

Exploring the limits for reduction of plastid genomes: A case study of the mycoheterotrophic orchids *Epipogium aphyllum* and *Epipogium roseum*

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Abstract

© The Author(s) 2015. The question on the patterns and limits of reduction of plastid genomes in nonphotosynthetic plants and the reasons of their conservation is one of the intriguing topics in plant genome evolution. Here, we report sequencing and analysis of plastid genome in nonphotosynthetic orchids *Epipogium aphyllum* and *Epipogium roseum*, which, with sizes of 31 and 19 kbp, respectively, represent the smallest plastid genomes characterized by now. Besides drastic reduction, which is expected, we found several unusual features of these "minimal" plastomes: Multiple rearrangements, highly biased nucleotide composition, and unprecedentedly high substitution rate. Only 27 and 29 genes remained intact in the plastomes of *E. aphyllum* and *E. roseum*-those encoding ribosomal components, transfer RNAs, and three additional housekeeping genes (*infA*, *clpP*, and *accD*). We found no signs of relaxed selection acting on these genes. We hypothesize that the main reason for retention of plastid genomes in *Epipogium* is the necessity to translate messenger RNAs (mRNAs) of *accD* and/or *clpP* proteins which are essential for cell metabolism. However, these genes are absent in plastomes of several plant species; their absence is compensated by the presence of a functional copy arisen by gene transfer from plastid to the nuclear genome. This suggests that there is no single set of plastid-encoded essential genes, but rather different sets for different species and that the retention of a gene in the plastome depends on the interaction between the nucleus and plastids.

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Keywords

Gene loss, Genome reduction, Nonphotosynthetic plants, Orchids, Plastid genome