

MOLECULAR SYSTEMATICS

MBOTCC-6
Unit-III

M. Sc. Sem-II
(2018-20)

Molecular systematics signifies the use of molecular genetics to study the evolution of relationships among individuals and species. Organisms are classified on the basis of variations in protein and DNA. Molecular systematics uses variations in protein and DNA molecules to determine how similar or dissimilar sets of organisms are. These molecular differences provide a much more accurate taxonomic picture. The objective of this approach is to provide insight into the history of groups of organisms and the evolutionary processes that create diversity among species.

It came into play when genetic data could be used to separate groups of individuals or local populations belonging to one species that could not be distinguished by their extrinsic characters.

Molecular systematics requires phylogenetic analysis as a tool for evaluating phylogenetic relationships of living organisms. Suitable molecular markers are to be selected based on systematic questions.

Molecular phylogenetic analysis is done on the basis of desirable genetic markers.

DNA sequence divergence between various taxa needs to be estimated to determine their phylogenies. Elegant molecular methods are available for this purpose.

Character Each nucleotide position is a character and the actual nucleotide present

...Contd. p. 2

at a particular site is a character state. A character can be phylogenetically informative when nucleotide changes are shared by two or more taxa. A character can be phylogenetically uninformative when all nucleotides are the same among taxa, or when only a single taxon has a different nucleotide.

Restriction enzyme mapping is a less direct method of determining sequence divergence. These are enzymes that recognize specific sequences in the DNA and cut the DNA strands.

Restriction fragment pattern gives a restriction map of the stretch of DNA. The extent to which two restriction maps (or restriction fragment patterns) are similar serves as an estimator of sequence similarity or difference. DNA hybridization is another indirect way of obtaining estimates of DNA sequence divergence between two taxa.

In each of the above phenetic approaches, the data would be in the form of a single number indicating the similarity or difference between the DNAs of each pair of species studied.

Cladistic approaches include direct sequencing, restriction maps and restriction fragments. In each case, one would look for shared derived character states among taxa. With restriction sites, shared loss is unreliable as a uniting ~~nucleotide~~ character because the nucleotide change could have

occurred anywhere in the recognition sequence. !3!

Molecular approaches to systematics gives information about the rates of molecular evolution. If DNA or protein evolved at a constant rate in all species then one could use estimates of sequence divergence to build very reliable phylogenies.

If there was a molecular clock, we could determine the "true phylogeny". However, the fact is that there is no molecular clock. Nonetheless molecular tools have allowed major leaps in our understanding of biological diversity.

