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Title: Evolutionary and biotechnology implications of plastid genome variation in the inverted-repeat-lacking clade of legumes
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Abstract: Land plant plastid genomes (plastomes) provide a tractable model for evolutionary study in that they are relatively compact and gene dense. Among the groups that display an appropriate level of variation for structural features, the inverted-repeat-lacking clade (IRLC) of papilionoid legumes presents the potential to advance general understanding of the mechanisms of genomic evolution. Here, are presented six complete plastome sequences from economically important species of the IRLC, a lineage previously represented by only five completed plastomes. A number of characters are compared across the IRLC including gene retention and divergence, syteny, repeat structure and functional gene transfer to the nucleus. The loss of clpP intron 2 was identified in one newly sequenced member of IRLC, *Glycyrrhiza glabra*. Using deeply sequenced nuclear transcriptomes from two species helped clarify the nature of the functional transfer of accD to the nucleus in *Trifolium*, which likely occurred in the lineage leading to subgenus *Trifolium*. Legumes are second only to cereal crops in agricultural importance based on area harvested and total production. Genetic improvement via plastid transformation of IRLC crop species is an appealing proposition. Comparative analyses of intergenic spacer regions emphasize the need for complete genome sequences for developing transformation vectors for plastid genetic engineering of legume crops.

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