

## **PRINCIPLES OF ZOOLOGICAL NOMENCLATURE**

Nomenclature provides names to species and higher taxa, to facilitate communication among zoologists. According to Article 1 of the **code**:

“Zoological nomenclature is the system of scientific names applied to taxonomic units of animals (*taxa*) known to occur in nature, whether living or extinct.” The nomenclature should fulfil the following three basic requirements:

**Uniqueness:** The name of a taxon is like the index number of a file. It gives immediate access to all information in literature, available about a particular taxon. Every name must be unique because it is key to the entire literature. Uniqueness has been achieved by adopting *binominal nomenclature*, as proposed by Linnaeus in the X edition of *Systema Naturae* in 1758.

According to binominal nomenclature, each species name should consist of the first generic and second species name. Species name should not duplicate under any genus, e.g. *Panthera leo*, *Panthera tigris*, *Panthera pardus*. A combination of the two makes the name unique.

**Universality:** Scientific names should be known to all and be universally accepted. Vernacular names would be difficult to keep track of, and scientists will have to learn names in several languages of the world. To avoid this, zoologists have adopted by international agreement a single language, *Latin*, which is a dead language and therefore does not evolve and is acceptable to everybody.

One need not learn Latin language in order to give name. Any word in any language, if latinized by changing the ending by suffixing *-us*, *-a*, or *-ensis* is acceptable as valid Latin name, e.g., *japonica*, *indicus*, *chinensis*. Use of Latin is also advantageous due to the fact that most of the ancient scientific literature is written either in Latin or Greek and it would be easy to refer to the old literature if names are given in Latin.

**Stability:** Zoological names would lose their utility if they were changed frequently and arbitrarily. It would create confusion if we call an object *spoon* today and *apple* next week. *International Code of Zoological Nomenclature* has been designed to bring about stability. Taxonomists are bound to follow the rules given in the **code** before assigning names to taxa. Most of the changes in names are due to taxonomists' errors. Lot of name changing has taken place during the last 200 years. International Code of Zoological Nomenclature safeguards against frequent name changing.

### **International Code of Zoological Nomenclature**

Adopted by the 15th International Congress of Zoology (London) and published on November 6, 1961.

*The object of the code is to promote stability and universality in the scientific name of animals, and to ensure that each name is unique and distinct.*

The Swedish naturalist Carl von Linne who changed his name to a binomen, Carolus Linnaeus, was the father a set of rules of nomenclature published in *Critica Botanica* (1737), *Philosophia Botanica* (1751) and in the 10th edition of *Systema Naturae* (1758). The confusion that prevailed after Linnaeus was solved in the 5th International Congress of Zoology in Berlin in 1901. The original code was, however, adopted in 1904 in the 6th International Congress of Zoology in Bern and published in 1905 in Paris as, “*Regles Internationales de la Nomenclature Zoologique.*”

The most recent version (a modified version of 1961 code) was published in 1964 in parallel in French and English. It was adopted by the 16th International Congress of Zoology, Washington (1963) with modifications in articles 11, 31, 39 and 60.

**International Congress of Zoology** is a legislative body, which adopts by voting the constitution and proposals put before it by the commission.

**International Commission on Zoological Nomenclature** is a judicial body elected by the International Congress of Zoology. It is protector of the code and deals with the interpretations, disputes and implementation of the **code**. Amendments have to be routed through the commission.

**International Code of Zoological Nomenclature (1964)** is the system of rules and recommendations authorized by the International Congress of Zoology. The object of the code is to promote stability and universality in the scientific names of animals and to ensure that each name is unique and distinct. Code does not restrict the freedom of taxonomic thought and action.

Before the present code, the following codes were prevalent in Europe and U.S.A.:

1. Strickland Code (1842) in Berlin.
2. W.H.Dall Code (1877) in USA.
3. Douville' Code (1881) in France.

#### **Salient features of the "Code"**

The 1964 code consists of a *Preamble*, *86 Articles*, *5 Appendices*, a *Glossary* and a detailed *Index*, in parallel in English and French. Starting date of the code is 1st January 1758.

1. Names must either be Latin or Latinized.
2. Names of taxa higher than species should be uninominal.
3. Name of a species is binomen.
4. Name of a subspecies is a trinomen.
5. Name of a subgenus is placed in parenthesis between genus and species, e.g. *Xorides (Gonophonus) nigrus*.
6. Family name should end in DAE, e.g. Tipulidae.
7. Genus name should be a noun in nominative singular or treated as such, e.g. *Apis*, *Rana*.
8. Species name should be an adjective or noun in nominative singular agreeing in gender with the generic name, e.g. *Drosophila obscura*, *Felis tigris* etc. or a noun standing in apposition to the generic name, e.g. *Felis leo*.
9. Zoological nomenclature is independent of other systems.
10. All names given to the species from time to time should be mentioned in synonymy.
11. Author's name is not part of the name. Its use is optional and is suffixed, e.g. *Cancer pagurus* Linnaeus.
12. **Law of priority:** The valid name is the oldest name published and available.

13. **Synonymy:** Synonyms are different names assigned to the same taxon. They should be mentioned along with the valid taxon, e.g. *Erias vitelli* (= *Erias fabia*).

14. **Homonymy:** Homonyms are identical names in spelling for different species of the same genus and for different genera of a family. Junior homonym has to be rejected. Homonymy arises when an existing species' name is not known to the person assigning a name, or a species with identical name is transferred to the same genus.

15. **Holotype:** Single specimen on which description of the species is based. Red colored label is fixed on the specimen.

16. **Allotype:** Specimen of the opposite sex to holotype. Also carries a red label.

17. **Paratype:** All remaining specimens after the designation of holotype and allotype are assigned the status of paratypes. They carry yellow labels.

18. **Syntypes:** If no holotype is designated, all specimens that the author studied for the description of the species are called syntypes.

19. **Lectotype:** In the absence of a holotype, one specimen from syntypes can be designated as Lectotype and rest of the specimens as Paralectotypes.

20. **Neotype:** If all type-specimens are destroyed, a neotype that fits the description very well can be designated under exceptional circumstances.

### **MOLECULAR TAXONOMY**

With the rapidly growing knowledge of genetics and molecular biology, phylogeny has received a new motivation. Phylogeny provides a new source of evidence about the course of evolution. While comparing total genes of two different species, if the genetic differences between them are minor, they are liable to be closely related. In other word, the degree of genetic difference indicates the closeness of that relationship.

There may be huge practical and theoretical problems as animals have so many genes. Moreover the presence of particular genes does not define their effects. The action of genes depends upon the presence or absence of many other factors. Also a small change in genes can make a big difference in animals. For example, Humans share about 99% genes with Chimpanzees and it is that remaining 1% genes that make us Humans.

The rate of genetic change and the rate of species change are not same. Both rate of genetic change and the rate of species change have not remained constant through the evolution. During the evolution, when there is a change in a gene, its immediate product (molecules) changes slowly. The comparison of the amount of change in that gene product will reveal the familiarity of the relationship of different groups of animals. Therefore, molecules can be used as morphological characters to study the evolutionary history.

For example, compare a particular gene within a range of populations like shrimps, insects and spiders. This comparison must first the show that different insect populations resemble each other more closely than spiders or shrimps. Then secondly it must show which two of the three groups are most closely related. During comparison, molecular characters can be replaced for morphological characters to evaluate the relatedness of animals.

### **Molecules used in molecular taxonomy**

Initially molecular taxonomy studies were conducted using proteins which are the products of gene action. But currently work is concentrated much on DNA and the genes themselves. The following are the molecules used in the molecular taxonomical studies.

**Ribosomal DNA (rDNA):** The genes coding for small subunit of 18S ribosomal DNA (rDNA) are used in molecular taxonomy studies because,

- Mutations are unlikely to survive natural selection and these genes have very less mutations.
- These genes are highly conserved and have changed very slowly during evolution.
- They have important structural role.

The rDNA can therefore provide important clues regarding changes that occurred very early in evolution such as the segregation of classes within a phylum or origin of the new phyla.

**Genes regulating early development:** Genes acting early in development guide the fate of cells and thus may be very informative. Comparison between phyla is based on the molecular evidences obtained using ribosomal genes. The information about the divergence which has occurred during evolution can be obtained from these genes.

Using more than one gene and testing various aspects of evolutionary change may avoid some of the disadvantages which occur in using ribosomal genes (rDNA).

**Mitochondrial DNA (mtDNA):** The genes situated in the mitochondria are different from nuclear genes and these genes have useful sources of information. It is not the gene content of the mitochondria that is used but the order of genes round the chromosomal ring. In most animals, the contribution of sperm to the zygote is zero and therefore mitochondrial inheritance is confined only to the females. This uniparental dependence further simplifies the use of mtDNA.

Mitochondrial DNA changes comparatively fast in evolution and it is useful to determine changes that have occurred less than 15 million years ago. When the whole genome is sequenced, mitochondrial DNA gives the information about ancient changes.

### **Methods of obtaining molecular information**

The differences between proteins can be revealed and estimated using gel electrophoresis. But the techniques which are applied directly to DNA are more preferred.

**DNA hybridization:** DNA hybridization is based on the principle that, upon heating the bonds between corresponding nucleotides of DNA are broken and consequently double stranded DNA dissociates. These disassociated strands recombine when cooled and bonds are formed only at corresponding sites. When single strands of DNA from related species are put together they form hybrids. When such hybrid pairs are heated, they get separated at a temperature much lower than the one required to separate original DNA pair. This is because of the formation of less number of bonds. This temperature difference is used as a measure of genetic similarity between the two species.

**Restricted site analysis:** Restriction analysis is based on the working of restriction enzymes. Restriction enzymes perfectly cut DNA into fragments at expected sites. Fragments from different sources are compared to obtain information about a small part of the total molecule.

**Sequencing of nucleotides:** The sequencing of nucleotides allows the identification of each nucleotide in whole sequence of a DNA molecule. This comprehensive process has been made easier by the polymerase chain reaction (PCR), which amplifies a small quantity of material for rapid analysis and automated sequencing machine. PCR technique opened new avenues in exploration of molecular information.

### **Processing of the molecular information**

Molecular evidence gives a large number of well-defined characters. A given nucleotide at a given site on the DNA molecule is known as a character. Traditional methods of evaluating characters are not applicable to study molecular differences but phenetic analysis can be easily applied.

During the process of evolution, if molecular change increases at a constant rate then the amount of change is the measure of evolutionary distance. Though, genes do not always change at a constant rate.

### **Reliability of molecular taxonomy**

Day by day the number of animals being studied with the help of molecular taxonomy is increasing and consequently the confidence in molecular taxonomy is also growing. Though molecular taxonomy is reliable, it has few disadvantages over advantages.

#### **Advantages**

1. As the nature and precise position of the unit can be defined exactly, the data is equivalent.
2. The size of the data used in molecular taxonomy studies is enormous.
3. The analysis of the cladograms is done using statistical methods.
4. In case the molecule is unchanged (Example, genes coding for ribosomal RNA), the relationships can be traced far back in time.
5. Non-heritable variations are avoided in molecular taxonomy studies.

#### **Disadvantages**

1. In cladistics, it is assumed that change in a gene molecule will depend only on the mutation rate and the time elapsed. In other words, it is assumed that an unvarying molecular clock is ticking at a regular rate. But, the clock is known to be variable in certain conditions and the whole idea of functionally neutral changes in genes is debatable.
2. There is no record of past changes in characters. This is a very serious disadvantage as there are only four possible nucleotides for any given site in DNA molecule. There might have been changes from one nucleotide to another and back again. Such multiple hits cannot be analyzed.
3. There is no familiar intermediate condition between characters and no primitive condition for a given DNA site can be recognized.
4. The tracing of functional correlates of character is very rare.
5. As sequence similarity is the only guide it is difficult to root a tree derived from molecules. Moreover the likelihood of convergence is usually impossible.

### **SEROTAXONOMY**

The study of antigen-antibody reaction is called serology. The substance capable of stimulating the formation of an antibody is antigen. A specific protein molecule produced by plasma cell in the immune system is antibody. The antibodies combine chemically with specific antigen and this combination elevates an immune response. The application of serology in solving taxonomic problems is called serotaxonomy.

Nuttall was the first biologist to compare immunochemical specificity of serum proteins for systematic purposes in 1901. Later in 1910, Dunbar showed theta proteins from pollen, seed and leaves of rice were serologically distinct. In 1914, Gholke established serology school in Germany and later Germany became the center of serological studies.

### **Process of Serotaxonomy**

The process of serotaxonomy involves the following steps:

1. The protein extract of the plant origin i.e. the antigen is extracted.
2. The antigen is injected into the blood stream of an experimental animal to form antibodies.
3. The experimental animal produces specific antibody in response to the antigen.
4. The serum with antibodies is called antiserum. Antiserum is made to react in vitro with antigenic protein as well as proteins of other taxa, whose affinities are to be determined.
5. The amount of precipitation shows the degree of homology.

For example, to know the closeness of the taxon A with B, C, D, E

The proteins from A are extracted and are injected into the experimental animal rabbit or mice. The experimental animal in return produces antibodies. These antibodies are extracted from the blood of the experimental animal in the form of antiserum.

- When this antiserum is allowed to react with the original protein extract from A, complete coagulation takes place.
- When this antiserum is allowed to react with the protein extracts from other taxa B, C, D, E the degree of coagulation varies.
- The degrees of coagulation are compared to know the closeness of the taxa. More the degree of coagulation more is the closeness.

### **Importance of serotaxonomy**

There are several instances where the serological data has been used to classify angiosperms. Some of them are mentioned below:

1. In 1983, Fairbrothers used serological data in classification of orders and assignment of families in Apiales, Fagales, Magnoliales, Juglandales, Rubiales, Ranunculales etc
2. Again in 1959, Fairbrothers and Jhonson separated six species of Bromus on the basis of the serological data.
3. On the basis of the serotaxonomic studies Fairbrothers and Jhonson showed that genera Magnolia and Michelia show closest affinity within Magnoliaceae

4. Simon in 1971 demonstrated close relationship between Nymphaeaceae and Nelumbonaceae based on serological data.
5. Kloss applied serotaxonomic data in the classification of Leguminosae.

### **CLADISTICS**

Cladistics is the method of assuming relationships between organisms. This method has its own set of assumptions, procedures, and limitations. This is the best method for phylogenetic analysis, as it provides a clear and open hypothesis to determine relationships of organisms.

According to cladistics, members of a group share a common evolutionary history. They are related very closely, to members of the same group than to other. The members of the group share unique features which were not present in their distant ancestors. These shared and derived features are called synapomorphies.

It is not enough for an organism just to share features, because two organisms may share many features and still may not be considered as the members of same group. For example, let us consider starfish, jellyfish and human. The jellyfish and starfish live in water, they both have radial symmetry and both are invertebrates. By these external features we can say that they belong to same group. But as per evolutionary relationship starfish and human are more closely related.

#### **Need for Cladistics**

1. Cladistics is used for creating systems of classification. It is the most favored method to classify organisms because cladistics identifies and works through evolutionary theory.
2. Cladistics gives hypotheses about the relationships between organisms in such a way that calculates properties of those organisms. This calculation can be critical in cases when specific genes or biological compounds are studied to improve crop yield and disease resistance.
3. Cladistics explains mechanisms of evolution as it is undoubtedly evolutionary in nature. Therefore, cladistics helps in studying the changes in characters of living organisms over time. It also gives clues about the direction and frequency of change. With the help of cladistics we can compare the descendants of a single ancestor, patterns of their origin and extinction, relative size and diversity of the groups.

#### **Assumptions of cladistics**

##### **Assumption 1: All organisms have originated from a common ancestor**

Diversity of life on earth is due to the reproduction of existing organisms. The life on the planet Earth originated only once and hence all the organisms are related to one another in some way or the other. This relation can be studied on any given group of animals and significant deductions can be drawn. These meaningful patterns of relationships provide a great deal of information.

##### **Assumption 2: Bifurcating pattern of cladogenesis**

According to this assumption, new kinds of organisms evolve when existing species divide into exactly two groups. This assumption is debatable as biologists believe that multiple new lineages can evolve from a single population at the same time. Moreover there is also a possibility of interbreeding between distinct groups.

##### **Assumption 3: Features of organisms change over time**



Cladistics assumes that the features of the living organisms change over time. It is because of this change that one can observe and recognize different lineages or groups. In cladistics the original feature is called as plesiomorphic or primitive feature whereas the changed feature is called as apomorphic or derived feature.

### **Methodology of a Cladistic Analysis: Construction of Cladograms**

1. Choose the taxa whose evolutionary relationships interest you. These taxa must be clades if you hope to come up with reasonable results.
2. Determine the characteristic features of the organisms and examine each taxon to determine the character states. All taxa must be unique.
3. Determine the polarity of characters.
4. Group taxa by synapomorphies, shared derived characteristics and not by plesiomorphies original characteristics.
5. Work out conflicts that arise by parsimony method to minimize the number of conflicts.
6. Build your cladogram following these rules:
  - \* All taxa go on the endpoints of the cladogram, never at nodes.
  - \* All cladogram nodes must have a list of synapomorphies which are common to all taxa above the node.
  - \* All synapomorphies appear on the cladogram only once unless the character state was derived separately by evolutionary parallelism.

### **Inferences from Cladistics: Understanding Cladogram**

The phylogenetic analysis gives out a theory of relationship of different taxa. This theory can be denoted as a cladogram. Cladograms are branching diagrams which are similar to family trees. Just as we can trace our ancestry with the help of family tree, we can trace the ancestry of the organisms with the help of cladogram. Both cladograms and family trees are very rich in information.

For example, see the family tree given below, Pink dots can be considered as female and the blue square can be considered as male. The ancestors in this family give rise to three progeny in first generation (shown as progeny 1). One of them mates to produce second generation (shown as progeny 2)

### **CRITICISMS OF CLADISM**

Cladism has often been confused with phylogenetic classification. Cladists consider only the branching of taxa and not the subsequent divergence. If one line is exposed to so much selection pressure that it becomes genetically very different from its nearest relatives then it would be biological absurdity to call them near relatives. Cladists ignore different rates of evolutionary change leading to speedy or unequal divergence. They consider evolutionary rates to be same in all phyletic lines. Cladism confuses genetic with genealogical relationship.

Ranking of taxa according to the branching point is always misleading. For example, it might necessitate inclusion of chimpanzee in family Hominidae rather than in Pongidae because its branching point from hominids is recent as compared to gibbons.



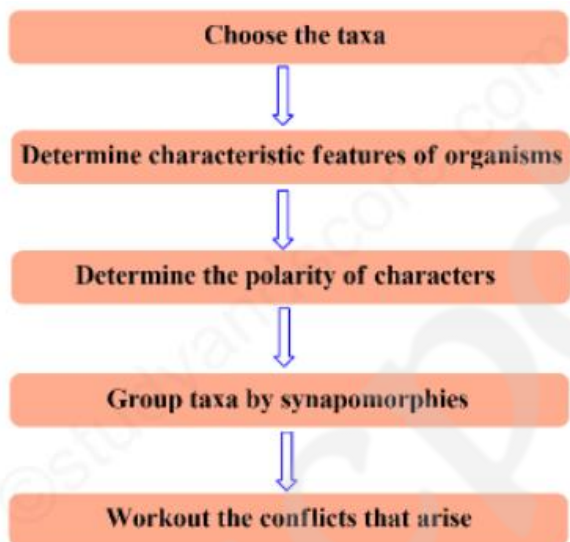
The principle of *recency of common ancestry* is used to determine hierarchy of taxa in which temporal (time) distance rather than evolutionary differences are taken into consideration. Then if fish and Amphibia are classes, reptiles should be placed in order and mammals in family, just because fish and amphibians evolved much earlier than the reptiles and mammals have the most recent origin.

Cladists' view that the parent taxon expires after splitting is not true and it may continue with little change along with the sister group. For example, reptiles gave rise to birds and mammals but the reptilian line still continues.

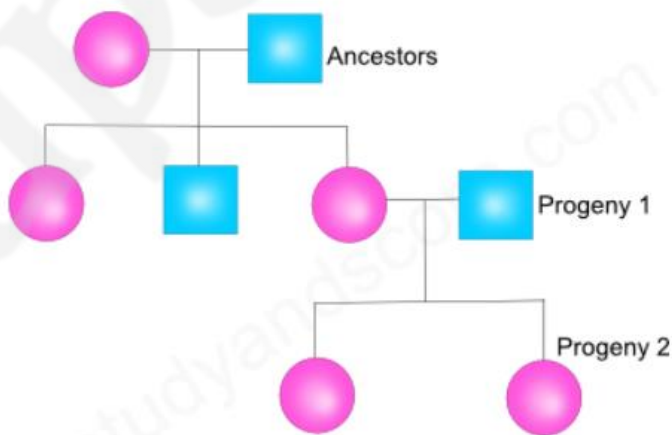
According to Hennig (1966), no species having arisen from the stem species can be placed outside the parent taxon. That means birds after having arisen from reptiles will have to be placed within class Reptilia.

Cladism is difficult to apply in the absence of fossil record or with poor fossil history. Then branching point will have to be determined by observed similarity.

Hennig (1966) ignores rate of evolution and asserts, "Decisive is the fact that the process of species cleavage is the characteristic feature of evolution."



Methodology of cladistic analysis



Family tree tracing ancestors