

TAXON

International Journal of Taxonomy, Phylogeny and Evolution

Electronic Supplement to

Relationships among wild relatives of the tomato, potato, and pepino

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Taxon 65: 262–276

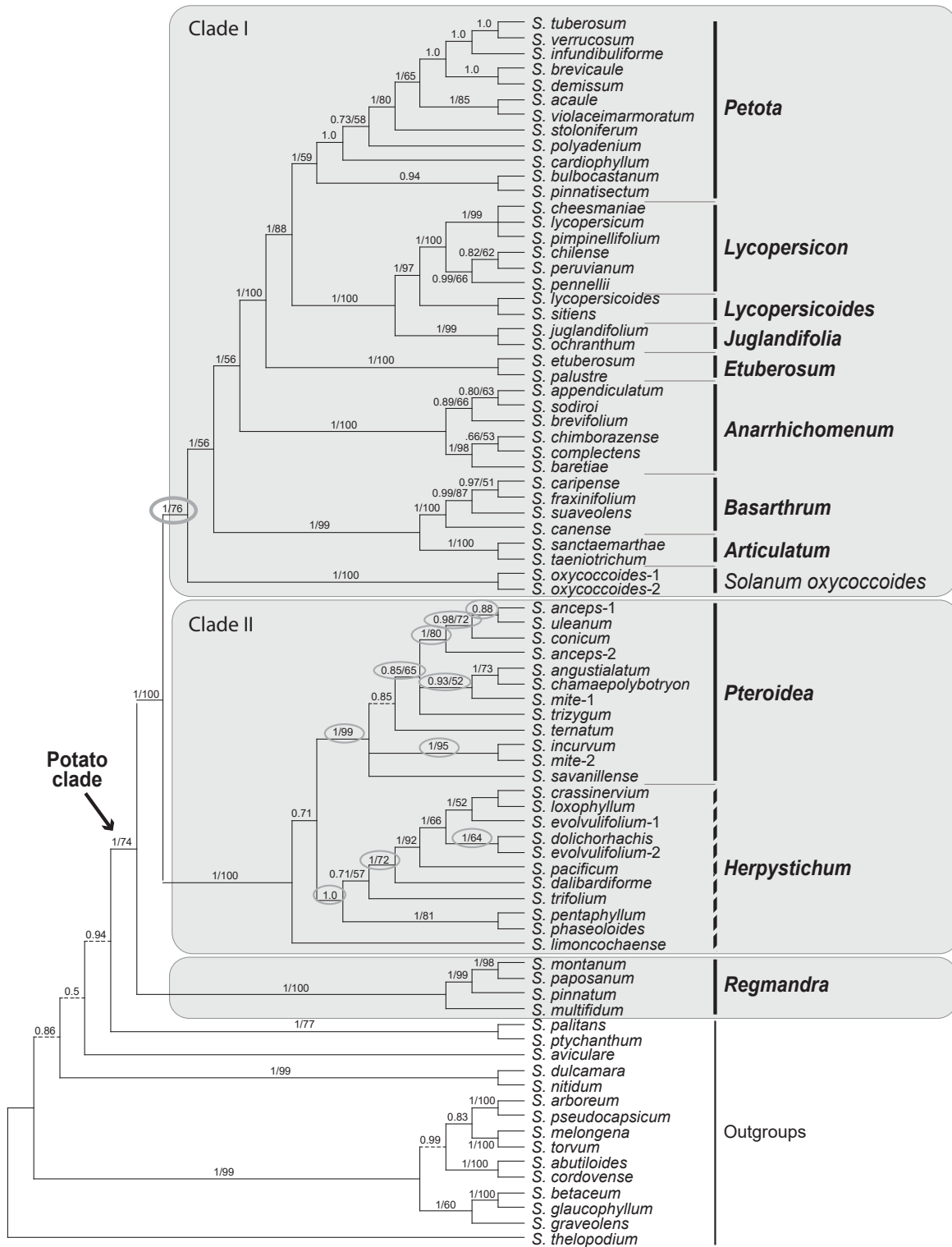


Fig. S1. The 50% majority-rule, post burn-in tree from Bayesian analysis of concatenated nuclear ITS and GBSSI (*waxy*) data. Branches not present in the MP strict consensus tree are indicated by dashed lines. Branch support values are Bayesian posterior probabilities >0.5/maximum parsimony bootstrap >50. Nodes that are in conflict with the chloroplast tree in Fig. S2 are circled, and bold circle indicates node that influences relationships among the lineages addressed in this study. Major lineages of the Potato clade are indicated by the gray boxes. Sections of *Solanum* are indicated on the right; the diagonally hatched bar indicates that section *Herpystichum* is paraphyletic on this tree.

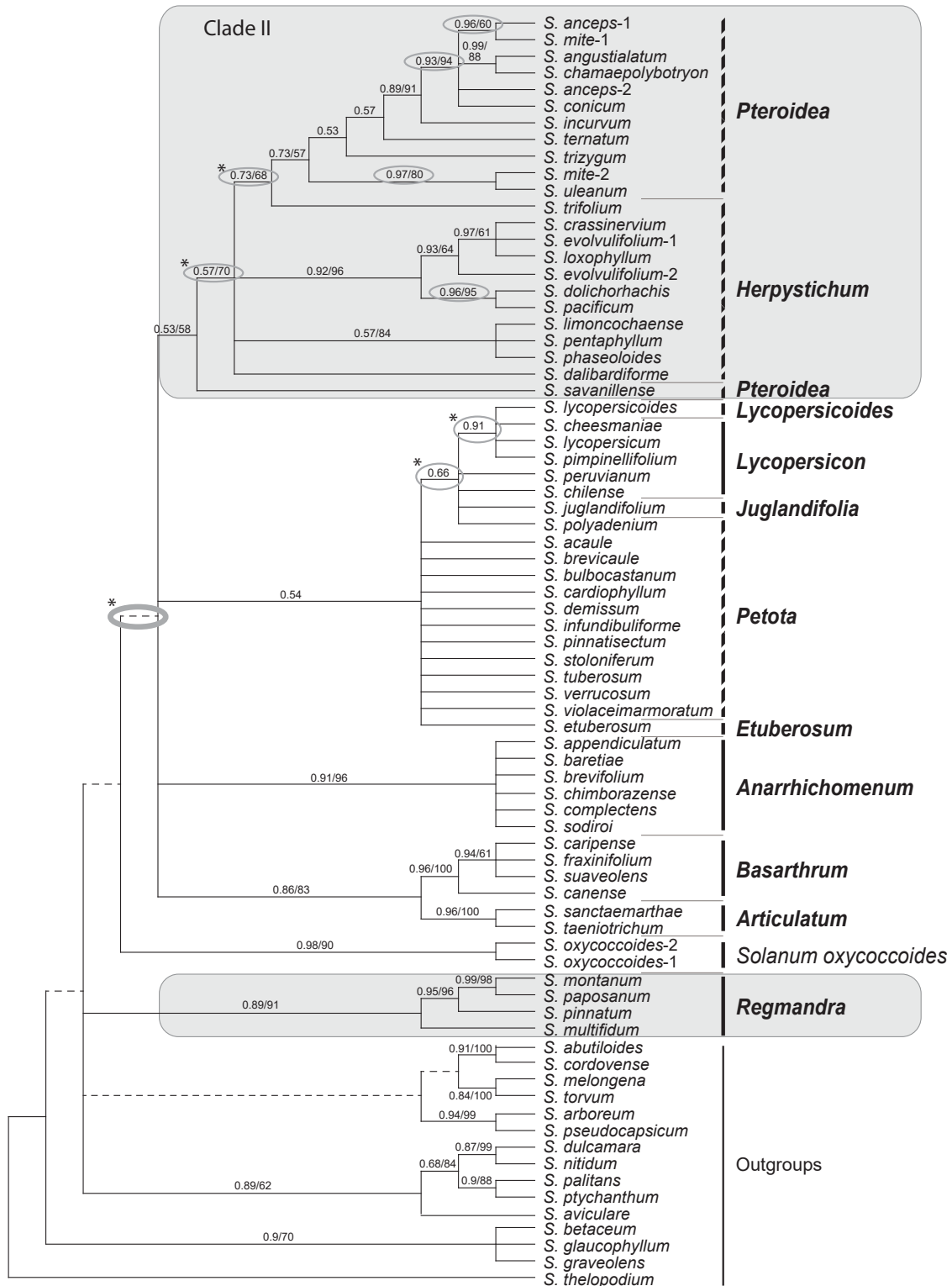


Fig. S2. The 50% majority-rule tree from maximum parsimony analysis of concatenated sequences of the chloroplast markers *trnT-trnF* and *trnS-trnG* from species of the Potato clade. The MP tree is presented here because it had greater resolution than the BI tree. Branches not present in the 50% majority-rule BI tree are indicated by dashed lines. Nodes that are in conflict with the nuclear tree in Fig. S1 are circled. Asterisks (*) identify nodes that are incongruent with the topology in Fig. 2, and bold circle indicates node that influences relationships among the lineages addressed in this study. Branch support values are Bayesian posterior probabilities >0.5/maximum parsimony bootstrap >50. Major lineages of the Potato clade are indicated by the gray boxes; Clade I is not monophyletic in this tree and is not boxed. Sections of *Solanum* are indicated on the right; diagonally hatched bars indicate sections that are not resolved as monophyletic on this tree (excluding unresolved clades).

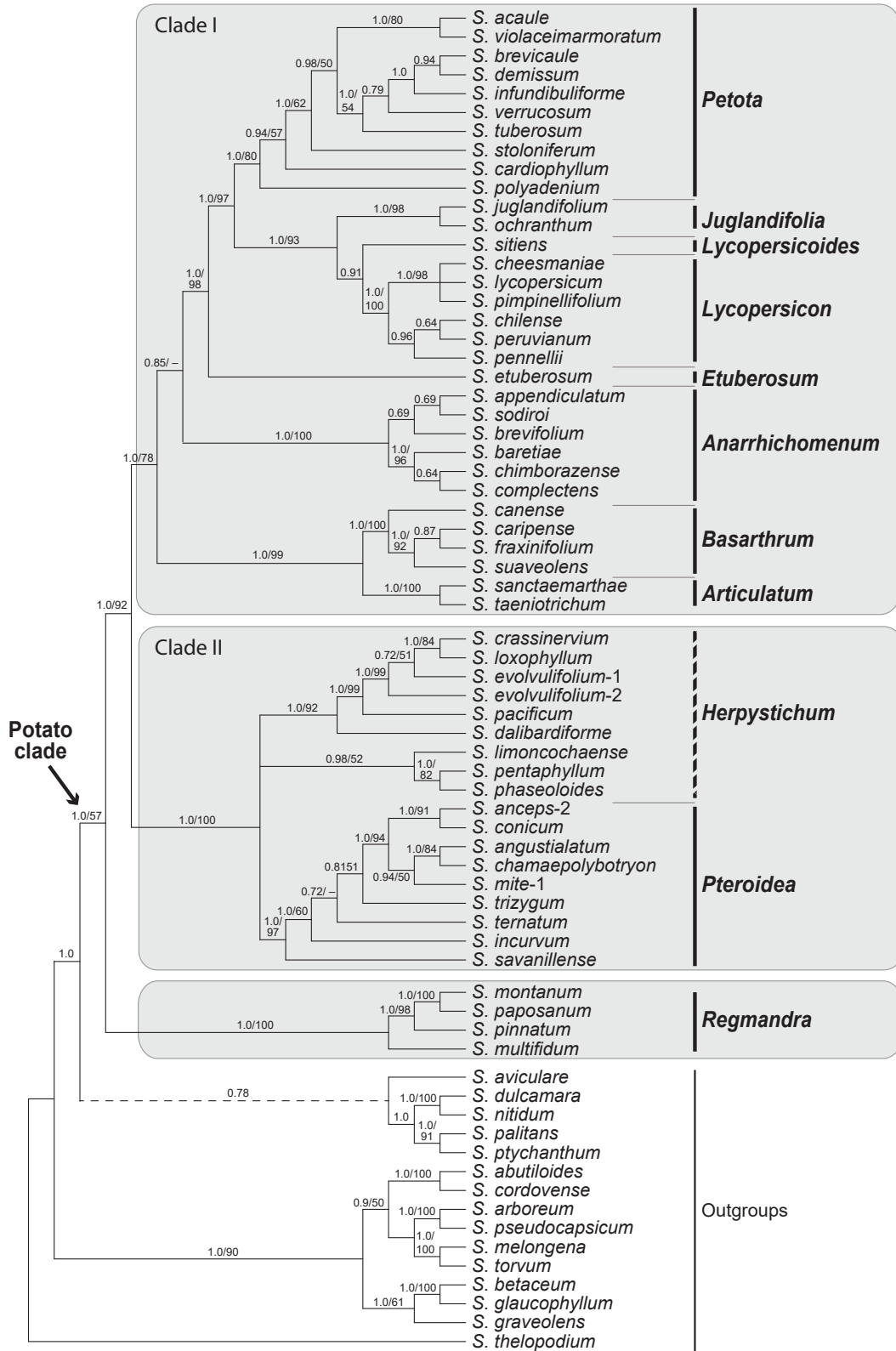


Fig. S3. The 50% majority-rule, post burn-in tree from Bayesian analysis of the combined *trnS-trnG*, *trnT-trnF*, GBSSI (*waxy*), and ITS data with eight accessions of ten species causing conflict between nuclear and plastid data (highlighted in Figs. S1 and S2) removed from the data matrix. Branches not present in the MP strict consensus tree are indicated by dashed lines. Branch support values are Bayesian posterior probabilities >0.5/maximum parsimony bootstrap >50. The three major lineages of the Potato clade are indicated by the gray boxes. Sections of *Solanum* are indicated on the right; the diagonally hatched bar indicates that sect. *Herpystichum* is not monophyletic on this tree.

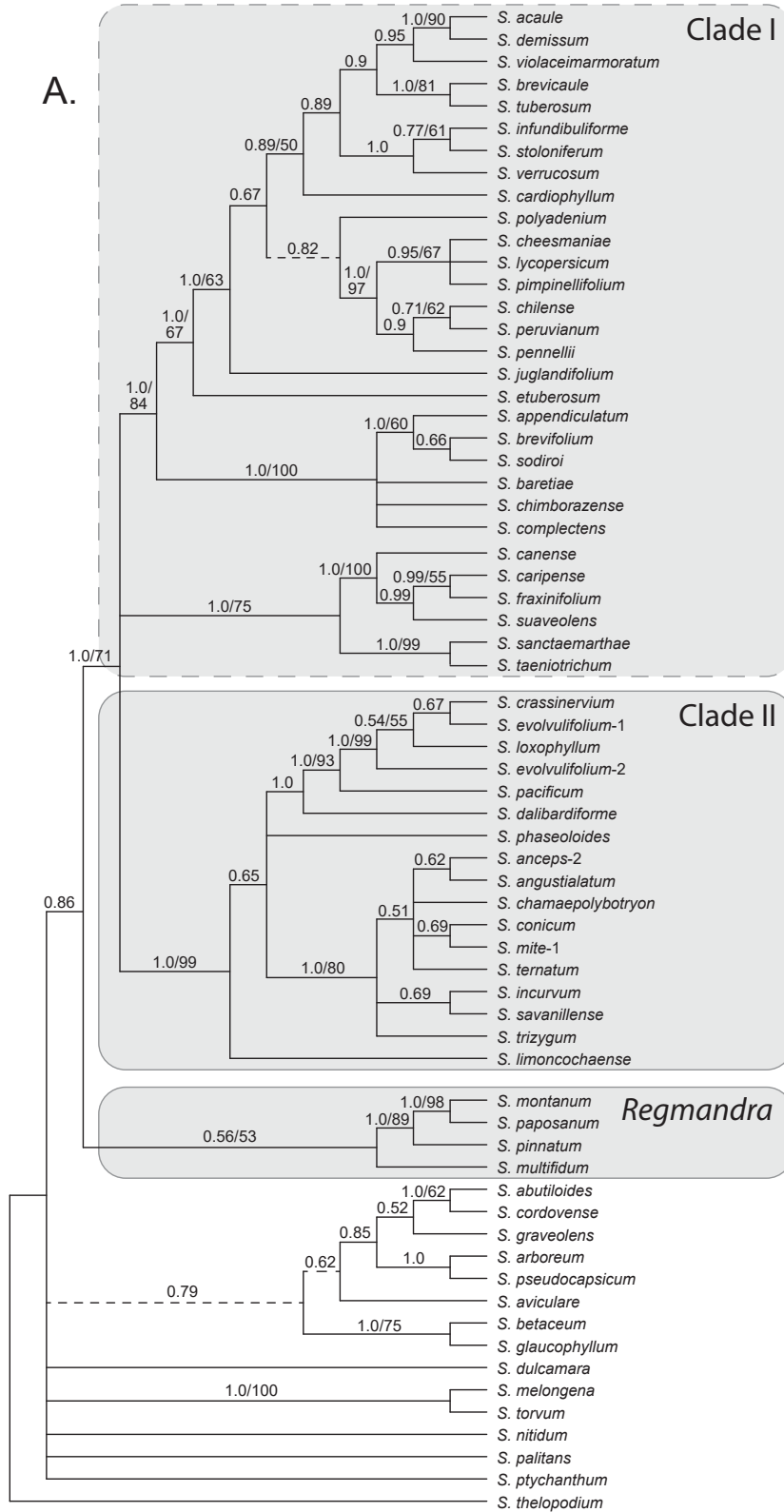


Fig. S4. The 50% majority-rule, post burn-in trees from Bayesian analysis of **A**, nuclear ribosomal ITS and **B**, GBSSI (*waxy*) sequences with eleven accessions of ten species causing conflict between nuclear and plastid data (highlighted in Figs. S1 and S2) removed from the data matrix. Branches not present in the MP strict consensus tree are indicated by dashed lines. Branch support values are Bayesian posterior probabilities >0.5/maximum parsimony bootstrap >50. The three major lineages of the Potato clade are indicated by the gray boxes. The dashed line around the gray box in A indicates that the clade is not monophyletic in this analysis. Sections of *Solanum* are indicated on the right; the diagonally hatched bar indicates that sect. *Herpystichum* is not monophyletic on this tree.

