe and Africa is similarly remote from its Latin American origins. Commercial soybean production in the United States and Latin America dominates soy output in Asia, the soybean's centre of origin. A similar story holds for potatoes, a predominantly European crop originating in the Andes, as well as sugar cane and sugar beets.

The disjunction between major locations of production and centres of diversity holds also for crops that are grown almost exclusively in the South. Coffee in Latin America, India, Indonesia and sub-Saharan Africa, rubber and oil palms in Southeast Asia, cocoa in Africa, and bananas in Africa, Latin America and the Caribbean all tend to flourish away from their genetic origins. (Tea is a mixed case; while still important in its birthplace in India and China, it also flourishes in Sri Lanka, Africa and New Guinea, for example.)

Thus most of the world's agricultural output, North and South, grows in areas far from the historical sources of its germplasm. If producers were required to share the value of their output with countries that provided the crops, working out the details could be tricky. But certainly the North would be overwhelmingly a net payer. In fact, most countries, North and South, would be net payers, and almost all major producers of a given crop would be net payers for that crop.

Speculations on such payments are very likely moot. Recent assignments of rights to germplasm have 'grandfathered' access to germplasm currently held in gene banks including those of the international centres of the Consultative Group on International Agricultural Research, under the auspices of the International Plant Genetic Resources Institute (IPGRI). Hence in assessing the prospective gains from farmers' rights, scenarios of interest include: (i) payment and/or prior approval required by countries in centres of diversity for rights to search for or acquire germplasm in centres of diversity; and (ii) payment and/or prior approval required by national and/or international gene banks on behalf of depositing countries for access to or use of germplasm.

We discuss these scenarios below. An essential consideration is the extent of current demand for the germplasm held by farmers in centres of diversity, which is the topic addressed in the next section.

The Demand for Continuing Access to Farmers' Landraces

Writers supporting the case for compensation of farmers in centres of diversity dispute the inferences drawn above from the figures of Kloppenburg and Kleinman (1987). They argue that the North is especially dependent on access to exotic germplasm. Even if they are located outside centres of diversity, 'poor farmers in developing countries are far less dependent upon exotic germplasm since they are surrounded by much greater variability' (Fowler and Mooney, 1990, p. 199). The North has a higher reservation price for access to germplasm: '[T]he political 'pain threshold' for Australia, Europe, and North America – with their highly uniform plant varieties and mechanized food processing – is much lower than the threshold for Africa, Asia, or Latin America' (Fowler and Mooney, 1990, p. 200).

Certainly the North, with its greater wealth, has a higher capacity to pay, and a lower elasticity of demand for food as a whole. What these facts do or do not imply for any 'pain threshold' is an interesting question. But here the discussion focuses on a narrower issue: How dependent is the North on continued access to exotic germplasm?

The argument for continued dependence of the North in particular rests on a set of premises about the major crops:

- Major crops are held to be dominated by a small number of cultivars at any one time.
- Cultivars are relatively quickly superseded as they fall prey to disease or are supplanted by newly bred cultivars with higher yields.
- Output from the set of these cultivars is more variable than from landraces due to the small numbers of cultivars and the high vulnerability of each to stress, pests and disease.
- The flow of new cultivars depends critically on the introduction of new germplasm into the set of elite lines from which they are bred.

We will consider each of these propositions in turn.

Dominance of a Small Set of Cultivars

There is no doubt about the high uniformity of cultivars of major crops in the North relative to the centres of diversity. In 1969, the National Research Council (1972) reported that of 13 major crops (maize, soybeans, wheat, cotton, millet, dry beans, snap beans, peanuts, peas, potatoes, rice, sugar beet, sweet potato) the average number of major varieties was about four, and they accounted for an average of 70% of area planted. Though these figures are now out of date, the general continued dominance of a small number of cultivars in the United States is undisputed. In Europe, a narrow set of popular cultivars dominates major crops in many countries (Vellvé, 1992, Ch. 2), and there is little doubt that a similar situation exists in Canada and Australia.

A major reason for the typical dominance of a small number of varieties in production is their superior performance, from the farmer's viewpoint, over a relatively wide range of environmental conditions. The spread of 'high-yield varieties' has been a major source of increased cereal production as population has continued to increase, while acreage expansion has ceased to be a major means of increasing food supply.

An observation that a small set of cultivars accounts for a large share of production does not necessarily imply a corresponding reduction in the variety of germplasm used by farmers. Farmers may maintain their old cultivars on part of their land, even as they adopt widely marketed high-performance germplasm (see Chapter 6).

Short Useful Life of High-yield Cultivars

It is true in general that modern high-yield crop cultivars follow a typical cycle of introduction, diffusion and obsolescence (Reid and Miller, 1989). Duvick conducted a survey of major crops that indicated the typical life span of a cultivar was 7–9 years and falling (Duvick, 1984, Tables 7 and 8).

Variability of New Cultivars

Though informal discussions in the literature often seem to imply greater variability of elite cultivars relative to landraces, empirical support of this proposition is surprising in its scarcity. Given increasing yields, the coefficient of variation (standard deviation divided by mean) is preferable to the variance or raw standard deviation. Change in variability is, of course, extremely difficult to measure in short time series. Singh and Byerlee (1990) show declining variability in wheat between 1951 and 1986, and no effect of high-yield germplasm on variability. Byerlee and Traxler (1995) show that the coefficients of variation of a set of modern wheat varieties released by CIMMYT has decreased as yields have risen. Even if given cultivars are no more variable than landraces, their very concentration could add to aggregate variability. Consistent with this hypothesis, Anderson *et al.* (1987) and Hazell (1989) do find increased correlations across countries and regions between the 1960s and 1971–1983, but their results may be dominated by the unusual crop failures of the 1970s. Furthermore, in storable crops, improvement in market competition might induce variation in planned production in response to changes in marketwide stocks (Williams and Wright, 1991).

Dependence of Breeders on Inflow of New Germplasm

In the aggregate, there appears to be widespread historical dependence on germplasm from centres of diversity. And the discussion above confirms the reliance on successive generations of improved seeds, each of short duration and containing a small set of high-yielding cultivars. Contrary to common assertions, the current system does not seem, relative to available historical evidence, especially subject to disruption from pests, diseases or other causes. But is it beholden to a *continued* flow of germplasm from centres of diversity?

Current Introduction of Landrace Germplasm Breeding in High-yield Cultivars

Some writers, noting the rapid turnover of popular cultivars, have suggested that modern growers substitute temporal for cross-sectional diversity. This might seem consistent with continued reliance on new genetic material from the centres of diversity, but the rapid turnover of varieties does not imply that there are continued large-scale inflows of germplasm.

In rice, Evenson and Gollin (1994) show that the amount of new germplasm introduced in IRRI releases seems to have declined in recent years, as these releases share much of the germplasm of previous releases. Importantly, all are reported to incorporate the same semi-dwarfism locus *sd-1*, and the Cina cytoplasm is still pervasive (National Research Council, 1993, p. 76). This does not mean that exotic germplasm has been completely ignored. IRRI breeders have effectively incorporated successive genes for pest and disease resistance from exotic germplasm; the complexity of this enterprise is illustrated in the account of Plucknett *et al.* (1987, Ch. 9) of the development of IR36. These genes enter as rare traits via successive backcrossing, so that the effective expansion of the germplasm is rather modest.

In maize, the major corn cultivars all trace back to six pure line ancestors in the USA. Though 77% of a sample of US corn breeders maintained that their base of germplasm was broader in 1981 than in 1970 (Duvick, 1984, Table 16, p. 169), Smith (1988) concluded that there was no change in genetic diversity of Corn Belt maize from 1981 to 1986, and Cox *et al.* (1988) found that less than 1% of US hybrid corn had non-North American exotic germplasm. Moreover, the National Research Council (1993, p. 73)notes that 'Most surveys have shown that there is little immediate prospect for a large-scale increase in diversity of hybrid maize' in the United States. Apparently, within the germplasm base of US hybrid corn (a small fraction of the total world germplasm), the pool of diversity remains sufficient to provide disease resistance in the high-input US environment and to support a remarkable and as yet undiminished rate of yield increase.

Clearly, genetic resources from the South, made available in recent decades to CIMMYT and other germplasm facilities, have not been of very significant benefit to corn producers in the North. One implication is that the maximum gain to be had by sources of corn germplasm via effective bargaining with Northern corn breeders may be modest indeed, if retroactive compensation is ruled out.

In wheat, for the United States, of 224 wheat cultivars released before 1975, only 31% had any germplasm introduced apart from their foundation germplasm (Cox, 1991, Table 3-1, p. 26), and none of this was introduced later than 1920 (Cox, 1991, p. 28). Of cultivars released subsequently, Cox found that 75% had some more recently introduced parentage, but usually it constituted only a small part of the cultivar's germplasm, typically introduced for disease resistance via crosses and back-crosses. He noted that 'The limited utilization of landraces is most striking ... ' (Cox, 1991, p. 29).

In soybeans, Sprecht and Williams (1984, p. 65) found that of 136 successful soybean cultivars released by US breeders from 1939 to 1981, 121 had cytoplasm from just five introductions. Only six ancestral strains accounted for nearly 60% of the germplasm in these 136 releases and for a similar percentage of germplasm in cultivars released from 1971 to 1981 (Sprecht and Williams, 1984, Table 3–7, p. 68), even though there was large turnover in the set of leading cultivars between 1970 and 1980 (Duvick, 1984, Table 4, p. 164).

In a more recent study, Gizlice *et al.* (1994, p. 1143) define the genetic base as the 'sets of genotypes that contain 99% of the genes found in modern cultivars'. They conclude that 'the soybean genetic base was largely formed before 1960. Nearly 75% of the genes in modern soybean cultivars is present in sixteen cultivars and a breeding line released before 1960. Breeders have remained dependent on this early genetic core of breeding material and have rarely introduced new germplasm' (p. 1149).

Thus, much of the germplasm of major crops and their wild and weedy relatives already resides in gene banks. But the effect of the vast increase in accessions since the 1970s on germplasm utilized for crop production has thus far been modest.

Allard (1992) offers a breeder's view of the need for an inflow of novel genetic material:

> Breeding in barley and corn, as well as in other major crops. has increasingly focused on crosses among elite materials and rates of progress indicate not only that this strategy has been successful but also that there has been little, if any, slowing of progress due to reduction of exploitable genetic material. ... It consequently seems unlikely that readily exploitable genetic variability will soon be exhausted ... (pp. 144–145).

What are the prospects for future crop germplasm demand?

Note that these major crops are precisely the ones with the volume most capable of supporting a competitive private breeding industry. It is sobering that their yields can continue to increase with little introduction of new genetic material into their breeding lines.

A frequent rationale offered by breeders for their low rate of introduction of new genetic material is that cultivars in genebanks or *in situ* are insufficiently described and documented, so their potential contributions as part of a breeding system can be hard to assess. This is not the whole story, however. Common beans, though a 'minor crop' in the United States, are a staple for millions of people. Moreover their genetic uniformity has led to some disastrous disruptions of production (e.g. the 1982 rust epidemic that caused pinto bean yield losses of 25–50% in Colorado and Wyoming; National Resource Council, 1993, p. 68). Yet

> The gap between identification of useful characters in exotic germplasm and the transfer of these potentially useful characters to cultivars had widened. It is economically prohibitive for private companies to commit the time and expense on cultivar development incorporating exotic germplasm in such a minor crop as common beans, and there is no longer much career incentive for public scientists to perform this work. Therefore, the gap ever widens' (Silbernagel and Hannan, 1992, pp. 2–3).

Apparently, the potential prevention of a multimillion dollar disaster offers insufficient incentive for private plant breeders even when well-identified, useful germplasm is available *gratis*. This gives us some clues as to the extent to which breeders believe they can hope to capture the social value of their work. It also gives us a reality check of the scope of concerns about 'profiteering' by seed companies using germplasm from the 'South'.

The Implications of New Technology

At present, the demand for new crop germplasm from farmers in centres of diversity, and from gene banks, is surprisingly modest. But at present the technology of crop breeding is changing rapidly. Is it possible that in the near future these changes will expand the demand for new germplasm?

The answer depends on the balance between countervailing trends. Advances in conventional breeding have increased the scope for incorporating genes from landraces that are distant relatives. Wide crosses have enabled wheat breeders to incorporate genes from other related grasses. This should, on the one hand, raise the demand for the germplasm of such grasses. But it might also reduce the demand for germplasm from closer relatives. Advances in genetic engineering are likely to increase the feasibility of such wide crosses and decrease the time needed to incorporate their effects in new cultivars.

However, genetic engineering is also expanding the sources of genetic change for crops much farther afield. Commercial cotton is now being grown incorporating a gene for pest resistance from *Bacillus thuringiensis*, and this gene is also being used by breeders of potatoes, tobacco and other crops. A fish gene has been transferred to potatoes to induce cold tolerance. Farmers' crops and their wild relatives are no longer the sole source of valuable genetic material for crop breeders. They have competition from genes found in the whole spectrum of terrestrial life forms. For yield increases and stress tolerance, which often entail combinations of genes, crop breeders are likely to concentrate mainly on their own elite lines as breeding materials, as they have in the past (see Duvick, 1984). The continued search for higher yields is unlikely to have a major effect in the near future on the demand for exotic germplasm.

In fact the supply of potentially useful genes is even wider. They can be synthesized via several methods (Orton, 1988) including irradiation (which produced new barley cultivars), chemically induced mutation, and somaclonal variation induced via *in vitro* propagation. In addition, transposable elements, which can relocate genes and alter their expression, are another source of genetic variation that might prove to be a fruitful source of genetic improvements.

How these countervailing effects will balance out is still to be seen. Effects may differ in the short and longer runs. But there seems to be no good reason to expect a dramatic change in the profile of utilization presented in the preceding section.

The Implications of TRIPS

The property rights regimes created in response to the GATT mandate for gradual compliance with TRIPS are still evolving in many countries. But concerns have been raised that plant patenting could mean that traditional farmers might lose the rights to cultivate their own landraces (see, for example, Rural Advancement Foundation International, 1994). Current CGIAR policy precludes such expropriation of materials in its gene banks, but judicial treatment of the legal claims of private breeding corporations is still evolving. Proponents of farmers' rights to their own germplasm have some cause to worry (see, for example, the panel discussion in Adams *et al.*, 1994, pp. 255–271). Researchers in the public as well as private sectors are naturally concerned if broad rights to biotechnology research in a given crop are claimed by large corporations, even if they realize that there is a high probability that such claims will eventually be denied via legal challenges.

On the other hand, there is little evidence that TRIPS will increase genetic diversity significantly via its intended stimulation of private crop breeding activity. In the absence of incentives for public or private breeders directed specifically at diversity, 'Decisions in applied breeding programs are based on breeding progress and not genetic diversity' (Gizlice *et al.*, 1993, p. 623). TRIPS will probably have, at most, a modest effect on the demand for genes from farmers' landraces.

The Bottom Line: the Financial Potential of Farmers' Rights

Popular discussions of the transfers to be had by enforcement of farmers' rights tend towards over-optimism for several reasons. First, there is a natural tendency to confuse the potential market value of plant genes with the potential value of pharmaceutical products derived from plants in centres of diversity. It is widely known that a single drug can have a multibillion dollar market. Even a typically modest percentage royalty can yield a hefty sum. Recently, Simpson *et al.* (1996) have shown that the pharmaceutical potential of natural plants cannot justify conservation of centres of diversity *at the margin* (i.e. cannot justify cessation of development of a small fraction of the remaining Amazonian rainforest), but they do not deny that the *total* value of the forest, potentially exploitable via management of access to the pharmaceutical industry, could be huge. In the case of agricultural genetic resources, the private market potential from the genes in traditional farmers' landraces is generally much more modest than for pharmaceuticals. (To put things in perspective, the commercial seed market worldwide is $15 billion per year; the comparable figure for pharmaceuticals is $235 billion.)

Other discussions focus on the profits of seed corporations to fix ideas about the value that might be appropriated by traditional farmers should their rights be fully recognized. As discussed above, the current gene flow from landraces to privately marketed cultivars of major crops is surprisingly modest. To have much force, rights must be retroactive (contrary to current trends) or greater future demand must be anticipated. Even so, this focus is misguided for two opposing reasons. First, the profits of the most successful corporations like Pioneer Hi-Bred (which had an operating profit of $384 million in 1994) are predominantly attributable to US corn sales and are in some large part due to the firm's investments in research, production and marketing, and to their managerial expertise. After all, the breeding lines on which their genetic material is based are, in general, available to competitors who earn far less money in the same market.

The True Beneficiaries of New Seeds

To focus on profits from seed sales as the measure of the total value of genetic resources is to miss the forest for the trees. The total benefits derived from use of agricultural genetic resources is far larger than the profits of seed sellers. The major achievement of breeders, using genes generally derived from landraces, has been to increase food supply from available resources, thus reducing food prices, or preventing food price increases, as population has multiplied over the past century.

The evidence on food prices is striking. Real prices of the world's major food sources (wheat, rice, and corn, as well as of soybeans) have declined dramatically since the second World War, and especially over the last several decades. Though other factors also contributed to this decline, the role of general progress in breeding in producing higher yields is indisputable.

The beneficiaries are principally food consumers in developed and developing countries. Some farm owners may gain, others may lose, from particular innovations. But it is important to keep the 'big picture' in mind. Consumers north and south are the major beneficiaries of new germplasm in food crops. Apart from the effects of trade barriers and domestic agricultural price policies, the gains accrue roughly in proportion to consumption. Though the rich generally consume more grains, directly and indirectly via animal products, the gains are much more crucial for the larger number of poor consumers in less developed countries.

Conclusions

Agricultural genetic resources are crucial for human civilization. The major beneficiaries of the advances in crop production in the present century based on these resources are consumers in all countries, North and South, and the benefits are huge. Once said, this may be obvious. But several of the most informative and interesting recent books on genetic resources do not contain terms such as price, productivity or food consumption in their indices. The major benefit of genetic resources is surprisingly absent from the discussion.

Despite the high total value of agricultural germplasm, any attempts to earn rents, akin to those on mineral deposits, from continued supply of agricultural germplasm to breeders will likely fail. Breeders of major crops are not highly dependent on flows of new germplasm into their breeding stock. Indeed the narrowness of the genetic base of crops like hybrid corn and soybeans in the United States is remarkable, given their continuing yield advances.

Unfortunately, there is a real danger that efforts to capture these meagre rents from the flow of new germplasm to breeders will severely compromise a worldwide breeding enterprise that has enjoyed historically unprecedented success in increasing food supplies to the benefit of all consumers. This worldwide enterprise relies on an intensive exchange of germplasm, mostly enhanced materials and released cultivars. (Each year 650,000 accessions are distributed by the CGIAR centres, of which 500,000 are 'improved material'.) Care must be taken that this exchange is not damaged too severely by taxes, fees or, worse still, individualized prior approval requirements. If it is, consumers everywhere will lose, and any possible gains to holders of rights to germplasm will be paltry by comparison.

Note

1. For example, 'The North's genetic dependence on the South is accelerating for many crops' (Fowler and Mooney, 1990, p. xii).

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17

Valuing Farmers' Rights

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In recent years, the ownership and control of plant genetic resources (PGRs) have emerged as contentious issues in the international arena – and as issues for popular organizing and concern. In India, for example, popular demonstrations drawing tens of thousands of people have focused on the arcane provisions within the General Agreement on Tariffs and Trades (GATT) concerning intellectual property rights (IPRs) for PGRs. A dozen international meetings and 'undertakings' over the past decade have sought to create a legal framework for IPRs in agriculture.

At stake in the debate is control of revenues accruing from the use of products that incorporate genetic resources. Such products can have enormous value. A single pharmaceutical product based on PGRs, for example, can earn billions of dollars per year in revenues.[1] Crop varieties developed by multinational agribusinesses can similarly generate millions of dollars in profits.

It has become an article of faith among some activists and politicians in the 'South' that the developing countries (particularly those in tropical climates) can reap substantial profits from their native genetic resources.[2] The argument usually holds that because the tropics are the source of most of the planet's biodiversity, tropical countries should be able to profit from selling these genetic resources (or earning royalties from their use) on a world market increasingly hungry for new genetic materials.

In this chapter, it is argued that there are significant potential hazards to the South in seeking to establish systems of IPRs that guarantee 'farmers' rights' or other forms of proprietary rights to the countries that are sources of genetic resources. In particular, this chapter reports the results of an effort to quantify international flows of genetic resources in rice.

Rice is the quintessential tropical crop. Perhaps no crop is more closely

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identified with tropical wetlands. Of perhaps 80,000 known landrace varieties of *Oryza sativa*, the common cultivated rice, by far the majority come from India, China, and the countries of South and Southeast Asia. Thus, a naive observer might assume that rice producers in the rest of the world owe compensation to the farmers of this region.

In fact, however, the situation is much more complex. Although cultivated rice originated in Southeast Asia perhaps 5000 years ago, rice has been grown for hundreds of years throughout Asia, in Africa, in Europe, in North and South America, and in Australia and Oceania. There are legitimate landrace varieties from all these regions – meaning traditional varieties developed by farmers over centuries, using pre-scientific methods of seed selection. In most countries today, the varieties of rice used by farmers incorporate genetic material from landraces that originated elsewhere. For example, the genealogy of the Indian variety Mandira contains 18 distinct landraces from seven countries.

This chapter reports the results of a genealogical analysis of 1709 released varieties and elite lines of rice.[3] For each variety, all the known landrace ancestors and other ultimate progenitors were identified (to the extent feasible). Then the extent to which the varieties grown in each country were drawing on genetic resources that originated in other countries was determined. The surprising result of this analysis was that many of the world's most important rice-growing countries (e.g. India, Bangladesh, Vietnam, the Philippines and Korea) appear to be greater *importers* of genetic resources than exporters. In other words, these countries might end up as net losers under a system of international compensation for farmers' rights. In contrast, the biggest net winner might be the USA, which (in the data) is the largest net exporter of rice genetic resources. Although it seems improbable that the US would be a *source* of rice germplasm, a number of traditional varieties from Texas, Arkansas and Louisiana have been used widely in national and international breeding programmes and have contributed germplasm to literally hundreds of varieties released around the world.

Although the data require some additional refinement, the initial results underscore the need for caution from those who are pressing for an international system of farmers' rights. It is not obvious that such a system would benefit either agricultural communities in poor countries or the indigenous peoples who are thought to have developed so much of crop genetic diversity. If the goal is to transfer resources to poor rural people in developing countries, a system of farmers' rights may not be an appropriate mechanism.

Property Rights and Genetic Resources

In the major cultivated crops, such as wheat and rice, tens of thousands of landraces and traditional varieties are cultivated by farmers around the globe. These varieties differ – sometimes subtly – in their genetic characteristics: taste and cooking properties, disease and stress tolerance, agronomic traits and local adaptation. The genetic richness of these species has resulted from centuries of selection by farmers, interacting with their natural and human ecologies.

Plant breeders and agricultural scientists have long recognized the value and importance of the genetic variation represented in these pools of crop varieties. Since the advent of scientific plant breeding methods at the beginning of the 20th century, breeders have consciously sought to transfer genetic properties across varieties through selection, cross-breeding, and most recently through a variety of biotechnologies.

But the new technologies also raise complex questions about IPRs and the relationships between farmers in developing countries and the modern international research establishment. Farmers and indigenous people have, in many respects, created the array of genetic diversity that now exists. Researchers in both public and private entities hope to use this diversity to achieve gains in productivity. Private sector researchers hope to use genetic resources for profit – perhaps by selling high-productivity seeds back to the very farmers who cultivated and nourished the original diversity.

Activists, scholars and politicians have argued that there is an inherent injustice in current international systems of property rights. The current system effectively deprives farmers of any compensation for the use of genetic resources that they have developed. In contrast, private researchers who can demonstrate 'inventive steps' in the development of new crop varieties are able to claim a variety of IPRs and the associated rents. A number of alternative property rights regimes have been proposed.

Several previous studies have documented the present system of IPRs for PGRs and have surveyed the alternative forms of protection that might be extended to indigenous peoples and to farmers in poor countries. Specifically, Brush (1992), Gollin (1993), Swanson (1994), Walden (1995) and Wright (1996), among others, offer overviews of current property rights regimes and analyses of alternatives. The following paragraphs offer only a brief summary of the main issues.

Property Rights and Genetic Resources: Conceptual Basis and Current Views

Economists typically view property rights as central to systems of incentives. Property rights shape individuals' choices, with genetic resources as with any other good. For example, the willingness of private researchers to develop new varieties of crop plants depends on the extent to which they can profit from their efforts. Similarly, the willingness of farmers and indigenous people to conserve traditional crop varieties or habitat will depend on the returns that they can achieve from conservation, especially relative to the returns attainable through alternative actions.

For many goods, property rights are straightforward: ownership of a car or a pair of shoes is a relatively uncomplicated concept. Ownership of land or oil deposits is equally straightforward. In economic terms, all of these goods are 'rivalrous', meaning that one person's ownership precludes another person's ownership of the same good. The same does not hold, however, for new inventions. Once an invention is made, it can be used by many people simultaneously. For example, the recipe for a new pharmaceutical product can easily be copied, once it has been discovered.

To encourage innovation and invention, most countries protect inventions through some form of IPR, such as patent protection. Other forms of IPR protection include trade secret protection, plant breeders' rights, petty patents, trademarks and copyrights. The best-known form of IPR protection, the utility patent, typically confers short-term monopoly rights on an inventor in exchange for eventual public dissemination of information about the invention.

Patents and other forms of IPR protection have traditionally been confined to reward individuals for innovation. Historically, as Gollin (1993) notes, intellectual property laws have sought to protect the creators of industrial and artistic products, rather than biological life forms. In the United States, however, court rulings have consistently extended patent protection to biological innovations, including genetically altered microbes, plants and animals (Gollin, 1993). However, 'products of nature' are not patentable, being considered part of the public domain.

This explains the dominant view in US legal circles that crop varieties resulting from modern research warrant some form of IPR protection, whereas unimproved landraces and traditional varieties do not merit such protection. Nonetheless, this view has been increasingly challenged in recent years as many have begun to argue that IPR protection is an appropriate way to safeguard agricultural genetic resources and other forms of biodiversity that might otherwise be lost. Gollin (1993) notes that advocates of IPR for genetic resources typically argue that 'if those who control a habitat hold proprietary rights to develop its biological resources, then they have a means for obtaining economic benefits from those resources, and consequently, an incentive to conserve rather than destroy them'. A different view holds that IPR laws can help to achieve certain equity goals; for example, Reid *et al.* (1993) ask 'How can the efforts of generations of farmers be equitably compensated through their descendants for developments in agriculture?'

IPR Laws and the 'South': Are Rents Real or Imagined?

Implicit in much of the debate over IPR and PGRs has been a belief that the developing countries stand to reap huge benefits from their 'ownership' of genetic resources. For example, Brush (1992) suggests that farmers' rights can be a means by which poor countries can 'redress the inequality of world development'. Swanson (1994, 1995) claims that IPR protection for biodiversity would create a flow of compensatory payments from the rich 'North' to the poor 'South'. Swanson writes that 'IPR regimes for natural resources should generate a net gain for Northern states, *although the flow of funds under their auspices will be unidirectional North-to-South*' (emphasis added).[4]

Conversely, it is argued that current systems of property rights and trade have effectively allowed rich countries to appropriate the benefits of genetic resources without paying 'fair' compensation to poor countries. Shiva (1993) maintains that rich countries have ruthlessly exploited – perhaps even stolen – the genetic resources of poor countries, giving little in return except environmental destruction and systems of social inequality. Similar views are expressed by Fowler and Mooney (1990), among others.

The implicit assumption in this argument is that genetic resources have in the past flowed primarily from poor farmers in the 'South' to rich farmers, agribusinesses, multinational corporations and consumers in the 'North'. But even a quick look at global agriculture suggests that the situation is far more complex. It is true that the original centres of diversity for most crop and livestock species are found in areas that today lie in developing countries. But it is equally true that the spread of these species around the world dates back surprisingly far, and that the flows of genetic materials in agriculture have been multi-directional. It is not true that genetic materials have flowed only from the South to the North; there have also been important and long-standing flows from North to South, North to North, and South to South.

Consider the case of wheat: the first domesticated wheats appear to have been grown in Mediterranean West Asia about 9000–9500 years ago. But there is evidence that cultivated emmer and einkorn wheats had spread to Italy by 6500–7200 years before the present (Harlan, 1995; Smith, 1995). Consequently, it is foolish to argue that present-day farmers in Syria or Jordan would alone be able to claim property rights to wheat germplasm. Wheat cultivation in North America dates back at least to the 17th century; farmers in North America have adapted these varieties over 300 years to meet the needs of their environments and economies. If farmers in Syria can claim compensation for the use of their wheat varieties, so can farmers in Poland or Russia, England or Argentina, Canada or the US.

Similarly, if rice farmers in Thailand should be compensated for the use of varieties characterized by 'jasmine fragrance', then it is equally true that Thai farmers should pay compensation to their European counterparts for the Holstein–Friesian cattle that they keep, the poultry and pigs that they raise, the maize varieties that they cultivate, and so on. Moreover, they should compensate Taiwan and Japan for the semi-dwarf materials used for certain of their rice varieties, and they should compensate Bangladeshi farmers for the genes used in breeding contemporary 'floating rice' varieties.

Flows of genetic resources have by no means been unidirectional. While the South may possess most of the world's species, this does not guarantee that it will receive most of the rents and royalties from genetic resources. The following section probes this issue in greater detail, considering the case of rice.

Data and Previous Findings on Genetic Flows

Several previous studies have looked at the flows of genetic material in cultivated crops. Evenson and Gollin (1997) provide an analysis of genetic flows in rice. Byerlee and Moya (1993), Smale *et al*. (1996), Smale and McBride (1996), and Maredia *et al*. (1995, 1996) document flows in wheat. These studies examine the borrowing of varieties and parental materials in national breeding programmes over time. This chapter goes beyond previous work by accounting for flows of ancestral germplasm in rice. The aim is to ask to what extent each rice-growing country is cultivating varieties that are based on 'foreign' landrace ancestors. This is the kind of calculation which would determine patterns of compensation under a global system of farmers' rights. For example, if farmers in Brazil are growing rice varieties that incorporate germplasm from Chinese landraces, the Convention on Biological Diversity (as currently interpreted) would suggest that Brazil would need to pay China some compensation. Similarly, if Chinese varieties incorporate germplasm from Brazilian landraces, a reciprocal flow of compensation would take place. There is not yet any agreement on how genetic contributions would be assessed or on how value would be assigned, but in principle the kind of analysis undertaken in this chapter would be relevant in assessing compensation levels.

This study draws on a database of 1709 modern rice varieties released since the early 1960s.[5] For each of these released varieties, a complete genealogy was assembled. This included the date and origin of the cross on which the variety was based, as well as the data and origin of all parents, grandparents and other ancestors. Thus ancestry was traced back to original progenitors – in most cases, landraces or wild species.[6] Table 17.1 gives the frequency of release by country and by time period. Where release dates were not available, approximate dates were estimated based on available information. The data set includes materials from numerous countries, but it is relatively more complete for rice-producing countries of South and Southeast Asia than for those from other regions. India, in particular, is represented in the data set at a level that appears to be disproportionately large, with 643 varieties. Although India's breeding programmes have a long and productive history, the data set probably reflects a bias towards India based on the extensive and available data.[7] For a number of reasons, Japanese varieties were not included in this analysis.[8] The data indicate that numbers of released varieties rose steadily during the 1970s but have stabilized over the past 15 years. In some countries and regions, however, such as Latin America, varietal release totals have climbed markedly in the most recent period.

Previous analysis of these data (Evenson and Gollin, 1997) indicated that the international borrowing of modern varieties has been widespread. Flows of advanced varieties have included both direct release in one country of varieties developed elsewhere and indirect borrowing, chiefly through the use of foreign-developed varieties as parent materials. Of the 1709 released varieties, 390 (24%) were the result of a cross made outside the releasing country. The IRRI

Table 17.1. Numbers of varieties included in the data set, by country and by time period.

Country/region	Pre-1965	1966–70	1971–75	1976–80	1981–85	1986–91	Total
Africa	3	7	6	17	26	2	61
Bangladesh	1	7	8	11	4	33	64
Burma	0	4	6	21	37	8	76
China	9	1	8	30	31	12	91
India	10	68	136	139	125	166	644
Indonesia	1	2	5	21	10	9	48
Korea	0	5	11	35	40	15	106
Latin America	7	9	48	32	43	100	239
Nepal	0	0	1	10	4	2	17
Oceania	0	1	4	1	0	0	6
Pakistan	0	4	2	3	3	0	12
The Philippines	3	4	13	23	8	2	53
Sri Lanka	3	14	4	8	21	3	53
Taiwan	0	3	0	3	0	0	6
Thailand	1	2	4	8	5	3	23
USA	2	5	18	17	3	6	51
Vietnam	0	16	6	16	16	5	59
Other SE Asia	2	1	8	7	6	5	29
Other	0	7	15	15	15	19	71
Total	42	160	303	417	397	390	1709

was the source for 294 (17%) of these varieties. Other national programmes were the source for 96 releases. After IRRI, India was the next largest exporter of varieties, with 28 Indian varieties released elsewhere. India was also a large importer of varieties; 70 of its 643 varieties originated elsewhere, with 53 from IRRI. Sri Lankan varieties were released 11 times in other countries. Twelve Thai varieties were released in Myanmar. Myanmar was one of the largest importers of rice varieties; 43 of its 76 releases were imported varieties, including varieties from Bangladesh, China, India, Indonesia, IRRI, the Philippines, Sri Lanka, Thailand and Vietnam.

Perhaps more remarkable than the direct international flows of varieties have been the international flows of parents of the varieties. Nearly three-quarters of the varieties in the data set (1263) have at least one imported parent. Including imported varieties, 810 releases (47%) have at least one parent from IRRI, and 619 (36%) have at least one parent from another national programme. Excluding imported varieties, more than 500 varieties have at least one parent from IRRI. Excluding both imported varieties and those with IRRI parents, more than 350 released varieties have at least one parent from another national programme. This indicates that importing of parent materials is taking place across national programmes on a large scale.

The extent of international exchange – both of varieties and of parents – implies that a large majority of the varieties in the data set were developed using breeding lines from outside the country of release. In fact, only 145 varieties out of 1709 (8.5%) were developed entirely from own-country parents, grandparents and other ancestors. Most of these were simple varieties with fewer than four ancestors in their pedigree. The extent of this international flow of germplasm is extraordinary. No country in the data set has failed to take advantage of unimproved or improved germplasm from other countries.

But the flows of germplasm described above are essentially flows of advanced lines, primarily developed in public institutions. It is not clear whether these would be covered by any form of IPR protection under the Convention on Biological Diversity. There are no issues of farmers' rights that can be immediately discerned here. If India uses IRRI-bred varieties to develop its own modern lines, but the IRRI-bred varieties depend in turn on Indian germplasm, there is no issue of compensation.[9] Thus, in the next section, these flows of advanced lines and modern varieties are considered implicitly to represent flows of landrace materials.

International Flows of Rice Germplasm: Implications for Compensation

To arrive at specific estimates of compensation for genetic flows in rice, a matrix of germplasm exchange was calculated based on flows of landraces and other ultimate progenitors. This matrix reflects the full genealogies of the 1709 varieties in the database described above. Each variety can be traced to a set of ultimate progenitors. In most cases, these are landraces or pureline selections from landraces. Some are mutants. A few are of unknown type, or simply are not described in the available data. Most of the progenitors are identified by national origin – specifically, by the country from which they were collected.

For this analysis, each elite variety was traced to each of its distinct progenitors. (Duplicate progenitors were omitted; for example, if the landrace Cina occurred multiple times in a genealogy, it was considered only once.) The country of each progenitor was then identified. Each time that a progenitor from country i occurs as an ancestor of an elite variety in country j, it was considered to represent a flow of germplasm from i to j. In the germplasm flow matrix, then, the rows and columns reflect these flows. An element of the matrix, a_{ji}, thus represents the sum across all elite varieties in country j of the flows from country i.

Table 17.2 summarizes the results, some of which are startling. Several points deserve note. First, the extent of borrowing of genetic materials is enormous. Of the countries in this summary table, none approaches genetic self sufficiency; most are enormously dependent on foreign sources of germplasm. For Bangladesh, as an example, the 34 modern varieties in the data traced to 233 total ancestors (not all distinct), of which only four were identified as originating in Bangladesh, fewer than 2% of the total. Almost all the countries in the data show similarly low levels of genetic self-sufficiency in rice; only India

Table 17.2. Summary of international flows of landrace ancestors, selected countries.

Country	Total landrace progenitors in all released varieties	Own landraces	Borrowed landraces	Own landraces used in other countries	Net lending (borrowing), as share of total landraces
Bangladesh	233	4	229	10	(0.940)
Brazil	460	80	380	43	(0.733)
Burma	442	31	411	9	(0.910)
China	888	157	731	2052	1.488
India	3917	1559	2358	1749	(0.155)
Indonesia	463	43	420	420	0.000
Nepal	142	2	140	0	(0.986)
Nigeria	195	15	180	0	(0.923)
Pakistan	195	0	195	10	(0.949)
The Philippines	518	34	484	299	(0.357)
Sri Lanka	386	64	322	57	(0.687)
Taiwan	20	3	17	669	32.600
Thailand	154	27	127	220	0.604
United States	325	219	106	2420	7.120
Vietnam	517	20	497	89	(0.789)

Notes: In the last column, all numbers are given as shares of landraces used in domestic varieties; figures in parentheses are negative numbers. Numbers may exceed 1 if a country is a large net lender of landraces. Positive numbers indicate that a country is a net lender; negative numbers indicate that a country is a net borrower.

(39.8%) and the US (67.4%) provided more than 20% of their own landrace ancestors.

A second point to note is that most of the countries in the data are net borrowers of landraces; their modern varieties incorporate landraces *from* other countries more often than their landraces appear as ancestors to modern varieties *in* other countries. A few countries emerge as large net exporters of landraces: Taiwan, the US, China and Thailand. On the other side are large importers of germplasm: Bangladesh, Pakistan, Nepal, Nigeria and Vietnam. Indonesia emerges as exactly even; India is a small net importer.

Although it is difficult to extrapolate from these data to any ultimate system of compensation for farmers' rights, the results are provocative. The net importers of germplasm could well emerge as losers under the kind of compensation scheme now being considered. This includes a number of countries from the South which are often thought to be rich in genetic resources, such as Brazil and Burma. The net exporters of landraces might well be winners, including Taiwan and the US, neither of which is often thought to be a rich repository of PGRs for agriculture.

How can countries such as the US be *sources* of landrace materials in rice, which is after all a tropical crop? By some definitions, obviously, it would not be possible to regard the US as a source of native genetic materials in rice.[10] But rice cultivation in the US can be traced back at least 200 years. Farmers in the

US have indeed selected varieties that perform well under intensive growing conditions, and it is hard to imagine a system of farmers' rights that would not extend to these varieties equally as to varieties developed by indigenous people in the Philippines.

Limitations and Conclusions

The results presented here should be interpreted with caution. First, no effort has been made to weight the varietal releases by area planted or other measures of importance. Not all of the 1709 varieties are cultivated, and certainly they are not all of comparable importance. Second, there are undoubtedly errors in the data corresponding to the national attribution of certain landrace materials. Third, there are problems with the representation of different countries in the data. Some countries, such as India, are extensively represented with released varieties. Others, such as Taiwan, may be relatively under-represented. This means that Taiwan is likely to appear as a source of landraces relatively more often than as a user of landraces. Fourth, there is no effort here to weigh the genetic contributions of different ancestors; all landrace progenitors are viewed as having equal weight. But some ancestors may have large genetic contributions to a modern variety, while others have negligible genetic contributions; the fact that a landrace appears in the genealogy of a modern variety does not imply that its genes have in fact been passed down.

All these problems – and others – make it unwise to interpret the numbers of Table 17.2 as direct indications of who would gain and who would lose under farmers' rights compensation schemes. The figures presented here do, however, suggest that there are important empirical questions relating to gainers and losers under farmers' rights. Advocates of farmers' rights should not blithely assume that all compensation for genetic resources will flow from the North to the South. The South–South flows (and South–North flows) may be substantial.

More surprising, the results here suggest that the directions of compensatory payments may have little to do with biological centres of origin/diversity. Although India and Burma are countries that would generally be considered centres of origin and domestication for rice, they both emerge as net borrowers of landraces in the data considered here. The US, a relative newcomer to rice cultivation, emerges as a net lender. The implication is that richness in genetic resources, in itself, may not guarantee that the South will gain from the Convention on Biological Diversity and associated compensation schemes.

Much research will be required to clarify the empirical issues raised here. For rice and other crops, the international genetic flows may be fairly easy to document at a crude level of detail. But for a workable system of international compensation, the data and analytic techniques will require considerable refinement. At present, there are no central data sources on varieties of rice planted in different countries or on their ancestry. The same is true for wheat. For maize, the private sector presence may make data doubly difficult to acquire: private firms may be unwilling to provide information about the ancestry of their varieties, both to protect trade secrets and to avoid being forced to pay compensation for the genetic resources. Nevertheless, this study suggests that it is both feasible and useful to ask empirical questions about the international flows of genetic resources.

Notes

1. For example, Lovejoy (1997) claims that a compound derived from the South American pit viper and used to treat hypertension brings the Squibb Company $1.3 billion in annual sales.
2. I use the term 'South' – as opposed to terms such as 'poor countries' or 'developing countries' – when I want to refer not to a group of nations but to the people and discourses associated with the term. To my understanding, the 'South' is a construct which is identified with a political and economic entity standing in opposition to the 'North' and subject to international exploitation in the capitalist world system. When I speak of politicians and activists in the 'South', I intend to refer to those who would self-identify themselves in that fashion.
3. In most developing countries, new crop varieties are formally 'released' to farmers by national agricultural research systems or national seed boards. The release process may imply some kind of screening of new varieties for performance. The difference between released varieties and elite lines is that the latter have not gone through the formal legal process.
4. The same wording appears in both Swanson (1994) and Swanson (1995). Swanson's argument is that in spite of the compensatory payments that the North will be obliged to make, the net effect of IPR protection would be to encourage conservation of biodiversity in the South, leading to public good benefits that would outweigh the costs of royalty payments.
5. The data for this study were made available by the International Rice Research Institute (IRRI) in Los Baños, Philippines, as part of a study reported in Chapter 13.
6. Formally, a landrace is a farmer-developed variety selected over time in response to a specific physical environment and to specific social and economic constraints. In this chapter, however, I occasionally depart from this usage to include other varieties of rice that have been in common use by farmers for long periods of time and that pre-date modern breeding efforts.
7. It is reasonable to assume that most released varieties have been planted on significant acreage. Although some varieties are adopted widely, while others are planted in specific agroecological zones or geographic regions, most varietal releases are in fact used by farmers.
8. In particular, I had incomplete data on Japanese rice varieties and suspected that there has been relatively little recent flow of germplasm between Japan and the other countries in the study, since Japan grows primarily short-grained japonica rices and most of the other countries in the data focus on longer-grain indica and javanica rices.
9. There is of course the question of how *national* institutions compensate farmers for use of their germplasm, but this is an issue beyond the scope of international law. For example, can the Indian national agricultural research system use Indian landraces to

develop new rice varieties, without paying compensation to the farmers who have developed those landraces? The Convention on Biological Diversity has nothing to say about this question. More generally, there are numerous unresolved questions concerning the role of national governments as intermediaries in the compensation of farmers and indigenous peoples under the Convention.

10. It should be noted that so-called wild rice, which is native to the US, is not in fact a true rice and is not related to cultivated rices. The US landraces of rice included in this database are instead varieties of *Oryza sativa* and probably originated in the Philippines at some point in the past.

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Part V

The Implication of Development in Biotechnology

18

Impact of Biotechnology on the Demand for Rice Biodiversity

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Rice genetic diversity is the genetic material in improved rices, rice landraces in the field, the rice germplasm banks, and wild relatives of rice. One reason why policy-makers may wish to invest public money in conserving biodiversity is the contribution it can make to future economic growth. For policy-makers to determine whether they are investing enough money in the collection and conservation of genetic diversity, they must have some idea of the present discounted value of diversity and the cost of conserving diversity. Guesstimates of the value of diversity can be derived from estimates of the historical value of rice biodiversity and projections of the future demand for rice, the availability of inputs for rice production, and changes in the technology of breeding new varieties.

Evenson (1996) argues that because the present value of rice germplasm collections greatly exceeds the costs of adding to and maintaining them, near complete *ex situ* collection of landraces and wild and weedy species is justified. In addition he argues that near complete evaluation of rice genetic resources is justified. This chapter does not attempt to challenge the numbers behind these assertions; rather it concentrates on the question: Will biotechnology greatly increase or decrease the value of rice genetic resources?

This chapter will look at the impact of the new biotechnology. New biotechnology, which is what is meant by biotechnology in this chapter, consists of a group of tools: (i) tissue culture including wide hybridization, protoplast fusion, somoclonal and gametoclonal variation, and doubled haploids; (ii) genetic markers and mapping, cloning genes and studying gene expression; and (iii) genetic engineering – the transformation of plants with new genes.

Based on interviews with a number of key rice scientists our preliminary conclusions are: (i) so far biotechnology has at most caused a small increase in the use of rice biodiversity; (ii) the interaction of biotechnology and intellectual

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property rights (IPR) has not increased demand through increased private sector use of rice germplasm; and (iii) biotechnology is likely to increase substantially rather than decrease the value of rice biodiversity in the future. This suggests that Evenson's arguments for complete collection and evaluation of genetic resources are strengthened by the changes due to biotechnology.

Rice Genetic Diversity: How Much? Where? Cost?

Chang (1992) estimates the total accessions of rice in all germplasm banks to be 250,000. Of these, there were approximately 120,000 distinct accessions and 5000 wild accessions. Chang estimates that 10% of landraces remain uncollected.

The International Rice Genebank (IRG) at IRRI has more than 82,000 registered accessions, and of these almost 3000 are wild species and 1300 are *O. glaberrima*. If we take varietal name as an indicator, about 50,000 of the *O. sativa* accessions are unique (M. Jackson, personal communication, 1996). China has a collection of 61,000 accessions at the China National Rice Research Institute near Hangzhou, and the US has a collection of 16,476 accessions (N. Rutger, personal communication, 1996). There are also large germplasm collections in India, Thailand, Indonesia and Japan and another collections of wild-rice germplasm at the National Institute of Genetics, Mishima, Japan (Oka, 1991). ORSTOM and IRAT–CIRAD have about 4000 samples of seeds of wild and cultivated African rice and some Asian landraces that have been cultivated for a long time in Africa (Board on Science and Technology for International Development, 1996, p. 31).

Small scale efforts at *in situ* preservation of germplasm are being tried by some government research programmes and by non-governmental organizations (NGOs). Jackson (personal communication, 1996) reports some attempts to preserve wild species in Thailand and attempts by NGOs to preserve landraces in the Philippines, Vietnam and Thailand.

Landraces remain to be collected in remote areas. One country in particular where there is much diversity is Laos. IRRI is collecting samples there now. Wild species still have not been extensively collected in Australia, East, Central and South Africa, and South America. In some Asian countries there are still areas where collection remains to be done (Jackson, personal communication, 1996).

The cost of maintaining the IRG is about $700,000 annually. The cost of all rice germplasm collections is approximately $3–4 million (Evenson 1996).

Economic Contribution of Rice Biodiversity

The demand for biodiversity in rice is a derived demand which comes from the value of individual rice genes and groups of genes as an input into the process of producing more rice or more valuable rice. Changes in the demand for rice lead to the demand for higher yielding varieties and varieties with certain quality characteristics. Changes in demand include both changes in total quantity demanded due to growth in population and *per capita* income and changes in quality demanded. The changes in quality traits are often associated with *per capita* income growth – for example, the greater demand for japonica rice in parts of China or the demand for basmati type rices in South Asia. Production problems such as attacks by new diseases, pests or climate change lead to the demand for varieties resistant to these problems and for pest control and agronomic measures that can control the problem. Occasionally scientific theories lead to the demand for genetic characteristics, e.g. the search for male sterility to produce hybrids or the search for apomixis.

Public and private plant breeders respond to this demand by trying to produce rice varieties that retain the good traits of the old varieties and incorporate the new traits that are needed. They first screen the lines that they are using in their current breeding programme for the desired characteristics. If the characteristics are not found there, breeders make a wider search of elite lines that are being used in other breeding programmes. If they still do not find what they need, they go to the national gene banks or international collections such as the one at IRRI. In these collections they will use the common cultivated rice species *O. sativa* first, because characteristics from this species would be far easier to move into currently used varieties before searching accessions to the other 19 species. If the breeders still cannot find the characteristic that they need and the economic benefits are potentially very large, they may try to collect wild varieties or landraces with the required characteristics.

Most progress in increasing rice genetic potential for yields and resistance to pests, disease and other problems has been made by crossing material that was already in breeders' collections. These small collections consist of elite lines that have been developed through long national breeding programmes and breeding by the international centres along with local landraces to meet local conditions and tastes. Most of the $3.5 billion annual contribution of modern varieties in indica rice regions (Evenson, 1996) was due to conventional breeding.

The US case shows how often breeders use either the germplasm banks or wild species. California, Arkansas, Texas and Louisiana have government rice breeding programmes. Each breeder would have hundreds or perhaps a few thousand lines in his working collection which is what he uses to reproduce a regular stream of new varieties. If he has a disease or pest problem for which his collection does not have any resistant varieties, he can go to the National Small Grains Collection at Aberdeen, Idaho, which maintains the working collection of the 16,476 rice accessions that makes up the US rice germplasm collection. In a few unusual cases breeders may have to go to the IRRI germplasm collection for landraces or wild species.

Robert Evenson and Douglas Gollin (Chapter 13) provide evidence that a steady but small infusion of landraces has contributed to yields and resistance of rice in Asia and that occasionally characteristics from wild species have been important. They calculated that the present value of landraces added by IRRI was $86 million and that of the landraces added by NARS was $33 million.

In addition, there are a number of important examples of the importance of wild species in Asia. Perhaps the most important was the male sterile rice plant discovered in Hainan Island by Professor Yuan Longping's assistants in 1970 (Hunan Hybrid Rice Research Centre, 1994). 'The wild plant is believed to have originated from a cross of a local Indica variety with wild *O. spontaneum*' (Poehlman, 1987, p. 356). This breakthrough allowed commercial production of hybrid rice in China. In 1990, hybrid rice based on this and other male sterile lines covered 15.9 Mha, almost half of the rice area of China, as well as some of the area in Vietnam. It was responsible for a 10–20% or about 1 t ha^{-1} increase in yield in this area which amounts to an increase of 15.9 Mt of rice (Huang and Rozelle, 1995).

There are also some important examples of disease resistance being incorporated into commercial rice from wild relatives. Grassy stunt virus, which was transmitted by brown plant hoppers, was a problem in Southeast and South Asia in the 1970s. IRRI grew out much of their collection and inoculated it with grassy stunt virus. Eventually they found resistance in a wild species *O. nivara* that had been collected in India. This characteristic is now incorporated into all of IRRI's advanced lines.

Almost all of the research on rice has been conducted by the public sector, and most of that in public research institutes and universities in Asia. In addition, international rice research institutes such as IRRI, CIAT, IITA and WARDA have made important contributions. The largest countries in Asia have very large research programmes. A survey of scientists in Chinese provinces found that, on average, 410 scientists were working on rice improvement in the years 1975–1987 (Lin, 1991). About 1000 scientists were working at 50+ locations on all types of rice research in India in 1987.

There is very little private sector rice breeding anywhere in the world, other than a handful of private companies, primarily in Japan and India. Private breeding in Japan is a new phenomenon due in part to the government's eliminating its monopoly on rice breeding in the 1980s, the successful example of hybrid rice in China, and perhaps the introduction of plant breeders' rights. The recent increase in interest in India has been due to the commercial introduction of hybrids. Several new firms, such as Hindustan Lever, have been breeding rice since 1991, and the three firms that had started before 1991 have expanded.

Impact of Biotechnology

Biotechnology is affecting plant breeding in a number of different ways.

1. Advances in tissue culture and embryo rescue make it possible to use wild and weedy rice to develop new varieties that are resistant to diseases and pests for which genetic resistance had not been available.

2. Molecular markers have greatly increased the speed of screening germplasm of cultivated and wild rice by allowing the identification of a characteristic in the tissue of seedlings rather than waiting a season for the characteristic to express itself in the mature plant.

3. Recent advances in cloning genes and transforming plants greatly reduce the cost of using characteristics from landraces and wild relatives. Instead of requiring many years of backcrossing first to incorporate useful traits into high-yield varieties and then to eliminate harmful traits, the process can be reduced to a few years through biotechnology.

4. Genetic markers and maps will allow the identification of alleles for traits that are present in rice but which would never show up through conventional breeding.

5. Characteristics from other crops, from bacteria, and from animals can now be incorporated into rice, and the characteristics from rice can be incorporated into other crops.

In addition to its impact on the technology of plant breeding, biotechnology can reduce the cost of evaluating rice germplasm and wild relatives as they are collected or evaluating collections that are already in germplasm banks. The tools of biotechnology may make it easier to protect breeders' IPR by making hybrids easier to produce. In addition, in countries where new plant varieties can be protected with patents or plant variety protection laws, biotechnology may make it easier to prove that someone is copying your variety.

Like plant breeding, almost all of the rice biotechnology research in Asia is conducted by public sector research. By the autumn of 1992, India's total investment in rice biotechnology research was about $9 million at 19 institutions, which spent about $800,000 a year on current expenses. Seventy scientists, of whom 68 had PhDs, were working on rice biotechnology (Parthasarathy, 1993). Based on the number of Rockefeller Foundation projects in India and China, it appears that China was allocating perhaps twice as much annually to rice biotechnology as India. Unfortunately, we have not found any other sources of data on this. Comparing the number of conventional rice scientists in India with the number of biotech scientists shows that only a small share of total public research on rice is on biotechnology. Biotechnology is more expensive and better funded per scientist than conventional rice research.

IRRI's biotechnology research started with its wide crossing and anther culture programme in the 1980s. In the 1990s, IRRI worked with Cornell University and others to develop molecular markers for useful traits and a rice genome map. A molecular biology programme was initiated to increase basic understanding of rice and to develop and transfer the tools of biotechnology to national programmes. In the plant protection area, entomologists used biotechnology to study insect–plant interactions. IRRI purchased *Bt* genes for resistance to yellow stem borer from Ciba–Geigy for free use in developing countries. Plant pathologists are using biotechnology to study important rice diseases.

Two programmes have been established to encourage collaboration on rice biotechnology research among national programmes – the Rockefeller Foundation Rice Biotechnology Network and the IRRI Asian Rice Biotechnology Network. The Rockefeller Foundation has made a concerted effort to promote collaboration among developed and developing country scientists through financing the Rice Biotechnology Network, which brings scientists together, financing pre- and post-doctorates in the US and Europe, and financing collaborative research. Between 1984 and 1994, $62.7 million was committed to rice biotechnology research. In 1994, the budget for the Rice Biotechnology Network was $7.7 million.

The second programme to promote international collaboration is the Asian Rice Biotechnology Network (ARBN). It is led by IRRI and financed by the Asian Development Bank and the German aid agency. It was started in 1993. ARBN attempts to build or strengthen biotechnology research within research institutes and agricultural universities that have strong programmes of breeding, pathology, etc., for rice improvement and strong linkages with IRRI.

Relative to the size of public sector rice biotechnology research, private companies are carrying out only a limited amount of research. The number of private companies that are working on rice biotechnology is slightly larger than the number doing conventional rice breeding. In 1991, only a few companies were working on rice. Since then, Proagro/PGS and MAHYCO have established biotechnology laboratories working on rice in India. Agracetus and a number of other firms are working on rice biotechnology in the US.

Biotechnology in rice has made rapid progress in the last decade. In 1995, several breakthroughs in biotechnology occurred that should greatly enhance the productivity of rice breeding. First, transformation of indica rices using the ballistic gun and *Agrobacterium* has become relatively routine (G. Toenniessen, personal communication, 1996). Second, the first gene for disease resistance was cloned from an African wild rice, engineered into susceptible lines, and the transgenic plants showed resistance to the disease (bacterial leaf blight) (Song *et al*., 1995).

The techniques used in wide crossing (embryo rescue and tissue culture) were the first biotechnology techniques that encouraged breeders to use more than the elite lines and landraces that they usually use in their crossing programmes. It took 8–10 years of backcrossing and good luck to incorporate traits from a wild species, but it could be done. Thus, the only people who did this were international or government breeders who had long-term funding and a lot of patience.

Now, with the help of biotechnology, more breeders are exploiting traits from wild species because the time required has been cut to 2–3 years rather than 8–10 years. The head of IRG reports (M. Jackson, personal communication, 1996):

> There seems to have been an increase in interest in the wild species and in recent years we have received more requests for these materials. We assume this is related to developments in biotechnology which are permitting researchers to use germplasm more effectively.

Most of the other work on rice biotechnology has so far primarily made use of the genetic material that conventional breeders are already using. For example, in the search for resistance to bacterial leaf blight, mentioned above, biotechnology scientists started their search using segregated materials from crosses that already included wild species that were thought to have some resistance. Biotechnology essentially greatly speeded up the process of identifying and engineering the gene into commercial varieties.

Some of the most recent work is less dependent on the collections of conventional breeders and thus is making use of a much wider range of genetic material. A group at Cornell and IRRI is using genetic markers to identify alleles that would never be identified by conventional breeding because they are ‘hidden’ by dominant characteristics. Dr Susan McCouch from Cornell and IRRI reports (personal communication, 1996):

> I am able to say that our work with maps and markers is, in fact, providing evidence that wild or weedy ancestors can be productive sources of new genes for improvement of cultivated rice. We are demonstrating that marker-assisted breeding allows us to discover previously unidentified alleles hidden in low yielding wild ancestors that can boost yields of cultivated rice. The use of maps and markers not only provides an opportunity to identify these new alleles, but these tools also make it possible to speed up the process of moving them into locally adapted, highly productive cultivars. The concepts we are working with here at Cornell are aimed at broadening the pool of genetic diversity that breeders work with. ...

Today and in the near future it appears that, among the grasses, rice is more likely to be a source of genes and of probes for other species rather than other grasses being a major source of genes for rice. A few breeders of other grasses are starting to search rice genetic libraries for rice genes that control certain traits in rice and that they would like to have in other crops such as sorghum. The rice gene can be used to construct a probe. This probe can be used to screen germplasm of sorghum for the desired trait. If the trait is found, then it can be used in a conventional breeding programme or isolated and inserted into elite lines of sorghum. If the trait is not found, then the scientists might try to transform the sorghum by inserting the rice gene.

Another example of using the rice map for other crops is the CIMMYT/ORSTOM project studying apomixis in maize. They have not found apomixis in cultivated maize, but they recently identified the apomixis gene in a wild relative of maize, *Tripsacum*. Instead of going directly to maize to look for this gene and to study why it does not cause apomixis in the maize plant, they are first looking at the rice genetic maps. Using the markers from *Tripsacum*, they identify the region on the genetic map of rice where the apomixis gene is located. They then make probes from rice which can be used in *Tripsacum* and maize to study what turns apomixis on and off (D. Hoisington, personal communication, 1996).

These research projects are useful to rice scientists because they will identify and clone traits of rice which had not been done so far. Rice is chosen for a number of reasons: (i) the rice genome is smaller than that of most other grasses; (ii) more complete molecular maps of rice have been constructed; and (iii) bacterial artificial chromosome and yeast artificial chromosome libraries have been constructed and are more readily available because the Rockefeller Foundation has funded their construction, while libraries for corn, cotton and others are proprietary or more difficult to get access to.

Before the development of biotechnology, it was impossible to breed traits of crops other than rice or traits from bacteria or animals. Now that is possible. Are breeders now searching other crops for traits that they need in rice? The answer seems to be not yet. So far there have been no applications to the Rockefeller Foundation to do this type of research (G. Toenniessen, personal communication, 1996). The head of plant breeding at IRRI reports: ‘I do not know of any project underway which aims at cloning genes from other cereals for transformation of rice. One project which is being discussed aims at cloning gene(s) for apomixis from pennisetum or brachiaria (range grass from Brazil) and their introduction into rice’ (G. Khush, personal communication, 1996).

The most common use of non-crop genes that are being introduced into rice is *Bacillus thuringiensis* (*Bt*). The genes that produce poison to some insects are inserted into rice to protect against yellow stem borer and some other insect pests. Transgenic plants containing *Bt* are now being tested in a number of countries.

The use of genes from other crops, from bacteria or animals will become more important in the future. But in the near future it appears that the demand for rice germplasm is likely to be greater than the demand for non-rice genes by rice breeders.

Biotechnology – IPRs

Genetic engineering has allowed companies, universities and individuals in the US to patent genes, plant parts and plants. This has been the basis of the growth of the biotechnology industry in the US. This has greatly increased the amount of private sector research on plant biology. For the first time, large chemical firms and start-up companies are looking at rice improvement. While corn, soybeans and cotton have attracted more research dollars, rice has also been affected. For the first time firms like Monsanto, DuPont and Ciba–Geigy are trying to develop disease- and pest-resistant rice varieties.

Biotechnology is also strengthening IPRs by making it easier to produce F1 hybrid seed. P.G.S. Belgium has developed and patented a system to produce genetically engineered nuclear male sterility (NMS) in rice, and it is working with Japan Tobacco to develop NMS hybrids for Japan and Proagro to produce hybrids for rice in India.

The tools of biotechnology have also made it easier to identify varieties or hybrids that are being illegally sold or used as an inbred line in hybrids. This greatly strengthens the ability of private firms to enforce their IPRs where they exist.

Biotechnology has strengthened IPRs on rice in some countries, and this has led to increased private sector research on rice biology and rice breeding. However, we were not able to find any evidence that increased private rice research had led to an increased use of biodiversity. IRRI reports negligible use of IRG by private companies (M. Jackson, personal communication, 1996). The only evidence of increased interest in biodiversity due to these changes was the search for *Bt* strains which was carried out by Ciba–Geigy in the Philippines in the early 1990s.

From Use of Germplasm to Money for Maintenance and Collection of Germplasm

The overall impact of these changes has been a small increase in the use of *ex situ* collections of rice germplasm and wild and weedy relatives. This has not yet led to major increases in funding for germplasm collection and maintenance. Funding for IRRI's germplasm conservation, dissemination and evaluation has remained constant in recent years with the exception of a 1994 grant of US $3.3 million from the Swiss government for the collection of landrace varieties and wild species. The objective of the project is to complete the collection of rice germplasm before the turn of the century. Although IRRI is coordinating the work, it is actually being carried out in the national programmes and funds go to those programmes for this endeavour (M. Jackson, personal communication, 1996).

Over the last decade, national governments have paid more attention to germplasm preservation. In the 1980s, China, with the assistance of the Rockefeller Foundation and the World Bank, built up its national gene bank. At about the same time, India, with the assistance of the USAID made major investments in improved gene banks under their National Board for Plant Genetic Resources. These investments were induced by the increasing awareness of the value of biodiversity and were partially due to the fact that the environment is the latest development fad among donors. The awareness of the value of biodiversity is due in part to the well-publicized developments in biotechnology, but the concerns about being dependent on foreign germplasm collections and multinational seed companies were probably more immediate causes of the interest in *ex situ* preservation.

Conclusion

Rice biotechnology appears to have increased the demand for rice germplasm rather than reducing it. Some techniques have been particularly important in stimulating more use of rice germplasm. These include the early tissue culture and embryo rescue techniques that allowed the use of traits from wild and weedy relatives, the marker-aided selection, gene cloning and transformation. Recent work at Cornell to identify hidden alleles in rice has shown the potential of wild and weedy relatives as sources of genes to increase yields and reduce pest and disease attacks.

There appears to be no threat that the possibilities for importing genes from other plants and animals will reduce the demand for rice biodiversity. The demand of rice scientists for traits from other crops will not soon exceed the demand for rice genes, markers and traits by non-rice scientists. The use of *Bt* may have reduced the search for resistance to certain pests like yellow stem borer. However, there do not appear to be many more *Bt*s on the horizon.

Thus, Evenson's arguments for the complete collection and evaluation of genetic resources are strengthened by the changes due to biotechnology, not reduced by them. IRRI seems to be making some headway in that direction with its grant to collect most of the landraces and wild and weedy relatives. IRRI and many of the national rice collections could use more money for evaluation of the collections – particularly using the new techniques of biotechnology. If Evenson's numbers on the present value of rice biodiversity are in the right ballpark, increases in spending on these activities could easily be justified also. Experiments with *in situ* preservation may also be justified.

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Biotechnology and Genetic Resources

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Biotechnology changes the technology of plant breeding and alters the role of genetic resources. Conventional breeding methods allow breeders to make within-species crosses, i.e. to combine and recombine landraces and combinations of landraces within the major crop species. The first generation of biotechnology consisted of techniques allowing 'interspecific' crosses or combinations of genetic materials from closely related species. For example, in rice breeding, 'embryo resource' techniques were used to combine genetic resources from *Oryza nivara*, one of the 20-plus 'wild' or uncultivated species of rice, with *Oryza sativa*, the chief cultivated rice species to incorporate host plant resistance to the grassy stunt virus disease in rice. These 'wide crossing' techniques have been increasingly used over the past three or four decades.

More recent developments in biotechnology enable marker-aided plant breeding and 'transgenic' breeding. (Transgenic plants are defined as having genetic resources from an alien species incorporated into them.) There are several techniques for achieving transgenic plants now available to plant breeders. These have been available for most crops for more than a decade. Transgenic breeding is also increasing in importance.

How have these biotechnology developments affected the use of, and hence the value of, genetic resources as traditionally defined, i.e. landrace and related genetic resources in germplasm or gene bank collections?

In this chapter, a review of two evaluation studies of rice research programmes is provided to shed light on this question in the case of rice research. The first study reviewed is on evaluation of achievements of the Rice Biotechnology Program (funded by the Rockefeller Foundation) (Evenson 1996). The second is a research prioritization study for rice research in Asia (Evenson *et al.* 1996). Both studies indicated that the biotechnology techniques

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developed to date are best suited for qualitative ‘trait breeding’. This is because these techniques are suited to genetic transfer of very limited DNA or single-gene materials. As a consequence, both wide-crossing and transgenic breeding will have very similar objectives to those of conventional trait breeding.

These studies indicate that there is likely to be a considerable broadening of source genetic materials as the new techniques are increasingly employed. They do not indicate, however, that there will be a major shift away from genetic source materials that have been useful with conventional breeding methods.

The Rice Biotechnology Program Evaluation

The Rice Biotechnology Program supported more than 130 projects conducted in 26 countries (including projects in several international agricultural research centres). Many of the projects in developed countries were funded as ‘tool development’ projects (see below). Sixty-nine projects were located in developing countries.

Research objectives can be roughly grouped as follows (note that some projects had more than one objective):

- tool development: 68 projects;
- yield enhancement technologies: 75 projects;
- disease resistance technologies: 38 projects;
- insect resistance technologies: 19 projects;
- stress tolerance technology: 11 projects;
- grain quality technology: 12 projects;
- other: eight projects.

These research objectives reflected the ‘priority traits’ strategy built into the design of the programme. In particular, the disease resistance, insect resistance, stress tolerance and grain quality objectives are all related to traits controlled by one (or few) genes. These traits, in general, have essentially formed a significant part of conventional rice breeding strategy over the past two decades. It should be noted here, however, that while the priority traits strategy emphasizes single-gene traits, it does not preclude yield enhancement technology strategies. A larger number of projects in the programme were seeking yield enhancement objectives than were seeking specific resistance or tolerance objectives.

For the evaluation study, a specific set of research problem areas (RPAs) was specified. These included ‘biotechnology tools’ RPAs that would be useful to future researchers, five ‘yield enhancement’ RPAs, four disease resistance RPAs, four insect resistance RPAs, and five stress tolerance RPAs. These RPAs were defined so as to be confirmable with traits and achievements sought in conventional rice breeding programmes and with the priority traits strategy. Second, ‘time to accomplishment’ subjective probability estimates (SPEs) were obtained by asking for two estimates: an ‘optimistic’ estimate which had only a 25%

probability of achievement and a ‘conservative’ estimate which had a 75% probability of achievement.

SPEs must be provided by scientists with technical and scientific skills and objectivity. They cannot reasonably be obtained from non-scientists; but scientists are subject to possible bias. The bias and uncertainty as to estimates was limited by two procedures. The first was to obtain independent SPEs from a number of informants so that one can examine the distribution of SPEs. The second was to specifically allow for uncertainty of estimates by obtaining not a single point estimate, but a subjective probability distribution (SPD) estimate.

The SPEs reported in Tables 19.1–19.5 were from two groups of scientists participating in the Rice Biotechnology Program. The first group was composed of 60 respondents to a mail survey sent out in May 1993. The second group was approximately 70 respondents from participants at the Seventh Rice Biotechnology Conference in Bali, Indonesia, in May 1994. Fifteen respondents were common to both groups, and they provide some evidence for changes in SPEs over time.

The SPD dimension of the study was achieved by asking respondents for two estimates for time to achievement. All respondents were asked to presume that current international and national research programmes were expected to continue with a constant level of support. Researchers were, however, expected to change research programmes and research objectives in response to scientific and technological developments. One of the SPD estimates was an optimistic estimate described by the earliest date when a 25% probability of research objective could be achieved (or alternatively, this might be the date by which 25% of the programme’s multiple objectives would be achieved). Then a second, more conservative, date where a 75% probability of research objective could be achieved was obtained. These two dates allowed each respondent to express the range of uncertainty (the SPD) of their estimates.

The actual SPE distributions by RPA are organized in five tables reflecting the groups of RPAs. For each, the distribution of responses for the 25% and 75% probability levels are reported. For each group, the 1994 responses by respondent category (IARC scientists, NARS scientists, developed country scientists) can be summarized as follows.

1. SPEs: Biotechnology tool development. Table 19.1 summarizes the data from four tool development cases. In spite of considerable room for interpreting the questions, especially by those further from the applied end of the research spectrum, there is good agreement on the whole on tool development. Most of the relevant tools are to hand already, and the uncertainty has to do with routine use. The ranges (covering 75% of the estimates) are narrow for the 25% estimate and reasonable for the 75% estimate.

2. SPEs: insect resistance traits. Table 19.2 reports the evidence for transgenic insect resistance trait achievement to the field trial level (generally considered to be the routine breeding level). These estimates were generally of high quality (though poorest for gall midge resistance where substantial bimodalism is observed), the ranges are quite narrow, and median estimates of time to achievement were close; 1996–1998.

Table 19.1. Time assessment: biotechnology tool development response distribution.

	Year of achievement																		
Biological tool	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	Range	Median
I. Double haploid																			
25% prob.	13	11	22	8	3	2	4										1	1995–1997	(1996)
75% prob.	3	4	2	3	18	7	13	2		1		4		1			1	1997–2000	(1998)
II. Molecular markers																			
25% prob.	13	14	16	8	16	4	4		1		1						1	1995–1998	(1996)
75% prob.	5	2	5	2	9	9	18		1	3	2	1			1		1	1996–2000	(2000)
III. Pathogen markers																			
25% prob.	10	18	15	11	16	2	9			1		3					2	1995–2000	(1997)
75% prob.	1	3	5	7	8	8	19			5	0	14	1		1	1	10	1997–2005	(2000)
IV. Indica transformation																			
25% prob.	8	10	19	12	13	5	15	1	1	1		2					4	1996–2000	(1998)
75% prob.	3	2	11	7	9	4	20	3	8	3	1	6	2	1	1	1	16	1998–2005	(2000)
Respondent group (1994)																			
IARC scientists																			
25% prob.	1	2	8	4	3	6	2						6			1	1		
75% prob.		1		3	1	5	5	2	2				5			6	6		
Less developed countries' scientists																			
25% prob.	5	7	26	12	13	3	11		1				2						
75% prob.			3	3	12	8	24		5			1	14			6			
Developed countries' scientists																			
25% prob.	12	9	21	7	10	1	12						1				6		
75% prob.	9	2	5	4	13	7	15		1				12				16		

Table 19.2. Time assessment: insect resistance response distribution.

	Year of achievement																						
Biological tool	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2015	2020	2030	2050	Range	Median
I. Sucking insects																							
25% prob.	2	5	10	2	5	2	4			2		2		1			1	1	1			1996–2000	(1998)
75% prob.		2	2	2	5	6	9	2	4	3		2		2			4		1			1998–2003	(2000)
II. Leaf folder																							
25% prob.	1	6	6	2	7	3	1		1	1		1					1	2				1995–1998	(1998)
75% prob.			2	4	5	1	8		1	2		1	1	1	1		2	1	3			1997–2000	(2000)
III. Stem borer																							
25% prob.	3	6	10	5	10	3	3	1	1			2					2	2				1996–2000	(1996)
75% prob.		2	5	2	4	8	8	5	4			2	1	1	3		2	2	1	2		1995–2003	(2000)
IV. Gall midge																							
25% prob.	2	4	2	2	6	4	4			2	1	2					2	1				1994–2003	(1998)
75% prob.				1	3	4	7		2	3	1	2			1	2	3	4	2			1999–2010	(2000)
Respondent group (1994)																							
IARC scientists																							
25% prob.		2	6	4	6	7	1										2						
75% prob.			1	1	5	1	5	1	1			1				2	3	1					
Less developed countries' scientists																							
25% prob.	1	2	12	4	4	3	1		1		1						3						
75% prob.			1		1	10	9		1		1		2		1			4					
Developed countries' scientists																							
25% prob.	1	4	4	2	7	3	5			1		7		1				3					
75% prob.			1		3	4	1		4	4		2		2			4	5	3				

3. SPEs: disease resistance traits. Table 19.3 reports estimates for transgenic disease resistance traits. These estimates are of lower quality than for insect resistance traits. Bimodalism is observed in each case although it is mostly in the 75% estimates, hence the fairly broad ranges for these estimates (most bimodalism is from developed country scientists – see below). These might be regarded to be ‘medium to good’ quality estimates.
4. SPEs: abiotic stress tolerance. Table 19.4 reports estimates for transgenic abiotic stress tolerance traits. These estimates are of lower quality than those for insect and disease resistance. Ranges are broader, median dates are later and there is more bimodalism of the 75% estimates. But the estimates are still of ‘medium’ quality.
5. SPEs: yield enhancement. Table 19.5 reports the estimates for general yield enhancement RPAs. These range from reasonable to poor for apomixis and nitrogen fixation. Even here the term ‘poor’ refers to the broad range of estimates and does not necessarily mean that these are meaningless estimates.

The SPE time to achievement estimates were incorporated into an expected economic returns analysis.

The Research Priorities Study

The research priorities study was developed after the rice biotechnology study had been completed. This study sought SPE estimates both for research potential (RP) and for time to achievement. Perhaps its major innovation was that it used a combined RPA and research technique (RT) format, enabling comparisons among conventional breeding, wide-crossing, and transgenic and marker-aided breeding.

A formal questionnaire designed to elicit ratings of research potential and timing was administered to a total of 17 rice scientists (nine from IRRI, eight from NARS). Each scientist was asked to provide four numbers for research problem areas where they considered themselves to be qualified. The four numbers were:

1. A ‘rating’ of the potential (RP) for a research contribution to the RPA–RT problem area. Ratings were on a 1–5 scale.
2. A rating of the achievement to date (RA) by research on the RPA–RT problem area.
3. An assessment of the date (years from now) by which either a 25% achievement of the *remaining potential* (RP minus RA) would be achieved or by which there was a 25% likelihood of achievement.
4. An assessment of the date by which either a 75% achievement of the remaining potential was expected or by which a 75% likelihood of achievement was expected.

Table 19.3. Time assessment: disease resistance response distribution.

	Year of achievement																						
Biological tool	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2015	2020	2030	2050	Range	Median
I. Blast																							
25% prob.	1	8	8	2	21	4	9			2	2	3			1		3	3				1995–2005	(1998)
75% prob.		1	1	6	8	1	9	3	5	3		7			1	2	9	6				1995–2010	(2000)
II. Bacterial leaf																							
25% prob.	2	8	12	4	16	3	14			1		2			1		4	1				1986–2000	(1998)
75% prob.		1	1	4	9	5	11	2	1	2		7		1	1		8	4				1998–2010	(2000)
III. RSS virus																							
25% prob.		4	12	8	7	3	4					2										1996–2000	(1997)
75% prob.		1	2	2	8	2	5	2	2	1		3			1	1	5			2		1998–2010	(2002)
IV. Tungro virus																							
25% prob.	1	13	6	1	18	4	3	2			1	2					1					1995–1999	(1998)
75% prob.		2	3	2	11	3	7	1	5	1	1	4	1	1	2	1	5	3				1998–2002	(2000)
Respondent group (1994)																							
IARC scientists																							
25% prob.					12	5	1																
75% prob.		1	7	1	6	0	4	2	4			4					4						
Less developed countries' scientists																							
25% prob.	1	4	12	4	11	3	6	2								1							
75% prob.			1	1	11	6	7	3	6						2	2							
Developed countries' scientists																							
25% prob.		5	12	1	13	1	8					6					2	2					
75% prob.			1		11	2	7	2	2			7		1	2		9	5					

Table 19.4. Time assessment: abiotic stress tolerance response distribution.

	Year of achievement																					
Biological tool	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2015	2020	2030	2050	Range	Median
I. Drought		1	3	1	5	6	20	1	1	2	1	6					6	1				1998–2005	(2000)
25% prob.				1		1	4		3	5	1	9		3	2		9	7			1	2000–2015	(2005)
75% prob.																							
II. Flood																							
25% prob.			2	1	6	6	13			1	1	2			1		3	1				1998–2000	(2000)
75% prob.							3	1		4	1	10		1	1		6	6	3		1	2003–2015	(2005)
III. Cold																							
25% prob.		1	4	6	6	10	5		2	1		2				1	7					1997–2005	(1999)
75% prob.				3	2	3	4		1	7	1	7					7	5	1	1	1	2000–2015	(2005)
IV. Salt																							
25% prob.	1	2	5	7	2	7	10	1	4		1	5			2		1	11				1997–2005	(2000)
75% prob.				4	1		5	1	3	4		6				1	15	4		1	1	2000–2010	(2005)
V. Nutrient deficiency																							
25% prob.			3		6	4	6	1	2			2					3					1998–2005	(2000)
75% prob.							5	1	3	6		3					5	34	2		1	2000–2015	(2010)
Respondent group (1994)																							
IARC scientists																							
25% prob.			4	2	2	10	3			1		5					4	1					
75% prob.				1	1		1					8		1		1	7	4	1				
Less developed countries' scientists																							
25% prob.		1		3	5	8	7	1	1	7	3	6					1	2					
75% prob.				1			1				2	6		3	3	1	5	4					
Developed countries' scientists																							
25% prob.		1	4	1	7	3	17	1	2		4	1		1		10	7						
75% prob.							5		1	4	10		1	1		10	10	8					

Table 19.5. Time assessment: yield enhancement response distribution.

	Year of achievement																						
Biological tool	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2015	2020	2030	2050	Range	Median
I. Male sterility																							
25% prob.	7	9	12	4	4	3	11			1		1					12					1995–2000	(1996)
75% prob.	3	3	3	6	6	1	6	2	1	1	3	5				1	8	2				1997–2010	(2005)
II. Starch metabolism																							
25% prob.	1	1	4	5	14	1	9		2	1		2					5					1996–2000	(1998)
75% prob.			1		4		11		3		3	7	2				5	3	1	1	1	2000–2006	(2002)
III. Photosynthetic effect																							
25% prob.	2	1	2	7	5		5	1			2	3					2	2				1997–1999	(1999)
75% prob.		1	2	12	2	1	2		2	2		5	2		2	1	3	9		1		2005–2015	(2005)
IV. Apomixis																							
25% prob.		1	4	2	4	1	10	1	1	2		3			1	4	5	1	1			2000–2010	(2000)
75% prob.			2	2	1		7					3				3	7	7	1	1		2000–2015	(2010)
V. Nitrogen fixation																							
25% prob.			2		1		4			1		4		1	1		8	12	5		1	2010–2020	(2015)
75% prob.					1		5			2		3				1	7	12	10	3	6	2010–2050	(2020)
Respondent group (1994)																							
IARC scientists																							
25% prob.			2	1	3		4	1	1			4					5	3	1	1			
75% prob.				1	1		2				1	4	1			4	3	4	2	2			
Less developed countries' scientists																							
25% prob.	3		7	6	6	3	4	1	1		3	3	1		1		2	1					
75% prob.	1		2		4		4	2	2	1	2	4	2		2	1	8	2	1				
Developed countries' scientists																							
25% prob.	1		6	1	4	1	14					2	1				9	4	1	1			
75% prob.	1		1	1	2		6				2	5					9	11	2	2	2		

The elicitation of these four numbers was based on the following principles:

1. Scientists are more comfortable with a rating scale (1–5) than with a specific estimate of a productivity level. Rating scales linked to achievement were provided to scientists. These were:

- less than 10% achievement of loss elimination (or increase in biological efficiency);
- 10–25% achievement of loss elimination (or increase in biological efficiency);
- 25–50% achievement of loss elimination (or increase in biological efficiency);
- 50–75% achievement of loss elimination (or increase in biological efficiency);
- 75%+ achievement of loss elimination (or increase in biological efficiency).

The distribution of these ratings obtained from the sample of respondents were then quantified into a mean percentage achievement measure (the variance was also computed).

2. The distinction between RA and RP was needed to clarify what was meant by remaining research potential. By specifying both RP and RA we attempted to capture more clearly the *incremental* potential for further gains. In many RPA–RT classes, respondents indicated that while substantial RP for problem solutions existed in the past, research programmes had already achieved all or most of this potential, i.e. they had 'exhausted' much of the potential (see Evenson, 1996, Ch. 5). For research priority setting, we base the future research potential on the *remaining potential*, i.e. RP−RA.

Achievement-to-date ratings were based on research programming to date. Respondents were asked to visualize the continuation of current research programmes with some strengthening and normal responsiveness to research opportunities in estimating RP and time to achievement. Note that by utilizing these RP−RA concepts in this way we are attempting to rule out the possibility of specifying an arbitrary research programme to obtain RP estimates. Respondents have the experience to rate actual programmes more accurately than hypothetical programmes.

3. Scientists need some scope for expressing the variance in their subjective probability estimates. Our experience with the Rice Biotechnology study and with scientists indicates that eliciting two dates on time-to-achievement was an effective way to obtain a 'distribution' reflecting the degree of uncertainty of scientists.

Tables 19.6–19.10 summarize the scientists' responses to the ratings elicitation. It should be noted that not all respondents completed each block of RPA questions. They did, however, complete each RT question for the RPAs for which they responded. This was designed to achieve comparative consistency over RT.

Table 19.6. Scientists' ratings: insect loss RPAs.

	Management research				Conventional breeding				Wide crossing				Transgenic breeding			
RPA	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD
Yellow stemborer	5	10	0.24	0.20	8	13	0.16	0.12	9	15	0.22	0.18	7	13	0.54	0.32
Striped stemborer	4	11	0.32	0.22	9	12	0.15	0.10	9	12	0.20	0.20	7	10	0.52	0.46
Brown plant hopper	5	8	0.16	0.22	9	12	0.16	0.15	9	12	0.20	0.26	10	12	0.31	0.28
WB/brown plant hopper	4	10	0.23	0.18	7	11	0.16	0.17	10	13	0.27	0.22	9	14	0.20	0.24
Leaf folder	5	9	0.28	0.18	9	12	0.17	0.15	9	13	0.10	0.12	9	13	0.20	0.36
Hispa	6	13	0.12	0.10	11	15	0.20	0.10	8	14	0.20	0.16	10	12	0.33	0.42
Green leafhopper	5	10	0.17	0.22	7	12	0.20	0.10	10	16	0.30	0.26	9	13	0.30	0.20
Gall midge	5	10	0.30	0.21	7	12	0.30	0.21	9	15	0.28	0.26	9	15	0.32	0.30
Caseworm	6	11	0.30	0.21	8	17	0.16	0.09	11	19	0.15	0.18	10	15	0.36	0.40
Armyworm	6	11	0.30	0.17	9	15	0.16	0.09	11	16	0.15	0.18	10	15	0.36	0.40
Grasshopper	4	6	0.20	0.20	7	9	0.14	0.12	9	11	0.07	0.10	7	10	0.14	0.22
Mealy bug	4	7	0.20	0.10	8	12	0.14	0.12	9	11	0.10	0.10	7	10	0.30	0.42
Rice bug	4	7	0.20	0.14	8	12	0.20	0.16	9	11	0.07	0.10	7	10	0.14	0.22

For each RPA in Tables 19.6–19.10, four numbers are reported for each RT:

- mean years to 25% achievement of remaining potential (Y25);
- mean years to 75% achievement of remaining potential (Y75);
- mean estimated per cent of remaining potential (RP−RA);
- standard deviation of estimated per cent of remaining potential (SD).

Obviously, standard deviations of Y25 and Y75 could also have been computed. However, for purposes of displaying variation in estimated impacts of research programmes, variation in RP−RA is more relevant than variation in Y25 and Y75 which were designed to allow scientists to express their subjective variances. Thus the differences in Y25 and Y75 reflect the 'within scientists' subjective variation in estimates, while the standard deviations reported in Tables 19.6–19.10 reflected variations in estimates between scientists.

1. *Scientists' ratings: insect loss RPA.* We turn first to the insect loss RPAs summarized in Table 19.6. We note that there are differences in the RP−RA estimates both by RPA and by RT. Given the small scientist sample and the relatively high standard deviations across scientists, few of these differences are statistically significant. Most standard deviations are lower than the estimated RP−RA terms (note: scientists reported separate ratings for RP and RA). Most standard deviations for RP and RA separately were roughly one-third or so of the mean RP and RA estimates. The standard deviations of the differences, however, are relatively high. Should this be construed to mean that few differences across RPAs actually exist? If so, we can simply use 'congruence' rules to allocate over RPAs (see Evenson, 1996, Ch. 5).

We would argue that the procedure of separately identifying the RP and RA components probably results in an upward bias in the standard deviations and that differences over RTs are meaningful. We also consider differences over research techniques to be meaningful. Here we note that the highest RP−RA estimates are for the transgenic breeding techniques in all but one or two cases. Wide-crossing and tissue-culture techniques tend to be located between conventional breeding and transgenic techniques in these estimates.

Timing estimates also do not vary substantially by RPAs, but clearly do by RT. The management RTs are expected to yield results earlier than the genetic improvement techniques. Interestingly, transgenic techniques do not appear to have very different time estimates from conventional breeding or wide-crossing techniques.

2. *Scientists' ratings: disease loss RPAs.* Ratings for disease loss RPAs (Table 19.7) show similar patterns of variation over RPAs and RTs to those observed for insect loss RPAs. As with insect loss RPAs, there is more variation in the expected gains from working on the more important diseases, and transgenic techniques generally have the highest expected gains and the longest expected periods to achievement.

3. *Scientists' ratings: abiotic stress loss RPAs.* Abiotic stress loss RPAs (Table 19.8) again show patterns similar to those for other losses. Management solutions generally have lower expected contributions, however, and tend to have longer expected time-to-achievement estimates.

Table 19.7. Scientists' ratings: disease loss RPAs.

	Management research				Conventional breeding				Wide crossing				Transgenic breeding			
RPA	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD
Blast	6	14	0.30	0.20	5	12	0.20	0.26	6	13	0.22	0.20	8	13	0.40	0.28
Leaf scald	5	10	0.70	0.28	9	17	0.20	0.10	11	20	0.26	0.12	10	18	0.14	0.12
Cer leaf spot	5	25	0.26	0.12	10	17	0.30	0.12	11	20	0.30	0.12	11	19	0.20	0.16
Brown spot	8	15	0.20	0.16	8	12	0.30	0.12	9	15	0.30	0.12	10	18	0.20	0.16
Sheath rot	10	17	0.28	0.30	10	17	0.15	0.10	11	19	0.28	0.10	10	17	0.10	0.14
Sheath blight	6	15	0.36	0.32	10	16	0.08	0.10	8	16	0.24	0.20	7	13	0.34	0.26
Stem rot	10	17	0.20	0.10	10	15	0.20	0.10	8	16	0.20	0.10	7	13	0.20	0.10
Bacterial blight	9	12	0.20	0.16	6	13	0.22	0.28	5	11	0.36	0.22	8	12	0.25	0.20
Bacterial leaf streak	5	10	0.20	0.10	8	13	0.16	0.16	5	10	0.20	0.20	7	11	0.26	0.12
False smut	7	12	0.05	0.05	7	12	0.05	0.05	7	13	0.20	0.10	7	12	0.20	0.10
Glum blight	7	12	0.05	0.05	7	12	0.05	0.05	7	13	0.20	0.10	7	12	0.20	0.10
Tungro	10	17	0.22	0.22	5	14	0.22	0.12	7	14	0.32	0.10	8	15	0.48	0.40
Ragged stunt	10	17	0.20	0.10	7	12	0.16	0.16	7	14	0.20	0.10	8	15	0.20	0.20
UFRA	10	17	0.20	0.10	7	12	0.16	0.16	7	14	0.20	0.10	8	15	0.20	0.20

4. *Scientists' ratings: general pest loss RPAs.* The RTs specified for the control of weeds and other pests (Table 19.9) differ from those for other crop loss categories. The cultural and mechanical control options are expected to play the major role in weed control. Research has expected contributions to make in terms of biological control methods and bio-pesticides. Transgenic options for control also have some promise.

5. *Scientists' ratings: biological efficiency RPAs.* It is important that biological efficiency RPAs be included in priority setting. Since they do not have natural 'loss' units, it is sometimes difficult to specify meaningful RPAs. Consultation with scientists indicates that the RPAs in Table 19.10 are meaningful, but the priority setter should be particularly aware that the RPAs are subject to change as new scientific and technological options become available.

Implications for Genetic Resources

Both studies reviewed above reported general agreement on the traits-based RPA categories. The RPA–RT design permitted scientists to compare their projections across RTs. These comparisons support the judgement that both wide-crossing and transgenic techniques are suited to the qualitative traits strategy and that they are likely to contribute to achieving improved qualitative traits earlier than will be the case for the qualitative biological efficiency traits.

Rice breeders also expect continuity regarding genetic resource sources as new techniques are used. The new techniques are suited to extensions over conventional breeding techniques utilizing similar genetic resources. There are, of course, efforts to expand the genetic resource base for plant improvement and at some point in the near future, strategies for developing 'transgenic collections' will be formulated. It does not appear at this point that this will mean a significant reduction of use or of value of existing genetic resource collections.

When the scientists' SPEs were combined with crop loss data in the priority setting study, research resource allocation rules were developed for different regions in Asia. Implicitly, these calculations also allowed estimates of the contribution of genetic resources to productivity growth. These economic calculations showed that the economic returns to agricultural research will continue to be high in future decades, that plant breeding will continue to be of crucial importance, and that the collection, evaluation and maintenance of genetic resources will continue to be vital to the effectiveness of agricultural resources.

Table 19.8. Scientists' ratings: abiotic stress losses.

	Management research				Conventional breeding				Wide crossing				Transgenic breeding			
RPA	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD
Drought	6	14	0.12	0.12	8	16	0.22	0.14	10	17	0.22	0.24	12	16	0.32	0.22
Submergence	7	15	0.12	0.12	11	18	0.26	0.20	13	19	0.20	0.12	13	16	0.32	0.26
Cold	7	12	0.08	0.10	10	17	0.22	0.12	13	19	0.26	0.24	12	16	0.36	0.26
Heat	7	14	0.08	0.10	12	19	0.12	0.10	14	19	0.20	0.14	10	18	0.32	0.28
Acidity	7	12	0.14	0.14	6	11	0.20	0.16	7	14	0.12	0.16	10	16	0.24	0.16
Alkalinity	9	18	0.24	0.16	8	15	0.10	0.18	10	18	0.16	0.16	10	16	0.20	0.14
Salinity	8	13	0.20	0.14	7	14	0.20	0.14	9	16	0.20	0.18	10	15	0.30	0.20
Nutrient deficiency	7	14	0.16	0.10	7	17	0.14	0.16	11	18	0.08	0.10	13	17	0.12	0.18
Iron toxicity	7	14	0.14	0.14	7	19	0.16	0.14	9	15	0.24	0.26	10	16	0.20	0.20

Table 19.9. Scientists' ratings: rice pests.

	Cultural management				Mechanical control				Biological control				Bio-pesticides				Transgenic breeding			
Pests	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD
Weeds	5	11	0.20	0.10	12	18	0.25	0.10	4	10	0.20	0.10	5	11	0.15	0.20	10	19	0.30	0.11
Crabs	5	9	0.26	0.11	14	17	0.10	0.14	5	12	0.13	0.23	4	6	0.13	0.11	15	17	0.10	0.14
Rodents	5	9	0.25	0.10	15	18	0.06	0.11	4	9	0.20	0.16	11	16	0.15	0.10	14	17	0.10	0.14
Birds	5	15	0.00	0.00	5	17	0.00	0.00	2	5	0.20	0.16	5	17	0.10	0.14	4	18	0.00	0.00

Table 19.10. Scientists' ratings: biological efficiency potentials.

	Hybridization				Conventional breeding				Wide crossing			
RPA	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD
Plant design	7	13	0.23	0.14	4	11	0.22	0.12	8	15	0.23	0.14
Photosynthetic efficiency	8	17	0.10	0.11	9	16	0.20	0.13	8	18	0.17	0.23
Growth duration	7	15	0.23	0.15	6	10	0.23	0.15	8	15	0.26	0.20
Grain quality	7	14	0.40	0.23	5	11	0.30	0.15	8	13	0.23	0.23
	Tissue culture				Transgenic				Marker-aided selection			
	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD	Y25	Y75	RP−RA	SD
Plant design	5	11	0.17	0.14	9	17	0.33	0.24	10	17	0.32	0.19
Photosynthetic efficiency	8	15	0.10	0.11	10	17	0.36	0.27	11	19	0.36	0.08
Growth duration	4	9	0.20	0.25	7	17	0.24	0.26	8	14	0.36	0.22
Grain quality	6	13	0.26	0.16	8	14	0.36	0.36	9	15	0.54	0.22

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