

Plastid genome evolution across the genus *Cuscuta* (Convolvulaceae): two clades within subgenus *Grammica* exhibit extensive gene loss. *Thomas Braukmann, Maria Kuzmina, and Saša Stefanović*

SUPPLEMENTARY DATA

Table S1. *Cuscuta* and its autotrophic outgroups from Convolvulaceae surveyed for the presence/absence of 48 plastid protein coding genes. Plastid small (16S) and large (23S) ribosomal subunits were used as positive controls for presence of plastid DNA. To verify the presence of organellar DNA on the blots, mitochondrial *atp1* was used as additional positive control. Linear arrangement of species follows their presumptive phylogenetic relationships derived from García and Martín (2007), McNeal et al. (2007b), Stefanović et al. (2007) and Stefanović et al. (unpublished data). Based on slot-blot results, a “++” symbol indicates presence of full hybridization, “+” diminished hybridization, “—” absence of hybridization signal in comparison to positive controls, and “?” unable to score. Those species selected as representatives of all clades within *Cuscuta* for Fig. 1 are shown here in boldface, and species with sequenced plastomes (Funk et al., 2007; McNeal et al., 2007a) are underlined. Abbreviations of herbaria follow Index Herbarium.

