



Rapid Communication

Molecular Systematics in Plants: Tools and Approaches for Understanding Evolutionary Relationships

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ABSTRACT

Molecular systematics in plants uses DNA, RNA, and protein data to reconstruct evolutionary relationships and refine plant classification. Unlike traditional taxonomy, which relies primarily on morphology, molecular systematics provides precise genetic evidence to resolve ambiguous relationships, especially in groups influenced by convergent evolution, hybridization, or polyploidy. The development of molecular markers—such as chloroplast DNA regions, nuclear ribosomal ITS sequences, and single nucleotide polymorphisms (SNPs)—has greatly improved phylogenetic studies. Advanced sequencing technologies now allow whole-genome comparisons, enabling researchers to trace lineage divergence, identify cryptic species, and analyze evolutionary histories with high accuracy. Molecular systematics plays a central role in understanding plant biodiversity, biogeography, domestication, and conservation. By integrating molecular, morphological, and ecological data, modern plant systematics provides a comprehensive framework for resolving evolutionary patterns and supporting accurate taxonomic classification. This field continues to expand with improved analytical tools and growing genomic resources.

Keywords: Molecular Systematics, Plant Phylogeny, DNA Barcoding, Chloroplast DNA, ITS Sequences, Phylogenetics, Plant Evolution, Taxonomy, Molecular Markers, Genomics.

INTRODUCTION

Molecular systematics is a key discipline in plant biology that uses molecular data to understand evolutionary relationships and classify plant species. Traditional taxonomy relied heavily on morphology, but similar traits can arise independently through convergent evolution. Molecular evidence overcomes these limitations by providing direct insights into genetic divergence (Badr, 2008).

The rise of DNA sequencing revolutionized plant systematics. Early studies used chloroplast DNA, which evolves slowly and is maternally inherited in most plant species. Regions like *rbcL*, *matK*, and *trnL-F* remain widely used for reconstructing plant phylogenies at higher taxonomic levels. These sequences offer stable, informative markers for comparing distantly related lineages.

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Nuclear DNA markers also play a critical role. The Internal Transcribed Spacer (ITS) region is one of the most frequently used molecular markers in plant systematics due to its high variability. ITS sequences help resolve relationships among closely related species, providing finer taxonomic resolution than chloroplast markers (Soltis & Doyle, 2012).

Advancements in molecular techniques brought more sophisticated markers such as microsatellites, AFLPs, SNPs, and whole-genome data. These tools reveal genetic structure, hybridization patterns, and historical gene flow. They also help identify cryptic species that cannot be distinguished morphologically but differ genetically (Subbotin et al., 2013).

Plant evolution often involves hybridization and polyploidy, making systematics complex. Molecular tools are particularly valuable in detecting reticulate evolution, showing how genomes combine and diverge over time. Studies of allopolyploid species can differentiate parental lineages and reconstruct hybrid origins.

DNA barcoding has become a widely used approach in plant identification. Standard barcoding regions, such as *matK* and *rbcL*, provide universal genetic signatures that help botanists identify unknown plant samples. Barcoding is essential for biodiversity assessments, ecological studies, and authentication of medicinal plants (Xiao & De-yuan, 1997).

High-throughput sequencing technologies—such as next-generation sequencing (NGS), RAD-seq, and whole-genome sequencing—have transformed molecular systematics. These methods generate vast genomic datasets, allowing researchers to resolve deep evolutionary relationships and clarify taxonomic debates that previously seemed intractable.

Molecular systematics also contributes to understanding plant biogeography. Genetic data reveal how plant lineages migrated, adapted, and diversified across regions. Phylogeographic studies integrate molecular evidence with geological and climatic histories to explain plant distribution patterns.

Applications of molecular systematics extend to agriculture and conservation. Genomic tools help identify wild relatives of crops, trace domestication pathways, and guide breeding programs. Conservation biologists use molecular data to identify evolutionarily significant units and design strategies to preserve genetic diversity.

As molecular tools continue to advance, plant systematics becomes increasingly integrative, combining genetic, morphological, ecological, and biogeographic data. This holistic approach strengthens our understanding of plant evolution and enhances the accuracy of classification systems. Molecular systematics ultimately supports global efforts to document, protect, and utilize plant biodiversity (Hollingsworth et al., 1999).

CONCLUSION

Molecular systematics has transformed the study of plant evolution by providing precise genetic evidence to infer relationships that were previously obscured by morphological complexity. Through the use of chloroplast, nuclear, and genomic markers, researchers can clarify lineage divergence, detect hybridization, and understand the evolutionary history of plant species. The integration of advanced sequencing technologies and computational methods continues to refine phylogenetic frameworks and improve taxonomic accuracy. As global biodiversity faces increasing threats, molecular systematics plays a crucial role in plant conservation, breeding, and biological discovery. Its ongoing development will remain essential for advancing plant science and preserving the evolutionary heritage of plants worldwide.

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