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Title: Complete sequences of organelle genomes from the medicinal plant *Rhazya stricta* (Apocynaceae) and contrasting patterns of mitochondrial genome evolution across asterids

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Abstract: Background: *Rhazya stricta* is native to arid regions in South Asia and the Middle East and is used extensively in folk medicine to treat a wide range of diseases. In addition to generating genomic resources for this medicinally important plant, analyses of the complete plastid and mitochondrial genomes and a nuclear transcriptome from *Rhazya* provide insights into inter-compartmental transfers between genomes and the patterns of evolution among eight asterid mitochondrial genomes.

Results: The 154,841 bp plastid genome is highly conserved with gene content and order identical to the ancestral organization of angiosperms. The 548,608 bp mitochondrial genome exhibits a number of phenomena including the presence of recombinogenic repeats that generate a multipartite organization, transferred DNA from the plastid and nuclear genomes, and bidirectional DNA transfers between the mitochondrion and the nucleus. The mitochondrial genes *sdh3* and *rps14* have been transferred to the nucleus and have acquired targeting presequences. In the case of *rps14*, two copies are present in the nucleus; only one has a mitochondrial targeting presequence and may be functional. Phylogenetic analyses of both nuclear and mitochondrial copies of *rps14* across angiosperms suggests *Rhazya* has experienced a single transfer of this gene to the nucleus, followed by a duplication event. Furthermore, the phylogenetic distribution of gene losses and the high level of sequence divergence in targeting presequences suggest multiple, independent transfers of both *sdh3* and *rps14* across asterids. Comparative analyses of mitochondrial genomes of eight sequenced asterids indicates a complicated evolutionary history in this large angiosperm clade with considerable diversity in genome organization and size, repeat, gene and intron content, and amount of foreign DNA from the plastid and nuclear genomes.

Conclusions: Organelle genomes of *Rhazya stricta* provide valuable information for improving the understanding of mitochondrial genome evolution among angiosperms. The genomic data have enabled a rigorous examination of the gene transfer events. *Rhazya* is unique among the eight sequenced asterids in the types of events that have shaped the evolution of its mitochondrial genome. Furthermore, the organelle genomes of *R. stricta* provide valuable genomic resources for utilizing this important medicinal plant in biotechnology applications.

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