Supporting Information

Park and Potter 10.1073/pnas.1309948110

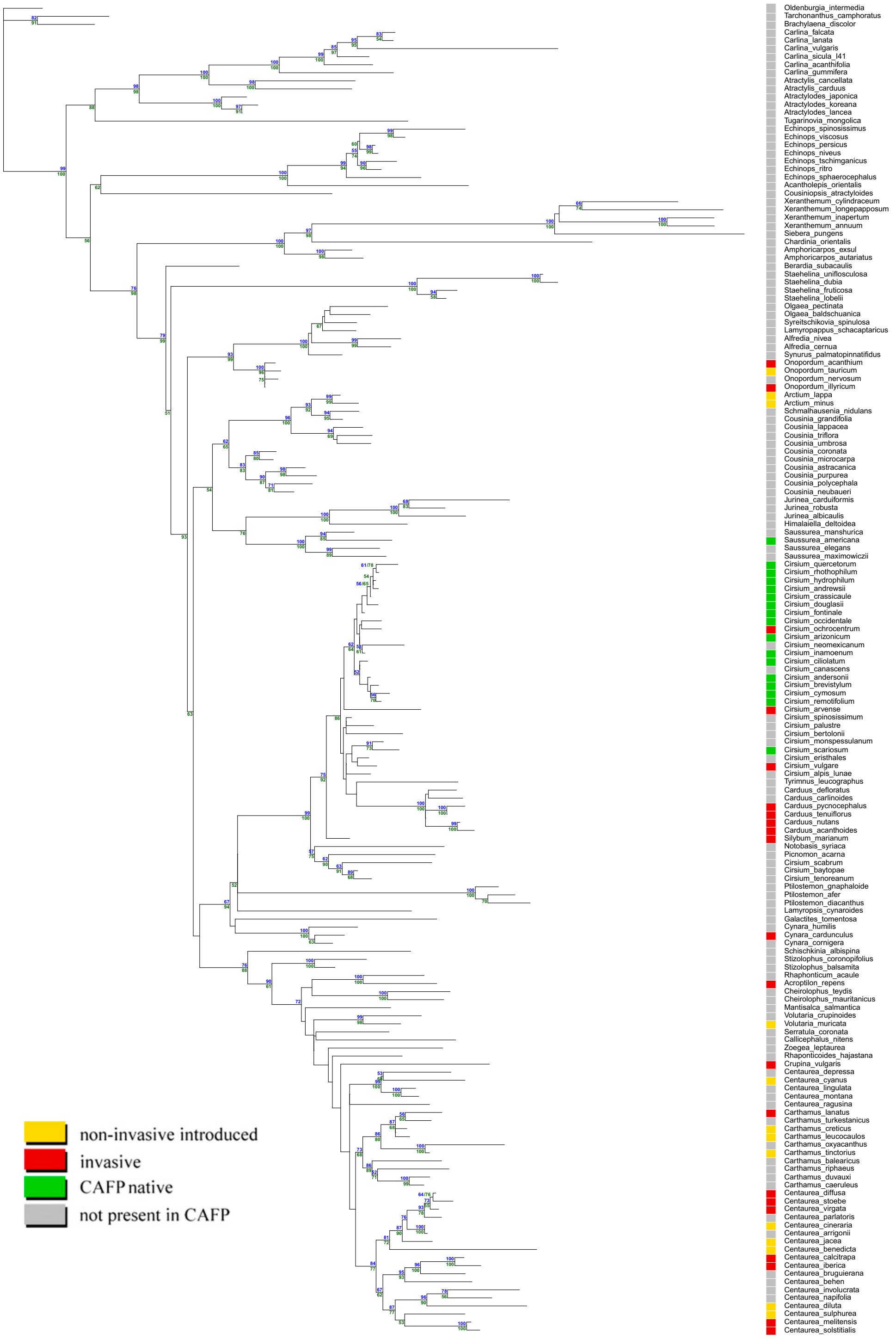

Fig. S1. Maximum likelihood tree of Cardueae based on sequences of and internal transcribed spacer (ITS), maturase K (matK), and intergenic spacer between *trnL* and *trnF* (*trnL-trnF* IGS; −ln L = −25,773.30). The tree was generated in Garli 2.0 (1). Blue numbers above branches indicate parsimony bootstrap support and green numbers below indicate maximum likelihood bootstrap support. The bootstrap analyses were run in PAUP (2) and Garli 2.0 (1), respectively, with 1,000 bootstrap replicates, using heuristic searches with 100 random addition sequence replicates per bootstrap replicate, and tree-bisection-reconnection

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(TBR) branch-swapping in the case of parsimony. The maximum llikelihood bootstrap analysis was run using the same parameters as for the original search outlined in *Methods*. Bootstrap values <50% are not shown. Tips represent species, which are color coded according to their invasive status.

1. Zwickl DJ (2006) Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. PhD dissertation (University of Texas at Austin, Austin, TX).
2. Swofford DL (2003) PAUP*: phylogenetic analysis using parsimony, version 4.0b10 (Sinauer Associates, Sunderland, MA).

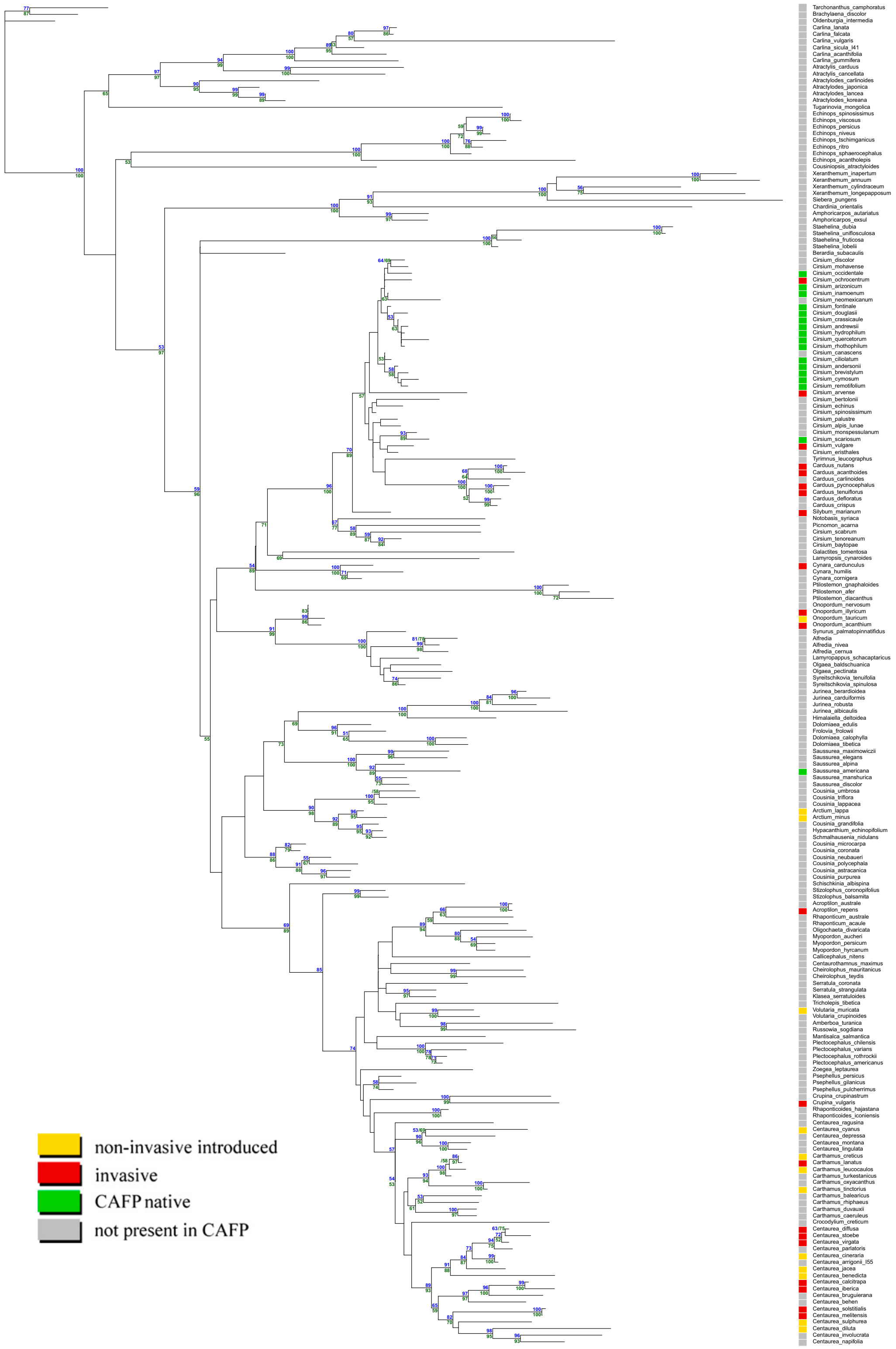

Fig. S2. Maximum likelihood tree of Cardueae based on sequences of ITS and *trnF* IGS (−ln L = −22,558.83). The tree was generated in Garli 2.0 (1). Blue numbers above branches indicate parsimony bootstrap support and green numbers below indicate maximum likelihood bootstrap support. The bootstrap analyses were run in PAUP (2) and Garli 2.0 (1), respectively, with 1,000 bootstrap replicates, using heuristic searches with 100 random addition sequence replicates per bootstrap replicate, and TBR branch-swapping in the case of parsimony. The maximum likelihood bootstrap analysis was run using the same parameters as for the original search outlined in *Methods*. Bootstrap values <50% are not shown. Tips represent species, which are color coded according to their invasive status.

1. Zwickl DJ (2006) Genetic algorithm approaches for the phylogenetic analysis of large biological sequence datasets under the maximum likelihood criterion. PhD dissertation (University of Texas at Austin, Austin, TX).
2. Swofford DL (2003) PAUP*: phylogenetic analysis using parsimony, version 4.0b10 (Sinauer Associates, Sunderland, MA).

Other Supporting Information Files

Table S1 (DOCX)
Table S2 (DOCX)
Table S3 (DOCX)