

Plastid Phylogenomics and Species Discrimination: Exploring the Power of Genomic Data

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Abstract

Plastid phylogenomics has emerged as a powerful tool for studying evolutionary relationships and resolving taxonomic uncertainties in various organisms. Plastids, being semi-autonomous organelles with their own genomes, provide a wealth of genetic information that can be harnessed to elucidate phylogenetic relationships and discriminate between closely related species. This manuscript provides a comprehensive overview of the applications and advancements in plastid phylogenomics for species discrimination. We discuss the principles of plastid genome organization, the methodologies employed in plastid phylogenomics, and the significant contributions of plastid phylogenomics towards species discrimination. We also highlight the challenges and future prospects of this rapidly evolving field.

Keywords: Heterogeneity • Laminopathies • RNA Interpretation

Introduction

Plastid phylogenomics has revolutionized our understanding of evolutionary relationships and has become an indispensable tool in species discrimination. Plastids are essential organelles found in plants and algae that perform photosynthesis and play a crucial role in various metabolic processes. These semi-autonomous organelles possess their own genomes, known as plastid genomes, which exhibit unique features and evolutionary patterns. The advent of high-throughput sequencing technologies has facilitated the generation of complete plastid genome sequences, enabling researchers to exploit the vast amount of genetic information encoded within these genomes.

Species discrimination, the accurate identification and differentiation of closely related species, is a fundamental task in various scientific disciplines, including taxonomy, conservation biology, ecology, and forensics. Traditional methods of species discrimination often rely on morphological characteristics, which can be subjective, influenced by environmental factors, and challenging to assess in certain life stages or cryptic species [1]. Plastid phylogenomics offers a powerful alternative by harnessing the conserved and informative nature of plastid genomes to resolve taxonomic uncertainties and discriminate between species.

Literature Review

The organization of plastid genomes is remarkably conserved, typically exhibiting a circular structure with a highly conserved set of genes involved in photosynthesis, gene expression, and other plastid-specific functions. However, plastid genomes also possess unique features, such as variable genome size, gene order rearrangements, and the presence of non-coding regions with potential regulatory roles. These genomic variations provide valuable insights into evolutionary processes, speciation events, and ecological

adaptations. Methodologies in plastid phylogenomics have rapidly evolved, driven by advancements in sequencing technologies, bioinformatics tools, and analytical approaches. Sample collection and DNA extraction methods have been optimized to obtain high-quality plastid DNA, while next-generation sequencing platforms have enabled efficient and cost-effective sequencing of plastid genomes. Genome assembly and annotation pipelines have been developed, allowing for the accurate reconstruction of complete plastid genomes. Data analysis and phylogenetic inference methods have been refined to incorporate plastid genome data, leading to robust phylogenetic reconstructions and accurate species discrimination [2].

Plastid phylogenomics has contributed significantly to species discrimination by providing a comprehensive framework for resolving taxonomic uncertainties and elucidating evolutionary relationships. It has been employed in various studies across diverse taxonomic groups, including plants, algae, and certain groups of protists. By comparing plastid genomes among closely related species, researchers can identify species-specific genetic markers, detect cryptic species, determine hybridization events, and infer evolutionary histories. Furthermore, the integration of plastid phylogenomics with other data sources, such as nuclear markers and morphological data, has further enhanced the accuracy and resolution of species discrimination analyses.

Despite its numerous advantages, plastid phylogenomics does present challenges and limitations. Incomplete or poorly annotated plastid genomes, limited taxonomic sampling, and the potential for hybridization and introgression events can affect the accuracy of species discrimination. Furthermore, certain evolutionary phenomena, such as convergence and long branch attraction, require careful consideration to avoid misleading interpretations. Looking ahead, there are promising avenues for future research in plastid phylogenomics [3]. Improving plastid genome assembly and annotation methods, integrating multi-locus approaches, exploring advancements in sequencing technologies, and applying plastid phylogenomics to conservation and forensic applications are areas of active investigation. These efforts aim to enhance the reliability and applicability of plastid phylogenomics for species discrimination, further expanding its potential in addressing taxonomic challenges and contributing to our understanding of biodiversity.

Discussion

Plastid genomes exhibit a remarkable level of conservation in their organization across a wide range of photosynthetic organisms, including plants and algae. The organization of plastid genomes is typically circular, but exceptions such as linear and multipartite genomes exist in certain algal groups. Plastid genomes are relatively small compared to nuclear genomes,

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ranging from around 100 kilobases to several hundred kilobases in size. Despite their compact size, plastid genomes encode a substantial number of genes, which are primarily involved in photosynthesis, gene expression, and plastid-specific functions.

The gene content of plastid genomes is highly conserved, with a core set of genes shared among different species. These genes include those encoding components of the photosynthetic machinery, such as the photosystem I and II complexes, cytochrome b6f complex, and ATP synthase. Plastid genomes also harbor genes responsible for plastid gene expression, including RNA polymerase subunits, ribosomal proteins, and transfer RNA (tRNA) genes. The presence of tRNA genes is particularly important for translation within the plastid compartment.

In addition to protein-coding genes, plastid genomes contain non-coding regions, including intergenic spacers and introns. Intergenic spacers are regions of non-coding DNA that separate genes and often harbor regulatory elements that influence gene expression. Introns, which are less common in plastid genomes compared to nuclear genomes, are sequences within genes that are transcribed but are later removed during RNA processing [4]. Introns in plastid genomes often contain tRNA or ribozyme sequences. Plastid genomes exhibit a high degree of conservation in terms of gene order and orientation within a particular taxonomic group, reflecting their shared evolutionary history. However, rearrangements in gene order and orientation do occur, especially among distantly related taxa. These rearrangements can provide valuable insights into evolutionary processes, such as genomic rearrangements associated with speciation events or adaptive evolution.

The overall structure and organization of plastid genomes are governed by a combination of evolutionary forces, including selection, genetic drift, and recombination events. The conservation of plastid genome organization is thought to be driven by functional constraints related to the coordination of gene expression and the maintenance of efficient photosynthetic processes [5]. Advancements in sequencing technologies have enabled the generation of complete plastid genome sequences with high accuracy and coverage. As a result, the field of plastid genomics has seen a rapid increase in the availability of plastid genome data, facilitating comparative analyses and phylogenetic investigations across diverse taxa.

Conclusion

The organization of plastid genomes exhibits a high level of conservation across photosynthetic organisms. Plastid genomes consist of a circular structure with a core set of genes involved in photosynthesis and gene expression. Non-coding regions, such as intergenic spacers and introns, contribute to regulatory functions. The study of plastid genome organization has

provided valuable insights into evolutionary processes, species relationships, and functional adaptations. With advancements in sequencing technologies, plastid genomics has become an indispensable tool for understanding plant and algal evolution. Further exploration of plastid genome organization will continue to enhance our understanding of the complex dynamics within plastids and their evolutionary significance.

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Conflict of Interest

There are no conflicts of interest by authors.

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