

SUPPLEMENTAL FIG. 1. One of 553 most parsimonious trees generated from nuclear monophyly of *Descurainia*. Branch lengths are indicated above branches; bootstrap values > 50%/Bayesian posterior probabilities are below branches. Dashed lines indicate branches that collapse in the strict consensus tree. Species marked with an * belong to the subtribe Descurainiinae as circumscribed by Schulz (1924); tribal classifications on the right-hand side are those proposed by Al-Shehbaz et al. 2006.

SUPPLEMENTAL FIG. 2. One of 8734 most parsimonious trees derived from cpDNA *trnL* data to assess the monophyly of *Descurainia*. Branch lengths are indicated above branches; bootstrap values >50%/Bayesian posterior probabilities are below branches. Dashed lines indicate branches that collapse in the strict consensus tree. Species marked with an * belong to the subtribe Descurainiinae as circumscribed by Schulz (1924); tribal classifications on the right-hand side are those proposed by Al-Shehbaz et al. 2006.