

Biometrics, numerical taxonomy and cladistics

CC VI: Plant Systematics

Unit 5

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Characters

- Description is the assignment of features or attributes to a taxon.
- The features are called characters.
- Two or more forms of a character are character states.

One example of a character is petal color, for which two character states are yellow and blue.

Another character is leaf shape, for which possible character states are elliptic, lanceolate, and ovate.

Variations

Variation is a deviation in structural, functional or developmental characters of an organism from its parents, from others in the same population. Genotypic variation is the difference in genotype within population or species as a result of mutation, recombination or gene interaction with some evolutionary significance. Phenotypic variation is variation in structural and functional characters resulting from environmental factors on one or more genotypes; this may not be of evolutionary significance.

Variation in Taxonomic and Systematic Characters

1. Geographic Variation in one or more characteristics over space.
2. Sexual Variation in one or more traits between or within a sex.
3. Individual Variation in one or more characteristics within the lifetime of an individual organism:

1. Geographic Variation

- As implied by the name this type of variation occurs over geographic space.
- This includes, but is not limited to, latitudinal, longitudinal, and altitudinal variation of characters.
- Usually, researchers examine variation in demes, populations, and species and look for any "geographic" correlation with any of this variation.
- Within logical boundaries, if a "geographic" component to the variation can be identified then one may hypothesize that the observed variation within the taxon may be clinal and may be correlated with an environmental component.
- If so, such a character may have a selective advantage in some geographic areas or, developmentally, characters may exist in some geographic areas because of temperature, light, or other physical influences early in ontogeny.

2. Sexual Variation

- As implied by the name of this type of variation males and females frequently vary from one another for characteristics.
- This is most often known as sexual dimorphism and the characteristics that do differ are often referred to as primary or secondary sexual features. These latter terms will be discussed below.
- Sexually dimorphic characters may not vary in larval and juvenile individuals; variation may be obtained only later in life.
- Adults may display these characters throughout the year or may only possess them during the breeding season.
- In the former case, usually the dimorphic characters are most extreme during the breeding season. Some species do not vary in secondary sexual features and sex is determined only by examination of gonadal tissue.

3. Individual Variation

1. Morphological Variation (Non Genetic Variation)

- Age variations Common in many groups of organisms to have different looking juveniles or larvae from adults.
- Many synonyms have resulted from this phenomenon. For example, Linnaeus described the immature striped goshawk as a different species from adult.
- This was obviously the result of molting pattern differences.
- Allometric Variations This type of variation is typically thought of as being under genetic control. Allometric growth or variation results when the size of some particular structure or number of structures is disproportionate relative to other structures or the rest of the body.

2. Seasonal Variation in Individuals.

- In species that survive for more than one year or more than one reproductive season, characteristics may vary depending upon the season. For example, the plumage of birds, antlers of some mammals, and general breeding coloration.

3. Social Variation.

- In some social insects (bees and wasps, termites) certain castes are developed (reproductive, workers, soldiers). The individuals may be males, females or both. The different structural types that are observed may be the result of different larval food or may be due to hormonal or other controls. Obviously these different forms should not be considered different species.

4. Ecological Variation Habitat Variation.

- Populations of a single species may occur in different habitats in the same region and are often visibly different depending upon the habitat that they are found in. Taxonomic treatment of local variants of this nature have fluctuated between two extremes.

5. Neurogenic or Neurohumoral Variation

- Color change in individuals due to regions in environment. Accomplished through the concentration or dispersal of color bearing bodies known as chromatophores. This has been observed in chameleons, some lower vertebrates, crustaceans, cephalopods, and flat fishes.

5. Host-Determined Variation

- Parasitic species may display different traits dependent upon the host on which they feed. Cocoons can vary in color depending upon wasp host.
- Some wasps may be winged or wingless, depending upon host. Some hosts may display different traits when parasitized.
- Color patterns may vary with fishes sometimes if they are parasitized (usually this is obvious).
- Density-Dependent Variation Crowding can influence morphological variations. This can be a result of reduced food supply or not. Under crowded conditions the phenotypes may vary from those reared under less crowded conditions: This phenomenon is particularly common with locusts.

6. Traumatic Variation

- This type of variation occurs with varying frequency depending on the group. It is usually obvious, but in some cases may be subtle and misleading. Parasite individual variation Typical patterns discovered in a host individual will include swelling, distortion, and perhaps mechanical injury.

7. Teratological or accidental Alterations in development.

- Usually these are externally induced but can be developmental and may be from hormonal control. External stimuli for aberrant morphologies may be mechanical, physical, or chemical. Post-mortem Changes Common in some museum specimens that have been fixed or preserved or pinned.

8. Genetic Variation

- Before, the same individual is actually or potentially subject to change in appearance. In addition to this non-inherited variation, there is much interpopulational variation which is primarily due to differences in genetic constitution.

9. Sex-Associated Variation

- Among the genetically determined variants within a population, there may be some that are sexually associated. They may be sex-linked or be otherwise associated with one or the other sex. Primary sex differences - Those that involve primary sex organs used in reproduction (gonads, genitalia). Where the sexes are otherwise quite similar, these will rarely be a source of taxonomic confusion. Secondary sex differences - Many groups display pronounced sexual dimorphism. These differences can be quite striking.

10. Continuous Variation

- Most common type of variation due to slight genetic differences which exist between individuals.
- No two individuals are exactly alike in a population genetically or morphologically. This is one of the foremost tasks of the taxonomist.
- Each character is likely to show different degrees of variation in a population. Likewise there will be differing degrees of variation between species for a character.

11. Discontinuous Variation

- Differences between individuals in a population are, in general, slight and intergrading.
- In some species, however, can be grouped into different classes determined by some characters. This discontinuous variation is frequently termed polymorphism.

Operational Taxonomic Unit (OTU)

- Operational taxonomic unit or OTU is considered as the basic unit used in numerical taxonomy. These units may refer to an individual, species, genus, or class. All throughout the taxonomic development, OTUs are the most commonly used units when analyzing gene sequence datasets.
- In numerical methods, the taxonomic units used are constantly not comparable to the formal taxonomic units. Therefore, the term operational taxonomic unit was coined.
- Since data is lacking on the correct OTUs in researches, various experiments have been conducted to evaluate the clustering method performance such as the rationality of OTU structure, the ability to cope with inflation of OTU, the stability of OTU, and the computational efficiency or runtime and memory requirements.
- OTUs or clusters with sequence similarity in the molecular level are widely accepted as an analytical unit used in microbial ecology.
- Nowadays, OTU is generally used in many contexts. In most cases, due to the absence of traditional biological classification systems, OTUs are used as pragmatic substituted terms for microbial individuals at different taxonomic levels.

Character Weighting and Coding

Polarity

- Polarity is the designation of relative ancestry to the character states of a morphocline. A change in character state represents a heritable evolutionary modification from a pre-existing structure or feature (termed plesiomorphic, ancestral, or primitive) to a new structure or feature (termed apomorphic, derived, or advanced).
- The designation of polarity is often one of the uncertain aspects of phylogenetic analysis. The methods used for polarity designation are:
 - comparison may be made within the concerned group shown in green (in-group comparison) or
 - with relatives outside the group shown in pink (outgroup comparison)

Character Coding and Weighting

- The coding of character states is done by assigning non-negative integer values

Binary or Two-state coding

- Binary characters are conveniently assigned 0 and 1 for two states. If it is possible to distinguish, plesiomorphic state is assigned 0 and apomorphic state 1 code Multistate Characters Multistate characters can be coded into number of states using non-negative integer numbers (0,1,2,3,4...) corresponding to transformation series (ordered or unordered).
- As part of a phylogenetic analysis, the characters may be assigned weights. Character weighting is the assignment of greater or lesser taxonomic importance to certain characters over other characters in determining phylogenetic relationships.
- More commonly the numerical taxonomy approach to give equal weighting to all the characters is adopted in the preliminary analysis, then characters which show the least homoplasy (similarity that is not the result of homology is termed homoplasy or analogy) are identified and given more weightage in the subsequent analysis, this process is known as successive weighting.

Character X Taxon Matrix

- The coded data may be organized in the form of a matrix or table with t number of rows (OTUs) and n number of columns (character-states). The character x taxon matrix supplies the data for constructing a phylogenetic tree or cladogram.
- Once the data have been codified and entered in the form of a matrix, the next step is to calculate the degree of similarity between every pair of OTUs.
- A number of formulae have been proposed by various authors to calculate similarity or dissimilarity (taxonomic distance) between the OTUs. :
 - Simple matching coefficient
 - Jaccard Coefficient of association
 - Yule coefficient
- Once the similarity or distance between every pair of taxa has been calculated, the data are presented in a second matrix with $t \times t$ dimensions where both rows and columns represent taxa.
- It must be noted that diagonal t value in the matrix represents self-comparison of taxa and thus 100% similarity. These values are redundant as such. The values in the triangle above this diagonal line would be similar to the triangle below.

Cluster analysis

- Data presented in OTUs x OTUs ($t \times t$) matrix are too exhaustive to provide any meaningful picture and need to be further condensed to enable a comparison of units.
- Cluster analysis is one such method in which OTUs are arranged in the order of decreasing similarity.
- The results of cluster analysis are commonly presented as dendrograms known as phenograms.
- Computer programs are used to efficient cluster analysis and help in the construction of cluster diagrams or phenograms. The various clustering procedures are classified under two categories:

Agglomerative methods: Agglomerative methods start with t clusters equal to the number of OTUs. These are successively merged until a single cluster has finally been formed. The most commonly used clustering method in biology is Sequential Agglomerative Hierarchic Non-overlapping clustering method (SAHN). The method is useful for achieving hierarchical classifications.

Divisive methods: Divisive methods as opposed to agglomerative methods, start with all t , OTUs as a single set, subdividing this into one or more subsets; this is continued until further subdivision is not necessary. The commonly used divisive method is association. The method has been mostly used in ecological data employing two state characters. It builds a dendrogram from the top downwards as opposed to cluster analysis, which builds a diagram from the bottom up.

Phenograms and Cladograms

Phenetics

- Phenetics is the study of relationships among a group of organisms on the basis of degree of similarity between them.
- A tree like diagram that represents phenetic relationships is called a phenogram.

Cladistics

- Phylogeny refers to the evolutionary history or pattern of descent of a group of organisms.
- Phylogenetic systematics, or cladistics, is that branch of systematics concerned with inferring phylogeny.
- A tree like diagram that represents ancestor-descendant relationships is called a cladogram.

Phenetics	Cladistics
Phenetics uses overall similarity – all characters are used. Current state of characters is considered without assigning any polarity. Taxa may be grouped together by shared <i>ancestral</i> features (known as symplesiomorphies) as well as by shared derived character states (synapomorphies). An outgroup is not included in analysis.	Cladistic uses only phylogenetically informative characters. Primitive and derived characters states must be identified and assigned a polarity. Taxa may be grouped together by shared derived character states (synapomorphies) only. An outgroup must be included in the analysis



Thank you

