

Molecular Phylogenetics – A tool for comparing genomes

NEHA SAWANT, POORVA GHOSH, B.A. AGLAVE AND M.O. LOKHANDE

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Molecular phylogenetics is a science that compares three or more genomes with each other and then is marked out to deduce the evolutionary relationship between them. Use of this science gives us gene true which is with different from species trees. The genome as are know is the entire DNA content of a all including all of the genes and all of the intergenes regions. These genomes evolve by gradual accumulation of mutations. The amount of nucleotide sequence difference between a pair of genomes should indicate how recently the 2 genomes shared a common ancestor. That is the fewer the difference the more recently the organisms have diverged and vice versa. Molecular phylogenetics predates DNA sequencing by several decades, derived from traditional method of classifying organisms according to there similarities and differences as practiced by Linnaeus in 18th century. But the data used was mainly on basis of morphological characters.

Molecular data was used quite early by the scientist Nuttall in 1904 by carrying out immunological tests to deduce relationships between varieties of organisms. And one of his objectives was to place humans in evolutionary position compared to other primates. Despite success his mark was net adopted until 1950 mainly due to technical limitation and also due to evolutionary changes in classification and phylogenetics too. These changes came to about with phentics and cladistics. There are two different methods but they place emphasis on the need for large datasets that can be analyzed by rigorous mathematical procedures. The difficulty in using these strenuous methods in morphological classification prompted a shift towards proteins and DNA which offer some advantages like.

- Many molecular characters can be stored at once
- These molecular characters are unambiguous and suitable compared to morphological ones.
- Molecular data are easily converted to numerical

form and hence as amenable to mathematical and statistical analysis.

Protein sequencing did not become routine until take 1960 and rapid DNA sequencing was not developed until ten years after that. Early studies therefore developed largely on indirect assessments of DNA or protein variations using one of the three methods.

Immunological data:

The data is obtained by studying the degree of cross reactivity of immunoglobulins and the proteins from different organisms.

Protein electrophoresis:

The similarity in electrophoresis properties of proteins is analyzed and data is obtained.

DNA- DNA Hybridization:

The data includes results of hybridization of DNA samples from the organisms being compared.

The objective of most phylogenetic studies is to reconstruct the tree like pattern that describes the evolutionary relationships between the organisms being studies the typical phylogenetic tree comprises of many basic terminologies which are sued in phylogenetic analysis external modes representing the genes that have been compared, whereas internal modes give the ancestral genes. The lengths of the branches indicate the degree of difference between the genes represented by the modes. The phylogenetic tree is also of two types one of which is unrooted and the other is rooted. The unrooted tree indicates the relationship between organisms being compared and does not tell us anything about the series of evolutionary events that led to these genes. However the rooted or inferred tree depicts the series of evolutionary events that are inferred from the data that were analyzed. The phylogenetic tree reconstruction involves following steps.

- Aligning the DNA sequences and obtaining comparative data.
- Conversion of comparative data into a reconstructed tree.
- Tests that are used to assign a degree of confidence to the tree as a whole and various segments within it.

Correspondence to:

B.A. AGLAVE, Department of Biotechnology, Institute of Life Sciences, H.P.T. Arts and R.Y.K. Science College, NASHIK (M.S.) INDIA

Authors' affiliations:

NEHA SAWANT, POORVA GOSH AND M.O. LOKHANDE, Department of Biotechnology, Institute of Life Sciences, H.P.T. Arts and R.Y.K. Science College, NASHIK (M.S.) INDIA