



The evolution of plant nuclear genes

Liang Chu*

*Corresponding author. E-mail: chuliang@zju.edu.cn

Department of Crop Science, Zhejiang University, Hangzhou, China

Received: 27-Jan-2022, Manuscript no: GJMEG-22-64875, **Editor assigned:** 31-Jan-2022, PreQC no: GJMEG-22-64875 (PQ), **Reviewed:** 10-Feb-2022, QC no GJMEG-22-64875, **Revised:** 23-Feb-2022, Manuscript no: GJMEG-22-64875 (R), **Published:** 01-Mar-2022, DOI: 10.15651/GJMEG.22.08.005

ABOUT THE STUDY

Most of the fluctuations in the rate of molecular evolution between seed plants are unexplored and remain unexplained. Although some attention has been paid to flowering plants, few reports have been made on the rate of molecular evolution of sister plant groups gymnosperms and differences in molecular evolution between seed plant groups have been tested in a phylogenetic framework increased. With the highly conserved morphology of gymnosperms and high macrosynteny at the genomic level, evidenced by similarities between extant species and fossil records, scientists believe that gymnosperms are slow-growing plants. However, some studies have provided contradictory results. Here we used 31,968 nucleotide sites derived from the orthologous gene from a wide range of taxonomic samples, including representatives of most conifers, cycads, ginkgo and many angiosperms with sequenced genomes.

Longer generation times and larger genome sizes are some of the factors explaining the slow rate of molecular evolution found in gymnosperms. In contrast to their slow molecular evolution, gymnosperms have higher substitution ratios than angiosperms. Finally, our study suggests that gymnosperms are larger and more efficient in purification and selection diversification than angiosperms, perhaps in relation to larger effective populations.

The rate of molecular evolution plays a central role in understanding many aspects of species biology. However, the causes of fluctuations in the rate of molecular evolution are not yet well understood, especially in plants. Here we show that height occupies about one-fifth of the dispersal of phylogenetic rates of chloroplasts and plant nuclear genomes.

This relationship applies to 138 flowering plants and explains species richness, UV exposure, latitude and changes in growth habits. Our observations can be explained by the relationship between size and plant genomic copy rate and we propose a mechanistic hypothesis to explain this, the "mitotic rate" hypothesis. This hypothesis could explain many different observations about the rate of molecular evolution throughout the tree of life. Our results have implications for understanding the evolutionary history and future of plant lineages in a changing world. Many factors have been proposed to control the rate of molecular evolution of plants, such as environmental energy, water availability, temperature, ultraviolet radiation, spacing rate, production time, metabolic rate, etc. The results of many studies are ambiguous or inconsistent and there is confusion about how some proposed mechanisms, especially the effects of generation time, work. Indeed, most of the differences in the rate of molecular evolution between plants remain unexplored and unexplained.

The molecular biology of plants has created a flood of data on genes and genomes. Evolutionary biology and taxonomy provide the context for integrating this information. This book summarizes contributions from evolutionary biologists, phylogenetic, developmental geneticists, biochemists and others working on different aspects of plant biology that touch on the molecular evolution of plants to varying degrees. The book is divided into three parts, the first part introducing a wide range of topics in evolutionary biology and summarizing the evolution of plant molecular phylogeny with an emphasis on model plant systems. The second segment shows a series of case studies on the evolution of gene families, and the third segment is the evolution of important plant processes such as disease resistance, root grain formation, hybridization, transposable elements and genomic evolution.