Comparative Analysis of Cuscuta Chloroplast Genomes for Developing Reliable Genetic Markers for Species Classification

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The genus Cuscuta (dodders) comprises parasitic plants with significant ecological and agricultural impacts, characterized by diverse host specificity that suggests rapid evolution. This interesting aspect of Cuscuta biology presents both a challenge for species classification and an opportunity to study adaptive mechanisms in plant parasitism. Species identification within this genus is challenging due to morphological similarities and complex parasitic lifestyles. This study aimed to develop reliable genetic markers for Cuscuta species identification using chloroplast (CP) genome analysis. High-throughput sequencing was employed to obtain complete CP genomes of several Cuscuta species. Comparative genomic analyses identified conserved regions and unique genetic variations among the species. Phylogenetic analyses using these genetic markers assessed evolutionary relationships within the genus. Potential markers for species identification were validated through PCR amplification and sequencing. The study successfully identified reliable genetic markers from Cuscuta CP genomes, enabling precise species classification. These markers not only serve as valuable tools for taxonomic studies and management strategies targeting Cuscuta infestations but also provide insights into the rapid evolution of Cuscuta species in relation to host specificity. This research contributes to our understanding of the adaptive mechanisms that allow Cuscuta to quickly evolve and exploit diverse host plants, offering new perspectives on plant-parasite coevolution and potential avenues for controlling these agricultural pests.