

Comparison of the Chloroplast Genomes and Phylogenomic Analysis of Elaeocarpaceae

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Abstract

Species of Elaeocarpaceae vary, but complete chloroplast genome data and systematic comparisons across the family are rarely reported. To understand the variation in chloroplast sequence size and structure in Elaeocarpaceae, the chloroplast genomes of 9 species were sequenced using the Illumina HiSeq 2000 platform and further assembled and annotated with *Elaeocarpus japonicus* and *Sloanea sinensis* (family Elaeocarpaceae) as references. A phylogenomic tree was constructed based on the complete chloroplast genomes of the 11 species representing 5 genera of Elaeocarpaceae. Chloroplast genome characteristics were examined by using Circoletto and IRscope software. The results revealed the following: (a) The 11 sequenced chloroplast genomes ranged in size from 157,546 bp to 159,400 bp. (b) The chloroplast genomes of *Elaeocarpus*, *Sloanea*, *Crinodendron* and *Vallea* lacked the *rpl32* gene in the small single-copy (SSC) region. The large single-copy (LSC) region of the chloroplast genomes lacked the *ndhK* gene in *Elaeocarpus*, *Vallea stipularis*, and *Aristotelia fruticosa*. The LSC region of the chloroplast genomes lacked the *infA* gene in *Elaeocarpus* and *Crinodendron patagua*. (c) Through inverted repeat (IR) expansion and contraction analysis, a significant difference was found between the LSC/IRB and IRA/LSC boundaries among these species. *Rps3* was detected in the neighboring regions of the LSC and IRb regions in *Elaeocarpus*. (d) Phylogenomic analysis revealed that the genus *Elaeocarpus* is closely related to *Crinodendron patagua* on an independent branch and *Aristotelia fruticosa* is closely related to *Vallea stipularis*, forming a clade with the genus *Sloanea*. Structural comparisons showed that Elaeocarpaceae diverged at 60 Mya, the genus *Elaeocarpus* diverged 53 Mya and that the genus *Sloanea* diverged 0.44 Mya. These results provide new insight into the evolution of the Elaeocarpaceae.

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