

Molecular Phylogenetics – A tool for comparing genomes

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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.

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– Using molecular to use to assign dates to branch points within the tree. Aligning the DNA sequences is the preliminary step towards construction of phylogenetic tree. Various methods are used for this purpose. Some of them are:

- DOT matrix method
- Similarity approach
- Distance method
- Multiple alignment.

Then this alignment data is converted into a phylogenetic tree. Various methods are used for the tree building purpose. This depends on the way in which multiple sequence alignment is converted into numerical data that can be analyzed mathematically in order to reconstruct the tree.

- Neighbor joining method
- Maximum parsimony method

Many other sophisticated methods are used for tree reconstruction. The reconstructed tree is then assessed for its accuracy because the tree is geometric rather than a numerical one. Molecular clocks enable the time of divergence of ancestral sequences to be estimated.

Molecular phylogenetics has evolved as an accurate and reliable method for evolutionary studies. Evolution gives the origin and development of life on earth and hence is an important aspect to be studied. Molecular phylogenetics has played an important role in understanding the evolution through the years as it uses the basic informative materials of life- DNA and proteins. There are various examples of use of phylogenetic trees.

DNA phylogenetics has clarified the evolutionary relationships between humans and other primates:

Knowing the evolutionary history of humans is one of the main objectives of phylogenetic trees. Using various techniques like DNA-DNA hybridization, restriction mapping and DNA sequencing, molecular data was obtained. This helped in comparisons of many different genes and to target these loci that are expected to show the greatest amount of dissimilarity. By 1997, 14 different molecular datasets had been obtained which enabled us to conclude with some conviction that the chimpanzee is the closest relative of humans and the gorilla is slightly more distant.

The oldest life on earth:

The planet was formed some 4 to 6 billion years ago and that by 3 – 5 billion years ago cellular life forms had appeared. The study of ancient microfossils has given the evidence of life 3-5 billion years ago. An attempt has been made to use molecular phylogenetics to date the

split between bacteria and archaea/eukaryotes but the result is not compatible with the existence of cyanobacteria microfossils from 3-5 billion years ago. For this purpose protein sequences were used instead of DNA sequences.

The origin of AIDS:

The global epidemics of AIDS has touched everyone's lives. AIDS is caused by human immunodeficiency virus 1 or HIV 1, a retrovirus that infects cells involved in the immune response. The starting point for this phylogenetic analysis is RNA extracted from virus particles, RT-PCR is therefore used to convert the RNA into a DNA copy and then to amplify the DNA so that sufficient amounts of nucleotides sequencing are obtained. This has helped in determining and understanding the origin of AIDS.

Problems with prions:

Prions are the proteinaceous infectious particles. More recently prions have come to the attention of a wider audience because they are the causative agents of neurological diseases such as Bovine Spongiform Encephalopathy (BSE) whose possible transmission to humans has caused great concerns in the UK and elsewhere. Using the sequence of prion genes of a phylogenetic tree can be constructed. The topology of such a tree gives much significant information about the evolution of humans.

Molecular phylogenetics is also used in intraspecific studies:

These studies use highly variable loci like multiallelic genes, microsatellite genes, mitochondrial DNA because they offer variability in various organisms. Hence molecular phylogenetics is useful in determining the origin of modern humans, patterns of more recent migrations and prehistoric human migrations in the new world.

Molecular phylogenetics has thus played an important role in determining the evolutionary history of the earth in recent times, as it uses the modern and reliable techniques for the same. Molecular phylogenetics has therefore grown in stature since the start of the 1990's, largely because of more rigorous methods for tree building, combined with the explosion of DNA sequence information obtained initially by PCR analysis and more recently by genome projects. The importance of molecular phylogenetics has also been enhanced by the successful application of tree reconstruction and other phylogenetic techniques to some of the more perplexing issues of biology.

