Research & Reviews: Journal of Ecology and Environmental Sciences e-ISSN: 2347-7830
p-ISSN: 2347-7822

The Tree of Life: Understanding Evolutionary Relationships through Phylogenetics

Stephen Twister*

Department of Ecology and Evolutionary Biology, University of California, Los Angeles, USA

Perspective

Received: 01-Jun-2022, Manuscript No. JEAES-22-64134; **Editor assigned:** 05- Jun-2022, Pre QC No. JEAES-22-64134 (PQ); **Reviewed:** 20- Jun-2022, QC No. JEAES-22-64134; **Revised:** 27-Jun-2022, Manuscript No. JEAES-22-64134 (A); **Published:** 04-Jul-2022, DOI: 10.4172/ 2347-7830.10.S2.005

***For Correspondence:** Stephen Twister, Department of Ecology and Evolutionary Biology, University of California, Los Angeles, USA

E-mail: step@medicine.edu

ABOUT THE STUDY

Phylogenetic is the study of evolutionary relationships among organisms, and it plays a crucial role in taxonomy, which is the science of classifying and naming organisms. By analysing the similarities and differences between various species, scientists can create a phylogenetic tree that shows the relationships between them. This tree is a visual representation of the evolutionary history of the species and is used to understand their genetic and morphological characteristics.

Molecular phylogeny is a more reliable basis for determining and analyzing phylogeny. By comparing the DNA or protein sequences of different organisms, we can identify the degree of similarity and difference between them. This method allows us to trace the evolutionary history of a species by analyzing its genetic material.

The use of molecular phylogeny has revolutionized the field of phylogenetics, providing a more accurate understanding of evolutionary relationships between organisms.

Phylogenetic can also be applied to linguistics. By analyzing the similarities and differences between languages, linguists can create a language family tree that shows the relationships between different languages. For example, the Indo-European language family includes languages such as English, French, German, and Hindi, which all share a common ancestor. The use of phylogenetic in linguistics allows us to understand the evolution of languages and the relationships between them.

The factors causing the trees demise are called Biotic and Abiotic. Abiotic factors include air pollution (acid rain) de-icing salt from roads, can be weather related floods and drought. Biotic factors are include pathogens, (any

e-ISSN: 2347-7830
p-ISSN: 2347-7822

microorganism bacterium or virus that causes disease) pandemics such as Dutch elm disease, Ash dieback, sudden oak death, fungi, insects and animals, especially humans.

From my point of view I would say that the greatest pathogen of them all is Honey fungus (Armillary mellea) it is the most common form of tree death I know of. I would go further and suggest that we called this fungus the" natural predator". It is truly awesome; it reproduces sexually through fruiting bodies releasing billions of basidiospores and more importantly asexually through rhizomorphs. Another common name for A. mellea is bootlace fungus; this refers to the rhizomorph simply because it looks like a black bootlace. A useful aid to identification, it is present all year round and is distinguished from all other fungi.

In the case of viruses, phylogenetic is a powerful tool for understanding their evolutionary history and the relationships between different strains. For example, the SARS-CoV-2 virus, which causes COVID-19, has been the subject of intense phylogenetic analysis since it first emerged in late 2019. A phylogenetic network of its genomes showed that these genomes are closely related and under evolutionary pressure. This information has been crucial in the development of vaccines and treatments for COVID-19.

Phylogenetic is essential in various fields including biology and virus research. By understanding the evolutionary relationships between different organisms, we can better understand their characteristics and behavior. This information is critical in the development of new drugs and treatments for diseases. In virus research, phylogenetic allows us to track the spread of viruses and understand their transmission patterns. By analyzing the genetic makeup of different strains, we can develop effective vaccines and treatments.

Phylogenetic analysis has also been used to understand the evolution of humans and our closest relatives, the great apes. By comparing the DNA sequences of humans and other primates, scientists have created a phylogenetic tree that shows the relationships between different species. This tree indicates that humans are more closely related to chimpanzees and bonobos than to gorillas or orangutans. This information has been crucial in our understanding of human evolution and the development of new treatments for diseases that affect humans and great apes.

In conclusion, phylogenetic is a powerful tool for understanding the evolutionary history of organisms and the relationships between them. By analyzing DNA sequences or morphological traits, scientists can create a phylogenetic tree that shows the evolutionary relationships between different species. This information is essential in the development of new drugs and treatments for diseases, as well as in virus research and linguistics. Phylogenetic analysis has revolutionized the field of biology and has provided us with a better understanding of the natural world.