

Unit 1**Module 1****Taxonomy****Taxonomy**

Theory and practice of grouping individuals into species, arranging species into larger groups, and giving those groups names, thus producing a classification.

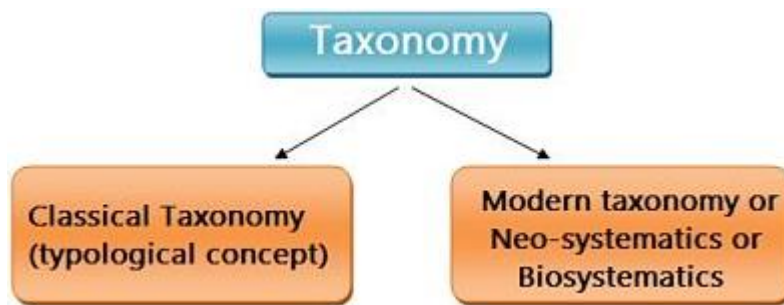
Taxonomy (from Ancient Greek τάξις (taxis) 'arrangement', and -νομία (-nomia) 'method') is the scientific study of naming, defining (circumscribing) and classifying groups of biological organisms based on shared characteristics. Organisms are grouped into taxa (singular: taxon) and these groups are given a taxonomic rank; groups of a given rank can be aggregated to form a more inclusive group of higher rank, thus creating a taxonomic hierarchy. The principal ranks in modern use are domain, kingdom, phylum (division is sometimes used in botany in place of phylum), class, order, family, genus, and species. The Swedish botanist Carl Linnaeus is regarded as the founder of the current system of taxonomy, as he developed a ranked system known as Linnaean taxonomy for categorising organisms and binomial nomenclature for naming organisms.

Systematics

The study of the identification, taxonomy, and nomenclature of organisms, including the classification of living things with regard to their natural relationships and the study of variation and the evolution of taxa.

Microtaxonomy and macrotaxonomy

The scientific work of deciding how to define species has been called microtaxonomy. By extension, macrotaxonomy is the study of groups at the higher taxonomic ranks subgenus and above.



Classical Taxonomy:

1. It is called old systematics or Alpha (α) – taxonomy or Taxonomy
2. It is pre – Darwinian
3. Species is considered as basic unit and is static
4. Classification is mainly based on morphological characters
5. This system is based on the observation of a few samples / individuals

Numerical taxonomy

Numerical taxonomy is defined as the numerical evaluation of the similarity between groups of organisms and the ordering of these groups into higher ranking taxa on the basis of these similarities. It may be defined as the branch of taxonomy that uses mathematical methods to evaluate observable differences and similarities between taxonomic groups.

Cladistics /Phylogeny

Cladistics refers to a biological classification system that involves the categorization of organisms based on shared traits. Organisms are typically grouped by how closely related they are and thus, cladistics can be used to trace ancestry back to shared common ancestors and the evolution of various characteristics. Although the classification of

organisms began in the early 1900's, cladistic analysis and specific methodology first originated in the 1960's by Willi Hennig, referred to as "phylogenetic systematics". This process involves creating phylogenies using morphological and molecular data to visualise evolutionary history and relationships between species.

- It is a relatively new system of classification that uses shared derived traits to establish evolutionary relationships.
- A derived trait is a feature that evolved only within the group under consideration.
- A phylogenetic tree based on a cladistic analysis is called a cladogram

Cladistic Methodologies

Cladistic methodologies involve the application of various molecular, anatomical, and genetic traits of organisms. Therefore, with the advent of computational modelling and molecular techniques (e.g., polymerase chain reaction [PCR]) cladistics are often used in evolutionary biology for the construction of phylogenetic trees. Cladistic data is also used to create cladograms (shown below), which consist of diagrams proposing a hypothesis of phylogenetic relationships between species based on shared characteristics. Thus, depending on a given dataset, the resulting cladogram may differ. For example, a cladogram based purely on morphological traits may produce different results from one constructed using genetic data. Today, highly advanced computational methods permit the use of multiple datasets to construct more accurate cladograms. Careful scientific analysis is required to rationally determine which cladogram may be a more correct representation.

Cladistic Character States

In the field of cladistics, specific terminology is used to describe particular characteristics, termed “character states” among groups of organisms.

1.Plesiomorphy

Plesiomorphy refers to the ancestral traits that a taxon retains throughout evolution. Two or more taxa can share plesiomorphies but reside in different groups. When this occurs, this is termed “symplesiomorphies”. An example of symplesiomorphy is quadrupedalism, or the ability to walk on four legs. Since this is an ancestral trait exhibited by reptiles, amphibians, and other taxa, this is a symplesiomorphy for mammals. Therefore, while symplesiomorphies can show distant evolutionary trends, it cannot be used to demonstrate more recently evolved characteristics.

2.Apomorphy

Apomorphy refers to a derived state used to define specific clades. Apomorphy can be further subdivided into “autapomorphies” and “synapomorphies”. Autapomorphies refer to traits that are exhibited only by one species or group, whereas synapomorphies refer to entire clades which can be classified by the presence of a particular trait. An example of synapomorphy includes the presence of digits, shared by all tetrapods. An example of an autapomorphy is the capacity of human verbal speech, which is not exhibited by other primates, and is thus, a distinguishing human trait.

3.Homoplasy

Homoplasy refers to a character state that is shared by at least two organisms but is not found in the common ancestor or predecessor. Thus, the trait is said to have evolved as a result of convergence or a reversal. A famous example of homoplasy is the evolution of warm-bloodedness in

both mammals and birds, despite the absence of this trait from the common ancestor. Therefore, evidence indicates that the trait of warm-bloodedness must have evolved separately within each clade.

Phylogenetic Tree

It is defined as a diagrammatic representation of evolutionary relationships among living organisms. This diagrammatic representation represents how different species evolved from a series of common ancestors.

The phylogenetic tree can also be defined as the two-dimensional graph representing the evolutionary relationship between an organism from various other organisms.

The phylogenetic tree is also called the "Tree of Life" or "Dendrogram" The idea of a phylogenetic tree arose from an ancient concept of a ladder-like progression from moderate to powerful forms of life. The term Phylogenetic or Phylogeny is derived from the ancient Greek word, which refers to race, origin or lineage.

Construction of the Phylogenetic tree

There are two different methods based on which the phylogenetic tree is constructed.

- **Character-based method**

This method is based directly on the sequence characters, therefore it is also called the discrete method. The character-based method uses the aligned characters for constructing the phylogenetic tree.

These aligned characters include either the DNA or protein sequences during the tree inference. The two most popular character-based methods are:

1. Maximum parsimony.

2. Maximum likelihood.

- **Distance-based method**

This method is based on the amount of the distance or the dissimilarity between the two aligned sequences. In this method of constructing the phylogenetic tree, the sequence data is transformed into pairwise distances and then the matrix is used for building a tree.

Steps for preparing the Phylogenetic Tree

Selection of an organism or a gene family



Selection of appropriate molecular markers



Amplification



Sequencing



Assembly



Alignment



Evolutionary model



Phylogenetic Analysis



Construction of a Tree

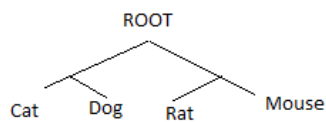


Evolution of a Phylogenetic Tree

Types of Phylogenetic Trees

1. Rooted tree

Make the inference about the most common ancestor of the leaves or branches of the tree.



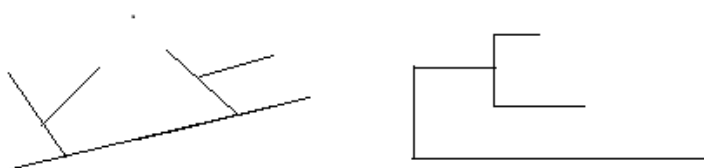
2. Un-rooted tree

Make an illustration about the leaves or branches and do not make any assumption regarding the most common ancestor



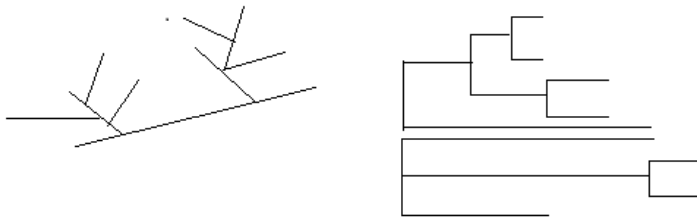
3. Bifurcating tree

This tree has a maximum of two descendants arising from each of the interior nodes.



4. The multifurcating tree

This tree has multiple descendants arising from each of the interior nodes.



Importance of Phylogenetic Tree

It is the fundamental tool to derive their most-useful evidence from the fields of anatomy, embryology, palaeontology and molecular genetics.

Other significances of the phylogenetic tree are:

- Used in the search for a new species.
- Used to study evolutionary histories
- To study how the species were spread geographically.
- To study the common ancestors of extant and extinct species.
- It is used to identify the most recent common ancestors and to recognize how closely related species are.
- To relate the milestones of the evolution of major life forms to the tree of life.
- To represent evolutionary relationships between organisms that are believed to have some common ancestry.
- With the help of the phylogenetic tree, the infectious microbes can be traced along with their evolutionary histories.

Biological Classification

Further onwards, the art of biological classification was introduced which basically puts organisms into groups. This is a part of Scientific Taxonomy. The classification system starts with a group with a wide variety of organisms and becomes more selective as the groups get more specific, as most classifications go. Linnaeus classified about 4,000 species using this method. He classified organisms into seven groups, based on their appearance.

The Eight Ranks

Today, there are eight ranks which can be used to classify an organism.

1. Domain
2. Kingdom
3. Phylum
4. Class
5. Order
6. Family
7. Genus
8. Species



Domain

A domain is the highest rank of organisms. The three-domain system of taxonomy was designed by Carl Woese in the year 1990. Taxonomic ranks should always be capitalised, except for species as it assists people to distinguish between bacteria (the organisms and the domain).

The three domains of life are Bacteria, Archaea, and Eukarya.

Kingdom

The Kingdom happens to be the highest classification after the domain into which living organisms are grouped. At present, there are five known kingdoms. All the living species are grouped into specific kingdoms based on factors like the types of cells they are composed of, mode of their nutrition and the total number of cells they hold.

The different kingdoms recognized today are Animalia, Plantae, Fungi, Protista, and Monera.

Phylum

The phylum or phyla is grouped next level after kingdom in the biological classification. The purpose of this level is to find some physical similarities among various organisms within a kingdom. There are 35 phyla in the kingdom Animalia.

Class

The organisms of a phylum are further divided into various classes. The classes were the most common rank proposed by Linnaeus. There are about 108 different classes in the kingdom Animalia that were introduced after the 19th century, proposed by Linnaeus which are still followed today.

Order

The organisms of a particular class are further distributed into orders. It is much more accurate than the classes. There are about 18-25 orders of mammals which are based on the classification of organisms. The sources differ. The art of taxonomy is mostly used to determine which order an organism belongs to.

Family

After the classification of organisms into orders, they are further grouped into families. It is the 8th major taxonomic rank in biological classification which can be subdivided into subfamilies. There are totally 12 families in the order Carnivora and 620 families in the class Plants.

Genus

The Genus or genera. It is even more specific compared to family and other groups. Genus is the first part of an organism's scientific name using binomial nomenclature followed by the second part is the species name.

The scientific name of an organism is always italicised, followed by the genus name which should be capitalised. Both Genus and species are the only taxonomic ranks that are italicised.

Species

Species is the last and major taxonomic rank which is subdivided into subspecies in certain cases only. There are more than 8.7 million different species of organisms on planet Earth. As each genus name is unique, the same species names can be used for different organisms. The species name should be always italicised, but never capitalised. The species of an organism would determine the second part of its binomial nomenclature.

Classification of Modern Humans

Domain – Eukaryota

Kingdom – Animalia

Phylum – Chordata

Class – Mammalia

Order – Primates

Family – Hominidae

Genus – Homo

Scientific Classification of Organisms

Five Kingdom Classification

The five-kingdom classification that we see today was not the initial result of the classification of living organisms. Carolus Linnaeus first came up with a two-kingdom classification, which included only kingdom Plantae and kingdom Animalia.

The two-kingdom classification lasted for a very long time but did not last forever because it did not take into account many major parameters while classifying. There was no differentiation of the eukaryotes and prokaryotes; neither unicellular and multicellular; nor photosynthetic and the non-photosynthetic.

Putting all the organisms in either plant or animal kingdom was insufficient because there were a lot of organisms which could not be classified as either plants or animals.

All this confusion led to a new mode of classification which had to take into account cell structure, the presence of cell walls, mode of reproduction and mode of nutrition. As a result, R H Whittaker came up with the concept of the five-kingdom classification.

The five-kingdom classification of living organisms included the following kingdoms:

1.Kingdom Monera

Bacteria are categorised underneath the Kingdom Monera.

Features of Monerans

- Bacteria occur everywhere and they are microscopic in nature.
- They possess a cell wall and are prokaryotic.
- The cell wall is formed of amino acids and polysaccharides.
- Bacteria can be heterotrophic and autotrophic.
- The heterotrophic bacteria can be parasitic or saprophytic. The autotrophic bacteria can be chemosynthetic or photosynthetic.

Types of Monerans

Bacteria can be classified into four types based on their shape:

1. Coccus (pl.: cocci) – These bacteria are spherical in shape
2. Bacillus (pl.: bacilli) – These bacteria are rod-shaped
3. Vibrium (pl.: vibrio) – These bacteria are comma-shaped bacteria
4. Spirillum (pl.: spirilla) – These bacteria are spiral-shaped bacteria

Monera has since been divided into Archaeobacteria and Eubacteria.

2. Kingdom Protista

Features of Protista

- They are unicellular and eukaryotic organisms.
- Some of them have cilia or flagella for mobility.
- Sexual reproduction is by a process of cell fusion and zygote formation.

Sub-groups of Protista

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1. Chrysophytes: The golden algae (desmids) and diatoms fall under this group. They are found in marine and freshwater habitats.
2. Dinoflagellates: They are usually photosynthetic and marine. The colour they appear in is dependent on the key pigments in their cells; they appear red, blue, brown, green or yellow.
3. Euglenoids: Most of them live in freshwater habitation in motionless water. The cell wall is absent in them, instead, there is a protein-rich layer called a pellicle.
4. Slime Moulds: These are saprophytic. The body moves along putrefying leaves and twigs and nourishes itself on organic material. Under favourable surroundings, they form an accumulation and are called Plasmodial slime moulds.
5. Protozoans: They are heterotrophs and survive either as parasites or predators.

3. Kingdom Fungi

The kingdom fungi include moulds, mushroom, yeast etc. They show a variety of applications in domestic as well as commercial purposes.

Features of Kingdom Fungi

- The fungi are filamentous, excluding yeast (single-celled)
- Their figure comprises slender, long thread-like constructions called hyphae. The web of hyphae is called mycelium.
- Some of the hyphae are unbroken tubes which are jam-packed with multinucleated cytoplasm. Such hyphae are labelled Coenocytic hyphae.
- The other type of hyphae has cross-walls or septae.
- The cell wall of fungi is composed of polysaccharides and chitin.
- Most of the fungi are saprophytes and are heterotrophic.
- Some of the fungi also survive as symbionts. Some are parasites. Some of the symbiont fungi live in association with algae, like lichens.



Some symbiont fungi live in association with roots of higher plants, such as mycorrhiza.

4.Kingdom Plantae

Features of Kingdom Plantae

- The kingdom Plantae is filled with all eukaryotes which have chloroplast.
- Most of them are autotrophic in nature, but some are heterotrophic as well.

The Cell wall mainly comprises cellulose.

Plants have two distinct phases in their lifecycle. These phases alternate with each other. The diploid saprophytic and the haploid gametophytic phase. The lengths of the diploid and haploid phases vary among dissimilar groups of plants. Alternation of Generation is what this phenomenon is called.

5.Kingdom Animalia

Features of Kingdom Animalia

- All multicellular eukaryotes which are heterotrophs and lack cell wall are set aside under this kingdom.
- The animals are directly or indirectly dependent on plants for food. Their mode of nutrition is holozoic. Holozoic nutrition encompasses ingestion of food and then the use of an internal cavity for digestion of food.
- Many of the animals are adept for locomotion.
- They reproduce by sexual mode of reproduction.

The five-kingdom classification of living organisms took a lot into consideration and is till now the most efficient system.

The older system of classification was based only on one single characteristic according to which two highly varied organisms were grouped together. For example, the fungi and plants were placed in the same group based on the presence of the cell wall. In the same way, unicellular and multicellular organisms were also grouped together.

Therefore, all the organisms were classified again into the five kingdoms known as the five-kingdom classification, starting with Monera, where all the prokaryotic unicellular organisms were placed together.

Following that, all the eukaryotic unicellular organisms were placed under the kingdom Protista.

The organisms were then classified based on the presence and absence of a cell wall. The ones without the cell wall were classified under kingdom Animalia and the ones with cell wall were classified under kingdom Plantae.

The organisms under kingdom Plantae were further classified into photosynthetic and non-photosynthetic, which included Plantae and fungi respectively.

This system of classification of living organisms is better than following the older classification of plants and animals because it eradicated the confusion of putting one species in two different kingdoms.

Three Domain System

The Archaea (archaebacteria)

The Archaea possess the following characteristics:

- Archaea are prokaryotic cells.
- Unlike the Bacteria and the Eukarya, the Archaea have membranes composed of branched hydrocarbon chains (many also containing rings within the hydrocarbon chains) attached to glycerol by ether linkages
- The cell walls of Archaea contain no peptidoglycan.
- Archaea are not sensitive to some antibiotics that affect the Bacteria, but are sensitive to some antibiotics that affect the Eukarya.
- Archaea contain rRNA that is unique to the Archaea as indicated by the presence of molecular regions distinctly different from the rRNA of Bacteria and Eukarya.

Archaea often live in extreme environments and include methanogens, extreme halophiles, and hyperthermophiles. One reason for this is that the ether-containing linkages in the Archaea membranes are more stable than the ester-containing linkages in the Bacteria and Eukarya and are better able to withstand higher temperatures and stronger acid concentrations.

The Bacteria (eubacteria)

Bacteria (also known as eubacteria or "true bacteria") are prokaryotic cells that are common in human daily life, encounter many more times than the archaeobacteria. Eubacteria can be found almost everywhere and kill thousands upon thousands of people each year, but also serve as antibiotics producers and food digesters in our stomachs. The Bacteria possess the following characteristics:

- Bacteria are prokaryotic cells.
- Like the Eukarya, they have membranes composed of unbranched fatty acid chains attached to glycerol by ester linkages

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- The cell walls of Bacteria, unlike the Archaea and the Eukarya, contain peptidoglycan.
- Bacteria are sensitive to traditional antibacterial antibiotics but are resistant to most antibiotics that affect Eukarya.
- Bacteria contain rRNA that is unique to the Bacteria as indicated by the presence of molecular regions distinctly different from the rRNA of Archaea and Eukarya.

Bacteria include mycoplasmas, cyanobacteria, Gram-positive bacteria, and Gram-negative bacteria.

The Eukarya (eukaryotes)

The Eukarya possess the following characteristics:

- Eukarya have eukaryotic cells.
- Like the Bacteria, they have membranes composed of unbranched fatty acid chains attached to glycerol by ester linkages. Not all Eukarya possess cells with a cell wall, but for those Eukarya having a cell wall, that wall contains no peptidoglycan.
- Eukarya are resistant to traditional antibacterial antibiotics but are sensitive to most antibiotics that affect eukaryotic cells.
- Eukarya contain rRNA that is unique to the Eukarya as indicated by the presence of molecular regions distinctly different from the rRNA of Archaea and Bacteria.

The Eukarya are subdivided into the following four kingdoms:

Protista Kingdom: Protists are simple, predominantly unicellular eukaryotic organisms. Examples include slime moulds, euglenoids, algae, and protozoans.

Fungi Kingdom: Fungi are unicellular or multicellular organisms with eukaryotic cell types. The cells have cell walls but are not organised into tissues. They do not carry out photosynthesis and obtain nutrients through absorption. Examples include sac fungi, club fungi, yeasts, and moulds.

Plantae Kingdom: Plants are multicellular organisms composed of eukaryotic cells. The cells are organised into tissues and have cell walls. They obtain nutrients by photosynthesis and absorption. Examples include mosses, ferns, conifers, and flowering plants.

Animalia Kingdom: Animals are multicellular organisms composed of eukaryotic cells. The cells are organised into tissues and lack cell walls. They do not carry out photosynthesis and obtain nutrients primarily by ingestion. Examples include sponges, worms, insects, and vertebrates.

It used to be thought that the changes that allow microorganisms to adapt to new environments or alter their virulence capabilities was a relatively slow process occurring within an organism primarily through mutations, chromosomal rearrangements, gene deletions and gene duplications. Those changes would then be passed on to that microbe's progeny and natural selection would occur. This gene transfer from a parent organism to its offspring is called vertical gene transmission.

It is now known that microbial genes are transferred not only vertically from a parent organism to its progeny, but also horizontally to relatives that are only distantly related, e.g., other species and other genera. This latter process is known as Horizontal gene transfer. Through mechanisms such as transformation, transduction, and conjugation, genetic elements such as plasmids, transposons, integrons, and even chromosomal DNA can readily be spread from one microorganism to another. As a result, the old three-branched "tree of life" in regard to microorganisms now appears to be more of a "net of life."

Microbes are known to live in remarkably diverse environments, many of which are extremely harsh. This amazing and rapid adaptability is a result of their ability to quickly modify their repertoire of protein functions by modifying, gaining, or losing their genes. This gene expansion predominantly takes place by horizontal transfer.

Binomial Nomenclature

The system of binomial nomenclature was introduced by Carl Linnaeus. Multiple local names make it extremely difficult to identify an organism globally and keep a track of the number of species. Thus, it creates a lot of confusion. To get rid of this confusion, a standard protocol came up. According to it, each and every organism would have one scientific name which would be used by everyone to identify an organism. This process of standardised naming is called Binomial Nomenclature.

All living species including plants, animals, birds and also some microbes have their own scientific names. For eg.,

- The scientific name of the tiger is presented as *Panthera tigris*. 'Panthera' represents the genus and 'Tigris' represents a particular species or specific epithet.
- The scientific name of humans is presented as *Homo sapiens*. 'Homo' represents the genus and 'sapiens' represents a particular species.
- The Indian bullfrog is scientifically written as *Rana tigrina*. 'Rana' is the name of the genus and 'tigrina' is the name of the specific species.

Rules of Binomial Nomenclature

A Biologist from all over the world follows a uniform set of principles for naming the organisms. There are two international codes which are

agreed upon by all the biologists over the entire world for the naming protocol. They are:

- International Code of Botanical Nomenclature (ICBN) – Deals with the biological nomenclature for plants
- International Code of Zoological Nomenclature (ICZN) – Deals with the biological nomenclature of animals.

These codes make sure that each organism gets a specific name and that name is globally identified.

The naming follows certain conventions. Each scientific name has two parts:

- Generic name
- Specific epithet

The rest of the binomial nomenclature rules for writing the scientific names of organisms include the following:

- All the scientific names of organisms are usually Latin. Hence, they are written in italics.
- There exist two parts of a name. The first word identifies the genus and the second word identifies the species.
- When the names are handwritten, they are underlined or italicised if typed. This is done to specify its Latin origin.
- The name of the genus starts with a capital letter and the name of the species starts with a small letter.

ICZN

The International Code of Zoological Nomenclature (ICZN) is a book containing a set of rules and recommendations on the formal naming of animals. Among Zoologists as well as in the book, it is often referred to simply as "the Code"

while Taxonomists refer to it as "the ICZN". It was first published in 1961, although it has precedents going back to 1842; the present edition is the fourth edition (1999). The Code is issued by the International Commission on Zoological Nomenclature. As the Commission may alter the Code without issuing a new edition of the book, it is not necessarily that the book may contain the actual provision that applies in a particular case. The Code deals with Zoological nomenclature, which is defined in the Glossary as –"The system of scientific names for animal taxa and the provisions for the formation, treatment and use of those names." Zoological nomenclature is independent of other systems of nomenclature. The rules and recommendations have one fundamental aim: to provide the maximum universality and continuity in the naming of all animals, except where taxonomic judgement dictates otherwise. The Code is meant to guide only the nomenclature of animals, while leaving the Zoologists freedom in classifying new taxa. In other words, whether a species itself is or is not an entity to be recognized is a subjective decision, but what name should be applied to it is not; the Code applies only to the latter, not to the former. A new animal name published without adherence to the Code may be deemed simply "unavailable" if it fails to meet certain criteria, or fall entirely out of the province of science. The rules in the Code determine what names are valid for any taxon in the family group, genus group, and species group. It has additional (but more limited) provisions on names in higher ranks. The Code recognizes no case law. Any dispute is to be decided first by applying the Code directly, and not by reference to precedent.

Principles

Animal names are regulated by six central principles, which were first set out in the third edition of the Code (1985):

- i) Principle of Binomial Nomenclature
- ii) Principle of Coordination

- iii) Principle of the First Reviser
- iv) Principle of Homonymy
- v) Principle of Priority
- vi) Principle of Typification

Structure

The Code divides names in the following manner:

- a) Names above the family group.
- b) Family-group names.
- c) Genus-group names.
- d) Species-group names

The names above the family group are regulated only as to the requirements for publication; there is no restriction to the number of ranks and the use of names is not restricted by priority. The names in the family group, the genus group and the species groups are fully regulated by the provisions in the Code. There is no limitation to the number of ranks allowed in the family group. In the genus group there are only two ranks: the genus and the subgenus. In the species group there are only two ranks: the species and the subspecies.

Gender agreement

In the species group gender agreement is of paramount importance. The name of a species is in two parts (a binomen) say, *Loxodonta africana*, and of a subspecies, in three parts (a trinomen) say *Canis lupus albus*, originally is a Latin phrase, and must be grammatically correct Latin. If the second part, the specific name or the third part, the subspecific name is adjectival in nature, its ending must agree in gender with the name of the genus. If it is a noun, or an arbitrary combination of letters, this does not apply. For instance, the generic name *Equus* is masculine; in the name *Equus africanus* the specific name *africanus* is an adjective and its ending

follows the gender of the generic name. In *Equus zebra* the specific name *zebra* is a noun, it is not correct to write *Equus zebra*. Similarly in *Equus quagga burchellii* the subspecific name *burchellii* is a noun in the genitive of the esteemed Burchell. If a species is moved, therefore, the spelling of an ending may need to be changed. Confusion over proper Latin grammar has led to many incorrectly-formed names appearing in print. An improper automated search may fail to find all the variant spellings of a given name (e.g., the spellings *atra* and *ater* may refer to the same species). Accordingly, many laymen and some scientists object to continued adherence to this long-standing rule.

Commission

The rules in the Code are to be followed by all users of Zoological names. However, its provisions can be interpreted, waived or modified in their application to a particular case when strict adherence would cause confusion. Such exceptions are not made by an individual scientist, no matter how well-respected within his or her field, but only by the International Commission on Zoological Nomenclature, acting on behalf of all Zoologists. The Commission takes such action in response to proposals submitted to it. For example: Carolus Linnaeus named the Domestic Cat, *Felis catus* in 1758; Johann Christian Daniel von Schreber named the Wildcat *Felis silvestris* in 1775. For taxonomists who consider these two kinds of cat to be a single species, the Principle of Priority applies which means that the species ought to be named *F. catus*, but in practice almost all Biologists have used *F. silvestris*. In 2003, the Commission issued a ruling (Opinion 2027) that "conserved the usage of 17 specific names based on wild species, which are predated by or contemporary with those based on domestic forms", confirming *F. silvestris* for the wild cat. Taxonomists who consider the domesticated cat to be the same species as the wild cat should use *F. silvestris*; taxonomists who consider the domesticated cat a subspecies of the wild cat should use *F. silvestris catus*;

taxonomists who consider the domesticated cats, a separate species, should use *F. catus*.

Principles

i) Principle of Binomial Nomenclature

In Zoology, the Principle of Binomial Nomenclature is one of the guiding principles of the International Code of Zoological Nomenclature. It states that the nomenclature for animals is binomial nomenclature: species have a name composed of two names, a "binomen": a generic name and a specific name. No other rank can have a name composed of two names. For example *Giraffa camelopardalis*; subspecies have a name composed of three names, a "trinomen": generic name, specific name, subspecific name:

Giraffa camelopardalis rothschildi taxa at a rank above species have a name composed of one name, a "uninominal name" i.e. *Giraffa* or *Giraffidae*. In botanical nomenclature, the equivalent for "binomial nomenclature" is "binary nomenclature" (or sometimes "binomial nomenclature").

ii) Principle of Coordination

In Zoology, the Principle of Coordination is one of the important principles of the International Code of Zoological Nomenclature. It states that the act of publishing a new Zoological name thereby automatically and simultaneously establishes all the corresponding names in the relevant other ranks, with the same type. For example In the species-group, publishing the species name (the binomen) *Giraffa camelopardalis* Linnaeus, 1758 also establishes the subspecies name (the trinomen) *Giraffa camelopardalis camelopardalis* Linnaeus, 1758. The same applies to the name of a subspecies; this establishes the corresponding species name. In

the genus-group, similarly, publishing the name of a genus also establishes the corresponding name of a subgenus (or vice versa): *Giraffa* Linnaeus, 1758 and *Giraffa* Linnaeus, 1758. In the family-group, publication of the name of a family, subfamily, superfamily (or any other such rank) also establishes the names in all the other ranks in the family group. Author citations for such names are the same as for the name actually published. It is immaterial if there is an actual taxon to which the automatically established name applies; if ever such a taxon is recognised, there is a name available for it.

iii) Principle of the First Reviser

In Zoology, the Principle of the First Reviser is one of the guiding principles of the International Code of Zoological Nomenclature. It supplements the Principle of Priority, which states that the first published name takes precedence. The Principle of the First Reviser deals with situations that cannot be resolved by priority, namely where there are two or more items that have the same date of publication (or the same year of publication when no details are known). These items may be two or more different names for the same taxon, two or more names with the same spelling used for different taxa, two or more different spellings of a particular name, etc. In such cases the first subsequent author who deals with the matter, makes a choice and publishes the decision in the required manner, the First Reviser, is to be followed.

iv) Principle of Homonymy

In Zoology, the Principle of Homonymy is one of the guiding principles of the International Code of Zoological Nomenclature. It states that any one name, in one particular spelling, may be used only once (within its group). This will be the first published name; any later name with the same spelling

(a homonym) is barred from being used. The Principles of Priority and the First Reviser apply here. For family-group names the termination (which is rank-bound) is not taken into account. In 1777 Johann Reinhold Forster published the name *Echidna* for a genus of moray eels. This meant that when Georges Cuvier proposed to use this name *Echidna* in 1797 for the spiny anteater he created a junior homonym. Later, in 1811, Johann Karl Wilhelm Illiger published the name *Tachyglossus*, as a replacement name, or *nomen novum*, and this is considered to be the valid name for the spiny anteater.

v) Principle of Priority

In Zoology, the scientific study of animals, the Principle of Priority is one of the guiding principles of the International Code of Zoological Nomenclature. It states that the correct formal scientific name for an animal taxon, the name that is to be used, called the valid name, is the oldest available name that applies to it. There are exceptions; another name may be given precedence by any provision of the Code or by any ruling of the Commission. It is the fundamental guiding precept that preserves the stability of Zoological nomenclature. It was first formulated in 1842 by a committee appointed by the British Association to consider the rules of Zoological nomenclature; the committee's report was written by Hugh Edwin Strickland. In 1855, John Edward Grey published the name *Antilocapra anteflexa* for a new species of pronghorn, based on a pair of horns. However, it is now thought that his specimen belonged to an unusual individual of an existing species, *Antilocapra americana*, with a name published by George Ord in 1815. The older name, by Ord, takes priority; with *Antilocapra anteflexa* becoming a junior synonym. In 1856, Johann Jakob Kaup published the name *Leptocephalus brevirostris* for a new species of eel. However, it was revealed in 1893 that the organism described by Kaup was in fact the juvenile form of the European eel. The European eel was named *Muraena anguilla* by Carolus Linnaeus in 1758 and moved to the genus *Anguilla* by Franz Paula von Schrank in 1798. So

Anguilla anguilla is now the valid name for the species, and *Leptocephalus brevirostris* is considered a junior synonym. The Common Chimpanzee was named *Simia troglodytes* by Johann Friedrich Blumenbach; when Lorenz Oken moved it to the new genus *Pan* in 1816, the specific name *troglodytes* had priority over any newly to be coined specific name, so the valid The name is now *Pan troglodytes* (Blumenbach, 1775). Two species of Madagascar snake were initially given the names *Pelophilus madagascariensis* Duméril & Bibron, 1844 and *Xiphosoma madagascariensis* Duméril & Bibron, 1844. The former was moved to the genus *Boa* in 1893 by George Albert Boulenger, resulting in the name *Boa madagascariensis* (Duméril & Bibron, 1844). This meant that when in 1991 Arnold G. Kluge of the Museum of Zoology at the University of Michigan moved *Xiphosoma madagascariensis* to the genus *Boa* as well; it could not have the name *Boa madagascariensis*. So Kluge gave the species the name *Boa manditra*.

HOMONYMY

This basic principle refers to the application of the same name to different taxa. The codes of nomenclature state that no two names above the species-group level may be the same in Zoology or Botany, although names may be duplicated between the two fields. Homonyms are of different types:

Senior homonyms:

The available name on the basis of priority that is as per the year of publication.

Junior homonyms:

A preoccupied name (not in use) on the basis of priority or by a ruling by a nomenclature body.

Primary homonyms:

In a species-group (species, subspecies, etc.) these are names that are the same and were proposed in the same genus-group taxon. The junior homonym must always be replaced either by a new name or a junior synonym (if one exists). Example: *Cottus pygmaeus* & pygmy sculpin. This species was described and later it was discovered that this name was already preoccupied by an old description of a *Cottus* from the Old World which means it is a primary homonym. A new name for the pygmy sculpin is currently being described.

Secondary Homonyms:

These are species that are placed in the same genus subsequent to their publication and they have the same specific epithets. The senior secondary homonym is the older of the two names. An alternative name will have to be provided either through description or junior synonyms for the junior homonym.

SYNONYMY

In scientific nomenclature, a synonym is a scientific name that applies to a taxon that goes by a different scientific name, although Zoologists use the term somewhat differently. For example, Linnaeus was the first to give a scientific name (under the currently used system of scientific nomenclature) to the Norway spruce, which he called *Pinus abies*. This name is no longer in use: it is now a synonym of the current scientific name which is *Picea abies*.

Unlike synonyms in other contexts, in taxonomy a synonym is not interchangeable with the name of which it is a synonym. In taxonomy, synonyms are not equals, but have a different status. For any taxon with a particular circumscription, position, and rank, only one scientific name is considered to be the correct one at any given time (this correct name is to

be determined by applying the relevant code of nomenclature). A synonym is always the synonym of a different scientific name and cannot exist in isolation. Given that the correct name of a taxon depends on the taxonomic viewpoint used (resulting in a particular circumscription, position and rank) a name that is one taxonomist's synonym may be another taxonomist's correct name (and vice versa). Synonyms may arise whenever the same taxon is described and named more than once, independently. They may also arise when existing taxa are changed, as when two taxa are joined to become one, a species is moved to a different genus, a variety is moved to a different species, etc. To the general user of scientific names, in fields such as agriculture, horticulture, ecology, general science, etc., a synonym is a name that was previously used as the correct scientific name (in handbooks and similar sources) but which has been displaced by another scientific name, which is now regarded as correct. Thus Oxford Dictionaries Online defines the term as "a taxonomic name which has the same application as another, especially one which has been superseded and is no longer valid." In handbooks and general texts, it is useful to have synonyms mentioned as such after the current scientific name, so as to avoid confusion. For example, if the much advertised name change should go through and the scientific name of the fruit fly were changed to *Sophophora melanogaster*, it would be very helpful if any mention of this name was accompanied by "(syn. *Drosophila melanogaster*)". Or to give another example, a mention of the name *Apatosaurus* is much helped by the addition "(syn. *Brontosaurus*)". Synonyms used in this way may not always meet the strict definitions of the term "synonyms" in the formal rules of nomenclature which govern scientific names .

Changes of scientific name have two causes: they may be taxonomic or nomenclatural. A name change may be caused by changes in the circumscription, position or rank of a taxon, representing a change in taxonomic, scientific insight (as would be the case for the fruit fly, mentioned above). A name change may be due to purely nomenclatural

reasons, that is, based on the rules of nomenclature; as for example when an older name is (re)discovered which has priority over the current name. Speaking in general, name changes for nomenclatural reasons have become less frequent over time as the rules of nomenclature allow for names to be conserved, so as to promote stability of scientific names. The Latin Caudata and Greek Urodela both mean "tailed" and have been used as a scientific name at the rank of order for the salamanders (as opposed to the tailless frogs). Thus they are synonyms.

In Zoological nomenclature, codified in the International Code of Zoological Nomenclature synonyms are different scientific names of the same rank that pertain to the same taxon, for example two names for the same species. The earliest such name is called the senior synonym, while the later name is the junior synonym. One basic principle of Zoological nomenclature is that the earliest correctly published (and thus available) name, the senior synonym, takes precedence and must be used for the taxon, if no other restrictions interfere. Synonyms are important because if the earliest name cannot be used (for example because the same spelling had previously been used for a name established for another taxon), then the next available junior synonym must be used for the taxon.

Objective synonyms refer to taxa with the same type and same rank (more or less the same taxon, although circumscription may vary, even widely). This may be species-group taxa of the same rank with the same type specimen, genus-group taxa of the same rank with the same type species or if their type species are themselves objective synonyms, or family-group taxa with the same type genus, etc. In the case of subjective synonyms there is no such shared type, so the synonymy is open to taxonomic judgement, meaning that there is room for debate: one researcher might consider the two (or more) types to refer to one and the same taxon, another might consider them to belong to different taxa. For example, John Edward Grey published the name *Antilocapra anteflexa* in 1855 for a

species of pronghorn, based on a pair of horns. However, it is now commonly accepted that his specimen was an unusual individual of the species *Antilocapra americana* published by George Ord in 1815. Ord's name thus takes precedence, with *Antilocapra anteflexa* being a junior subjective synonym.

Objective synonyms are common at the level of genera, because for various reasons two genera may contain the same type species; these are objective synonyms. In many cases researchers established new generic names because they thought this was necessary or did not know that others had previously established another genus for the same group of species. An example is the genus *Pomatia* Beck, 1837, which was established for a group of terrestrial snails containing as its type species the Burgundy or Roman snail *Helix pomatia* – since *Helix pomatia* was already the type species for the genus *Helix* Linnaeus, 1758, the genus *Pomatia* was an objective synonym (and useless). At the same occasion *Helix* is also a synonym of *Pomatia*, but it is older and so it has precedence. At the species level, subjective synonyms are common because of an unexpectedly large range of variation in a species, or simple ignorance about an earlier description, may lead a biologist to describe a newly discovered specimen as a new species. A common reason for objective synonyms at this level is the creation of a replacement name. It is possible for a junior synonym to be given precedence over a senior synonym, primarily when the senior name has not been used since 1899, and the junior

The name is in common use. The older name may be declared to be a *nomen oblitum*, and the junior name declared a *nomen protectum*. This rule exists primarily to prevent the confusion that would result if well-known name, with a large accompanying body of literature, were to be replaced by a completely unfamiliar name. An example is the European land snail *Petasina edentula* (Draparnaud, 1805). In 2002, researchers found that an older name *Helix depilata* Draparnaud, 1801 referred to the same species, but this name had never been used after 1899 and was fixed as a *nomen oblitum* under this rule by Falkner et al. 2002. Such a reversal of

precedence is also possible if the senior synonym was established after 1900, but only if the International Commission on Zoological Nomenclature (ICZN) approves an application. For example, the scientific name of the red imported fire ant, *Solenopsis invicta* was published by Buren in 1972, who did not know that this species was first named *Solenopsis saevissima wagneri* by Santschi in 1916; as there were thousands of publications using the name *invicta* before anyone discovered the synonymy, the ICZN, in 2001, ruled that *invicta* would be given precedence over *wagneri*.

To qualify as a synonym in zoology, a name must be properly published in according to the rules. Manuscript names and names that were mentioned without any description (*nomina nuda*) are not considered as synonyms in zoological nomenclature. In botanical nomenclature, a synonym is a name that is not correct for the circumscription, position, and rank of the taxon as considered in the particular botanical publication. It is always "a synonym of the correct scientific name", but which the name is correct depending on the taxonomic opinion of the author. In botany the various kinds of synonyms are:

- Homotypic, or nomenclatural, synonyms (sometimes indicated by \equiv) have the same type (specimen) and the same taxonomic rank. The Linnaean name *Pinus abies* L. has the same type as *Picea abies* (L.) H.Karst. When *Picea* is taken to be the correct genus for this species (there is almost complete consensus on that), *Pinus abies* is a homotypic synonym of *Picea abies*. However, if the species were considered to belong to *Pinus* (now unlikely) the relationship would be reversed and *Picea abies* would become a homotypic synonym of *Pinus abies*. A homotypic synonym need not share an epithet or name with the correct name; what matters is that it shares the type. For example, the name *Taraxacum officinale* for a species of dandelion has the same type as *Leontodon taraxacum* L. The latter is a homotypic synonym of *Taraxacum officinale* Wigg

- Heterotypic, or taxonomic, synonyms (sometimes indicated by =) have different types.

Some botanists split the common dandelion into many, quite restricted species. The name of each such species has its own type. When the common dandelion is regarded as including all those small species, the names of all those species are heterotypic synonyms of *Taraxacum officinale* Wigg. Reducing a taxon to a heterotypic synonym is termed "to sink in synonymy" or "as synonym". In botany, although a synonym must be a formally accepted scientific name (a validly published name): a listing of "synonyms", a "synonymy", often contains designations that for some reason did not make it as a formal name, such as manuscript names, or even misidentifications (although it is now the usual practice to list misidentifications separately).

LAW OF PRIORITY

According to the rule, the valid name of a taxon is the oldest available name applied to it, provided that the name is not invalidated by any provisions of this code or has not been suppressed by the commission. "Priority" means Priority of publication e.g; *Epitranus erythrogaster*, an insect species described by Cameron, 1888 and the same species was described by several authors

1. *Epitranus erythrogaster* Cameron, 1888
2. *Anacryptus sculpturatus* Crawford, 1910
3. *Anacryptus kankauensis* Masi, 1933
4. *Arrectoceroides ceylonensis* Mani, 1936

Since the Camerons' name *E. erythrogaster* is the earliest legitimate name, therefore,

it is accepted as a valid name (senior synonym) and rest of the names according to law

of priority becomes its invalid names (Jr. syn.)

(a) Exceptions:

A name that is not the oldest available name is nevertheless the valid name of the taxon in question

- (i) If it is conserved under section (b) of this article; or
- (ii) If the commission has expressly validated it.

(b) Limitations:

A name that has remained unused as a senior synonym in the primary Zoological literature for more than 50 years is to be considered a forgotten name (Nomen Oblitum).

(c) Family Group Names:

A family group taxon formed by the union of two or more taxa of that group takes the oldest valid family group name among those of its components.

(d) Genus and Species Group Names:

(i) A genus-group taxon formed by the union of two or more genus group taxa takes the oldest valid name among those of its components
e.g. The valid name of a genus formed by the union of genus A-us, 1850, and subgenus B-us, 1800, is B-us, 1800.

(ii) A species group taxon formed by the union of two or more species group taxa takes the oldest valid name among those of its components.

(iii) If the name of a genus or species having subordinate taxa is found to be invalid or unavailable, it must be replaced by the next oldest valid name
e.g., Genus Aus, 1850, contains the subgenera A-us, 1850, C-us, 1900, and D-us, 1860. If the name A-us is found to be a junior homonym, it is to be

replaced as the name of the genus by D-us, 1860, the next oldest valid name

Genus-1	Genus-2
Genus A-us, 1850	A-us, 1845
Genus A-us, 1850	A-us, 1845
Genus C-us, 1900	B-us, 1850
Genus D-us,	1860 C-us, 1855

Therefore genus A-us is to be replaced by D-us, 1860 (next oldest-available name) and the order of it will be-

- Genus D-us, 1860
- Subgenus D-us, 1860
- Subgenus C-us, 1900
- Subgenus A-us, 1850

Concept of Species

Species are often defined as a group of individuals with similar characteristics, where they can interbreed to produce fertile offspring.

Important Concept Of Species

In this concept, there is a finite number of varieties of living organisms that exist on earth. These types do not exhibit any relationship with each other. Such varieties are termed as species. This inequality is regarded as an unimportant and irrelevant phenomenon.

Aristotle and Plato stated this concept in their philosophies. In the year of 1954 and 1956, Cain regarded the Typological species concept as the morphospecies concept. As the members of the species or a taxon can be identified by their essential characteristics, a group of scientists refer to this as essentialist species concept.

Morphospecies concept states that the species can be differentiated from other species by their physical features and can be identified by their morphological attributes. This is called the morphological species concept.

Nominalistic Species Concept

The nominalistic species concept is the concept of Occam and his followers, of the belief that nature only produces individuals. Species are the creation of man. In nature, they lack definite existence. These concepts do not have any scientific basis.

It believes that the species have been invented to refer to big numbers of individuals jointly. During the 18th century in France, this concept was in demand and even now is used by some botanists.

Biological Species Concept

In the middle of the 18th century, a fresh concept called the biological species concept appeared. This concept was acknowledged in the later half of the nineteenth-century once Darwin's "Origin of Species" was published (in 1859). This is also known as the Newer Species concept.

K. Jordan was the first to formulate this concept in 1905. Later in 1940, Mayr supported this concept. As per this concept, "a species is a group of interbreeding natural population that is reproductively isolated from other such groups". Mayr described that the members of a species exhibit these attributes:

Reproductive community:

For the purpose of reproduction the individuals of a species recognize one another as potential mates.

Ecological Unit:

The species' members differ from each other due to many attributes, but all the members cooperatively form a unit. They interact with other species as a unit in any environment.

Genetical unit:

Species comprises a large, inter-communicating gene pool, although the individual is simply a non-permanent vessel comprising a small part of the contents of the gene pool for a shorter duration.

Evolutionary Species Concept

The flaws of the biological species concept had led the palaeontologists to formulate the evolutionary species concept.

- Simpson (in 1961) had defined it as “an evolutionary species is a lineage (an ancestral- descendant sequence of populations) evolving separately from others and with its own unitary evolutionary role and tendencies”.
- Wiley (in 1978) had provided a revised definition of the evolutionary species concept. He stated that “an evolutionary species are a single lineage of ancestral-descendant population which draws its identity from other such lineages and has its own evolutionary tendencies and historical fate”.

Types of Species

Taxonomic Species

It includes a group of morphologically similar organisms.

Microspecies

The population is obtained from a single parent.

Biological Species

It includes the population that involves sexually reproducing individuals.

Evolutionary Species

It is a combination of sexually reproducing organisms, phyletic lineages and uniparental organisms.

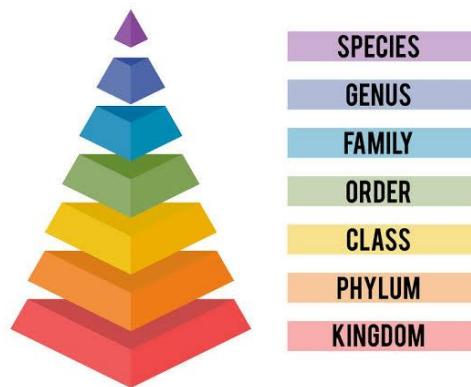
Successional Species

It includes phyletic lineages.

Taxonomic Hierarchy

Taxonomic hierarchy is the process of arranging various organisms into successive levels of the biological classification either in a decreasing or an increasing order from kingdom to species and vice versa.

HIERARCHY OF BIOLOGICAL CLASSIFICATION



Molecular Taxonomy (Molecular Systematics / Molecular Phylogenetics)

Molecular Taxonomy is the branch of phylogeny that analyses hereditary molecular differences, mainly in DNA sequences, to gain information and to establish genetic relationship between the members of different taxonomic categories.

The advent of DNA cloning and sequencing methods have contributed immensely to the development of molecular taxonomy and population genetics over the years. These modern methods have revolutionised the field of molecular taxonomy and population genetics with improved analytical power and precision.

The results of a molecular phylogenetic analysis are expressed in the form of a tree called a phylogenetic tree. Different molecular markers like allozymes, mitochondrial DNA, microsatellites, RFLP (Restriction Fragment Length Polymorphism), RAPD (Random amplified polymorphic DNA), AFLPs (Amplified Fragment Length Polymorphism), single nucleotide polymorphism – (SNP), microchips or arrays are used in analysis.

Uses of Molecular Taxonomy

ENTRI

1. Molecular taxonomy helps in establishing the relationship of different plant groups at DNA level
2. It unlocks the treasure chest of information on evolutionary history of organisms.

Mitochondrial DNA

- Mitochondrial DNA is the DNA found in the mitochondria of all eukaryotes.
- Abbreviation: mtDNA
- It is about 16,500 base pairs in size.
- It is both circular and linear.
- Number of Genes: 13
- The genes in the mitochondrial DNA take part in oxidative phosphorylation for the production of ATPs and in the synthesis of proteins.

RFLP (Restriction Fragment Length Polymorphism)

RFLPs is a molecular method of genetic analysis that allows identification of taxa based on unique patterns of restriction sites in specific regions of DNA. It refers to differences between taxa in restriction sites and therefore the lengths of fragments of DNA following cleavage with restriction enzymes.

Amplified Fragment Length Polymorphism (AFLP)

This method is similar to that of identifying RFLPs in that a restriction enzyme is used to cut DNA into numerous smaller pieces, each of which terminates in a characteristic nucleotide sequence due to the action of restriction enzymes. AFLP is largely used for population genetics studies, but has been used in studies of closely related species and even in some cases, for higher level cladistic analysis.

Random Amplified Polymorphic DNA (RAPD)

It is a method to identify genetic markers using a randomly synthesised primer that will anneal (recombine (DNA) in the double stranded form) to complementary regions located in various locations of isolated DNA. If another complementary site is present on the opposing DNA strand at a distance that is not too great (within the limits of PCR) then the reaction will amplify this region of DNA.

RAPDs like microsatellites may often be used for genetic studies within species but may also be successfully employed in phylogenetic studies to address relationships within a species or between closely related species. However, RAPD analysis has the major disadvantage that results are difficult to replicate and that the homology of similar bands in different taxa may be nuclear.

VNTR

VNTR or the Variable Number of Tandem Repeats are the repeated DNA sequences at a defined locus. The repeats are clustered together and oriented in the same direction. Individual repeats can be added or removed through replication and recombination errors. This forms alleles with different numbers of repeats.

The DNA segments vary in different individuals and are hence beneficial in identifying individuals in case of a crime scene or a paternity dispute. This is known as DNA fingerprinting.

The tandem repeat sequences of DNA are also termed as “satellite DNA”. These are of three main types:

- Satellite
- Minisatellite
- Microsatellite

Types Of VNTR

Satellite DNA

These are highly repetitive DNA sequences and each DNA sequence consists of several thousand base pairs. A satellite can measure up to 100 million base pairs. These are found occurring in the regions of heterochromatin. The Y chromosome has abundant satellites. This makes it convenient for the researchers studying paternal genetic transmission in mammals.

The density of the DNA is the function of its base and sequence. The satellite DNA with its highly repetitive DNA has a reduced density compared to the rest of the genome. Therefore, the name "satellite DNA" is coined.

The satellite DNA has several biological functions:

- Satellite DNA is present in the centromeric and pericentromeric regions. It regulates the functions of the centromere.
- They help in the formation of heterochromatin.
- Satellite RNA transcripts are found in plants, vertebrates, and invertebrates

Minisatellite

In a minisatellite, each repeat ranges from 9 to 100 base pairs. It is an array of tandem repeats 500 to 300,000 base pairs long.

Minisatellites have been found in association with important features of the human genome such as gene regulation, imprinting, and chromosomal

fragile sites. They provided the first highly polymorphic, multiallelic markers for linkage studies.

Most of the minisatellites are GC rich. They possess a strong strand symmetry.

Microsatellite

The repeats are very short, 2–6 base pairs each. The whole array ranges from 10,000 to 100,000 base pairs long. They are therefore called short tandem repeats or simple sequence repeats. They are usually found in insect and plant chromosomes, and euchromatin regions of vertebrates. Microsatellites are important to the population geneticists because of the variable number of repeats among the individuals of a population. Microsatellite markers are inherited from both the parents. Therefore, they are useful for paternity tests. Highly polymorphic loci increase our ability for parental analysis.

Microsatellites are not affected by natural selection. But they are influenced by gene flow, genetic drift, and mutation.

Importance of VNTR

- VNTRs are found on many chromosomes and vary in length among different individuals. Each variant helps in personal or parental identification.
- VNTRs are an important source of genetic marker RFLP which is used in the linkage analysis of genomes. A banding pattern unique to each individual is produced by the VNTRs.
- VNTR has its applications in forensic science, DNA fingerprinting, and other genetics and biology research.

Allozymes

Allozymes are enzymes with identical function but distinct electrophoretic migration patterns that are encoded by different alleles of the same locus. Allozyme electrophoresis provided the earliest assessment of the genetic variability of natural triatomine populations. Not more than a decade ago, allozymes were the markers of choice in triatomine molecular systematics, accounting for nearly 65% of the published work (Monteiro et al., 2001). Allozyme markers have, however, been gradually substituted by the more variable (and also codominant) PCR-based microsatellites.

To perform allozyme analysis, protein extracts are isolated from each individual being studied, applied to a support medium (traditionally starch gels) and submitted to electrophoresis. This separates proteins based on charge and size. Gels are then histochemically stained for a particular enzyme. Discrete bands are produced for different allozymes encoded by their respective alleles for that locus. The next step is to genetically interpret the pattern obtained for each individual assayed. This technique enables the genotyping of several specimens and loci simultaneously. As allozymes are codominant markers (i.e., both alleles are expressed in a given locus, which permits the identification of all alleles present in the sample), populations can be tested directly for deviations from the HWE.

The drawbacks include the need for fresh or frozen samples and for considerable practice with the methodology and gel scoring. There is also a particular weakness with respect to triatomines; while there is substantial variation in other insect groups such as mosquitoes and sandflies, the variability is very low in triatomines.

Significance of Molecular Taxonomy

- It helps to identify a very large number of species of plants and animals by the use of conserved molecular sequences.

ENTRI

- Using DNA data evolutionary patterns of biodiversity are now investigated.
- DNA taxonomy plays a vital role in phytogeography, which ultimately helps in genome mapping and biodiversity conservation.
- DNA- based molecular markers used for designing DNA based molecular probes, have also been developed under the branch of molecular systematics.

DNA Barcoding

Have you seen how scanners are used in supermarkets to distinguish the Universal Product Code (UPC)? In the same way we can also distinguish one species from another. DNA barcoding is a taxonomic method that uses a very short genetic sequence from a standard part of a genome. The genetic sequence used to identify a plant is known as “DNA tags” or “DNA barcodes”. Paul Hebert in 2003 proposed ‘DNA barcoding’ and he is considered as ‘Father of barcoding’.

The gene region that is being used as an effective barcode in plants is present in two genes of the chloroplast, matK and rbcL, and have been approved as the barcode regions for plants. Sequences of unknown species can be matched from a submitted sequence in GenBank using Blast (web-programme for searching the closely related sequence).

Significance of DNA Barcoding

- DNA barcoding greatly helps in identification and classification of organisms.
- It aids in mapping the extent of biodiversity.

DNA barcoding techniques require a large database of sequences for comparison and prior knowledge of the barcoding region. However, DNA

barcoding is a helpful tool to determine the authenticity of botanical material in whole, cut or powdered form.

Tree of Life

A phylogenetic tree shows the evolutionary relationships among different organisms. The Branches of the tree show where genetic or physical similarities and differences between organisms begin or end.

A phylogenetic tree is like a family tree. The root of the tree represents a distant ancestor of the species that appear at the ends of the branches. The branches separate at nodes, or points where ancestral lines split into new lines of evolution.

