Definition of CYTOTAXONOMY / What is CYTOTAXONOMY / Define CYTOTAXONOMY

Cytotaxonomy is a biology dealing with the classification and relationships of organisms using detail studies of chromosomes. The properties (number, structure, and behaviour) of chromosomes are of great value in taxonomy, because the chromosome number being the most widely used and quoted character in biology. Chromosome numbers are mainly determined at mitosis and quoted as the diploid number (2n). Another important taxonomic character is the position of the centromere. Meiotic behaviour sometimes shows the heterozygosity of inversions. Cytological data is significant than other taxonomic evidence.

Cytotaxonomical approach in classification

1. The Genetic Compliment

DNA is the essential materials of heredity (It comprises the genome and plasma). It is believed that the heterochromatic segments are associated with differences in the metaphase thickness. Even now, it is unknown that a given amount of DNA and protein is stimulated at mitosis to become distributed into a particular member of chromosomes.

2. DNA Hybridization:

The hybridization between single stranded DNA components from different origins can occurs provides a psychochemical means for assuming genetic relatedness among the species. It is known that DNA is extracted from organisms and made to hybridize in vitro with the cell lines of other organisms. The DNA matching techniques is much easier for solving complex taxonomic problems. The taxonomy implications of those have been studied by Hoyer et.al.1960 “The Incomplete fossil”.

3. Karyological Studies:

Chromosomal cytology has been more extensively used by plant taxonomists rather than animal taxonomists. The Karyotype characterised by chromosome numbers, size and morphology, is a definite and constant character of each individual species. The number shape banding of chromosomal can be determined by using various dissecting and staining techniques chromosomal taxonomy can be quite useful both in determining the phylogentic relationships of the taxa as well as in the segregation of sibling cryptic species.

Significance of cytotaxonomy

The **role of cytotaxonomy** is very important in taxonomic studies.

* Cytotaxonomy is more significant over physiological taxonomy because this process is dealing with the comparative study of chromosome and with this method minute variation among the individuals can be detected.
* DNA is present in the every chromosome and the variations in each DNA are responsible for the variation among the individuals, species, genus and everything.
* When the differences of physiological variations are too less among the individuals of same species and other higher taxa, Cytotaxonomy is a part of taxonomic biology that deals with the classification of organisms.
* Cytotaxonomy classifies these organisms based on their function and cellular (DNA) structure. As the cytologic data are directly derived from nucleus, the seat of hereditary material, they may be used for understanding the evolution and relationships of population. The chromosome number is usually constant in a species which makes it as an important taxonomic character.
* Chromosomes also vary in forms, size, and volume and in the amount of distribution of heterochromatin. These characteristics of karyotypes are taxonomically useful where the individual chromosomes are large enough for detailed microscopic observation.
* In this branch, another useful taxonomic character is the position of centromere. Meiotic behavior may show heterozygosity of inversions. This may be constant for a taxon, offering further taxonomic evidence.

So, the cytological data is regarded as having more significance than the other taxonomic evidence. For example, the class monocotyledons have usually got large sized chromosome than the dicotyledonous. The general, woody plants have got smaller chromosomes than their herbaceous relatives. In plant cells, mitochondria and chloroplast are major cell organelles which are used in molecular systematic.

**Cladistics Taxonomy**

Cladistics is a particular method of hypothesizing relationships among organisms. Like other methods, it has its own set of assumptions, procedures, and limitations. Cladistics is now accepted as the best method available for phylogenetic analysis, for it provides an explicit and testable hypothesis of organismal relationships.

The basic idea behind cladistics is that members of a group share a common evolutionary history, and are "closely related," more so to members of the same group than to other organisms. These groups are recognized by sharing unique features which were not present in distant ancestors. These *shared derived* characteristics are called *synapomorphies*.

**What assumptions do cladists make?**

There are three basic assumptions in cladistics:

1. Any groups of organisms are *related by descent* from a common ancestor.
2. There is a *bifurcating pattern* of cladogenesis.
3. *Change* in characteristics occurs in lineages over time.

The first assumption is a general assumption made for all evolutionary biology. It essentially means that life arose on earth only once, and therefore all organisms are related in some way or other. Because of this, we can take any collection of organisms and determine a meaningful pattern of relationships, provided we have the right kind of information. Again, the assumption states that all the diversity of life on earth has been produced through the reproduction of existing organisms.

The second assumption is perhaps the most controversial; that is, that new kinds of organisms may arise when existing species or populations divide into exactly two groups. There are many biologists who hold that multiple new [lineages](https://ucmp.berkeley.edu/glossary/gloss1phylo.html#lineage) can arise from a single originating population at the same time, or near enough in time to be indistinguishable from such an event. While this model could conceivably occur, it is not currently known how often this has actually happened. The other objection raised against this assumption is the possibility of interbreeding between distinct groups. This, however, is a general problem of reconstructing evolutionary history, and although it cannot currently be handled well by cladistic methods, no other system has yet been devised which accounts for it.

The final assumption that characteristics of organisms change over time is the most important assumption in cladistics. It is only when characteristics change that we are able to recognize different lineages or groups. The convention is to call the "original" state of the characteristic *plesiomorphic* and the "changed" state *apomorphic*. The terms "primitive" and "derived" have also been used for these states, but they are often avoided by cladists, since those terms have been much abused in the past.

*Significance of Cladistics Taxonomy:*

### Cladistics is useful for creating systems of classification.

Cladistics is now the most commonly used method to classify organisms. Why do we need to classify organisms? Well, consider the bewildering variety of organisms that have ever lived on Earth, from jellyfish to bacteria — that are what paleontologists do for a living. How is it possible that paleontologists, let alone other biologists, are able to communicate their ideas about such a diverse topic as the history of life? Well, it's obvious that a system of classification is needed. That is, we need words like beetle or conifer so that we can talk about many organisms at one time. In fact, the history of formal classification schemes in biology is long, dating from the 1700s, well before Darwin proposed his theory of natural selection. Today, cladistics is the method of choice for classifying life because it recognizes and employs evolutionary theory.

### Cladistics predicts the properties of organisms.

As with any other system in science, a model is most useful when it not only *describes* what has been observed, but when it *predicts* that which has not yet been observed. Cladistics produces hypotheses about the relationships of organisms in a way that, unlike other systems, predicts properties of the organisms. This can be especially important in cases when particular genes or biological compounds are being sought. Such genes and compounds are being sought all the time by companies interested in improving crop yield or disease resistance, and in the search for medicines. Only a hypothesis based on evolutionary theory, such as cladistic hypotheses, can be used for these endeavours.

### Cladistics helps to elucidate mechanisms of evolution.

Unlike previous systems of analyzing relationships, cladistics is explicitly evolutionary. Because of this it is possible to examine the way in which characters change within groups over time — the direction in which characters change, and the relative frequency with which they change. It is also possible to compare the descendants of a single ancestor to look at patterns of origin and extinction in these groups, or to look at relative size and diversity of the groups. Perhaps the most important feature of cladistic is its use in testing long-standing hypotheses about adaptation. For many years, since even before Darwin, it has been popular to tell "stories" about how certain traits of organisms came to be. With cladistics, it is possible to determine whether these stories have merit, or whether they should be abandoned in favor of a competing hypothesis. For instance, it was long said that the orb-weaving spiders, with their intricate and orderly webs, had evolved from spiders with cobweb-like webs. The cladistic analysis of these spiders showed that, in fact, orb-weaving was the primitive state, and that cobweb-weaving had evolved from spiders with more orderly webs. This situation has been repeated in many groups with many traits, including studies of parasitism, geographic distribution, and pollination.