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Plant Virus Diversity, Evolution and Epidemiology: A Mini Review

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Abstract

The goal of the field of phylogenetics has been to provide knowledge about the evolution of living organisms ever since Charles Darwin proposed that the "natural system" should be represented as a genealogical tree that will reflect the evolution of organisms and Haeckel created the first tree of life and coined the term "phylogeny." This objective has been the constant focus of Phylogenetics' development for more than a century. Early attempts to recreate trees relied on comparing phenotypes, notably morphological traits. It was suggested in 1904 that molecular data would offer a more mathematical method of determining the evolution of organisms than phenotypic traits.

Keywords: Evolution • Plant virus • Phylogeny

Introduction

The creation of effective methods for acquiring nucleic acid sequences made it possible to gather enough molecular information to infer phylogenetic trees, and the invention of computers made it possible to analyse this molecular information. The second was conceptual: The introduction of cladistics approaches, which are predicated on the notion that individuals within a group have an evolutionary history and are more closely connected to other individuals within that group than to any other organism. Cladistics, in contrast to earlier techniques, was overtly evolutionary and permitted the inference of ancestors' and descendents' character states. Moreover, this methodology not only was appropriate for describing relationships between organisms, but also to predict them, and therefore it could be used for hypothesis testing. Cladistics had a far-reaching impact of the field of phylogenetics, to such extent that today´s evolutionary biologists still utilize cladistics approaches.

The two main categories of cladistic approaches are character-based and distance-based. Using a computer to study systematic relationships, distance-based methods are likely the most established way. The foundation of distance-based phylogenetic reconstruction involves two phases. Secondly, the evolutionary distance—a measure of how much change has occurred along the evolutionary path that connects two taxa—is estimated for each pair of taxa. This distance is inversely correlated with the amount of substitutions between the daughter and parent sequences in nucleic acid or protein sequences. Then, using these estimates, a tree is inferred. Neighbor-Joining and Unweighted Pair Group Method with Arithmetic Mean (UPGMA) are the two most used distance-based techniques (NJ). Instead of converting character values into distance matrices, character-based approaches use actual characters (a nucleotide at each place). By reducing all sequence variation to a single number of evolutionary distances, this eliminates the loss of sequence information. The maximum likelihood (ML) and parsimony methods are the most often applied techniques of this kind. These approaches rely on the application of optimality criteria: for parsimony, this means limiting evolutionary change, and for ML, it means optimising a likelihood function that the modeller has established. Every input tree topology can be scored by explicitly establishing an objective function based on the optimality criterion. So, any two or more trees can be rated using the selected optimality criterion and this tree score enables for that.

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Literature Review

This study is to provide a concise summary of the contribution of Phylogenetics to our understanding of the interaction between the mechanisms that produce genetic variety and the forces of evolution that influence the genetic composition and dynamics of plant virus populations. The review is organised around three key areas that have benefited from phylogenetic inference development: Understanding the interactions between plant viral genetic variation and host defences, transmission method, and epidemiological dynamics, as well as the mechanisms and forces that influence the genetic variety of plant virus populations.

Plant virus taxonomy using phylogenetic

Early plant virus classifications were primarily the work of lone virologists. None of these initiatives were well-received by virologists. In order to create a single, accurate categorization of viruses, a group of 43 virologists from around the world founded the International Committee on Nomenclature of Viruses (ICNV) in 1966. They did this by commissioning host-specific working groups. In 1970, the ICNV published its first categorization of viruses, including plant viruses, establishing the characteristics of the viral particle as the most useful criteria for classifying viruses. This was the beginning of the field of virus taxonomy. The current name of the ICNV was adopted in 1974: International Committee on Taxonomy of Viruses (ICTV).

The ICTV therefore accepted a common definition of virus species as "a polythetic class of viruses that represents a reproducing lineage and occupies a particular ecological niche" as a result of which virus groups were reorganised into families and genera. Sequence data was still not widely available at this time, and phylogeny was only really used as a supplemental classification criterion for plant viruses. In fact, the taxonomy of viruses at this time had little to no implications for evolution or phylogeny.

It is possible for genotypes of the same or distinct virus species to recombine. Based on the idea that recombination events would cause topological changes in trees generated with alignments of the sequences at each side of the putative recombination break-point, early publications heavily utilised phylogenetic approaches to detect recombination. This is due to the fact that depending on the parental sequence on either side of the break-point, recombinants will occupy various positions in the tree. Recombination detection techniques have become more numerous and advanced over the past 20 years. Distance, phylogeny, compatibility, and distribution of substitutions methods have been generally categorised among these techniques, which are founded on various premises and employ various methodologies.

Discussion

In plant viruses with multipartite genomes, reassortment of genomic segments may also result in genetic exchange, which has a similar genetic and evolutionary impact as recombination strictly speaking. In fact, segment reassortment is also referred to as pseudorecombination by plant virologists. It is commonly accepted that evidence of pseudorecombination can be found inconsistencies in the topology of phylogenetic trees produced from various genomic regions. Using this technique, it has been demonstrated that intra-specific pseudorecombination influenced the evolution of the cucumber mosaic virus (CMV), the tomato rugose mosaic virus (EACMV), the pepGMV, and the PHYVV. The evolution of bipartite begomoviruses and the origin of the family Bromoviridae have both been linked to pseudorecombination at the inter-specific level, suggesting that pseudorecombination may control the speciation patterns of entire plant virus families.

Phylogenetic analysis and epidemiological data have demonstrated that pseudorecombination has a role in host adaptability and the emergence of disease outside of its effects on evolution.

A decrease in the genetic diversity of the newly born population and a strong geographical structure resulting from an increase in the genetic diversity between mother and daughter populations are the overall evolutionary effects of population bottlenecks that cause genetic drift. Genetic drift has been hypothesised as the cause of geographical structure in phylogenetic trees of TYLCV populations from the Mediterranean basin or American isolates of Sugarcane Yellow Leaf Virus and low genetic diversity in CMV populations from California or Wheat Yellow Mosaic Virus in China. If under differing selection pressures, selection, however, may also result in a loss in the variety of the daughter population and an increase in the diversity between populations. Phylogenies have not been widely employed to investigate the evolutionary repercussions of genetic drift in plant virus populations because it is difficult to tell if these effects are the result of selection or genetic drift.

In order to evaluate the severity and contributing factors of selection pressures on plant virus populations, phylogeny-based approaches have been frequently used. Plant viral genes are typically under significant negative selection, a characteristic that has been repeatedly noted in species-specific analyses, according to genome-wide assessments of dN/dS ratios in 38 plant virus species, including representatives of the largest families of plant viruses. The fact that many plant virus proteins have several functions necessitates a trade-off between them; the majority of mutations will negatively affect one or more of the protein's functions, while very few will enhance multiple functions or be helpful for one function while neutral for others.

Phylogeny-based investigations have revealed a substantial amount of diversity in selection pressures between plant viral protein-coding genes and between virus populations, despite the general finding of pervasive negative selection on plant virus protein-coding genes. In order to advance current understanding of key issues for pathology and evolutionary biology, such as the evolution of virulence, the creation of effective countermeasures, and the emergence of new diseases, phylodynamics unifies the interplaying epidemiological and evolutionary processes that drive pathogen spatiotemporal prevalence and phylogenetic patterns at various landscape scales. This section examines the role of phylodynamics in understanding the relationship between plant virus epidemiology and population evolution as well as the ecological factors that influence this interaction. Phylodynamics analyses of plant viruses have mainly concentrated on: I understanding when the current genetic diversity of plant virus populations was originated; (ii) examining how host defences and current disease control strategies affect virus evolution and epidemiology; (iii) identifying the origin and dispersion patterns of plant viruses at different landscape scales; and (iv) analysing the ecological factors shaping the evolution and epidemiology of plant virus [1-6].

Conclusion

Evolution of plant viruses: Multifactorial studies. Understanding the interactions between plant virus evolution, epidemiology, and ecology has benefited from advanced phylogenetic reconstruction techniques. Surprisingly, most investigations have concentrated on the impact of just one (or a small number) epidemiological or ecological characteristics on phylogenetic relationships. Yet, in nature, a variety of epidemiological and ecological characteristics combine to influence the evolution of plant viruses. Bayesian phylogenetic studies and generic linear model statistics have been integrated in recent approaches to account for the impact of many influences on the evolution of animal viruses. But until now, these techniques have only been used to study the factors that influence the emergence of the rabies virus.

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Conflict of Interest

There is no conflict of interest by author.

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