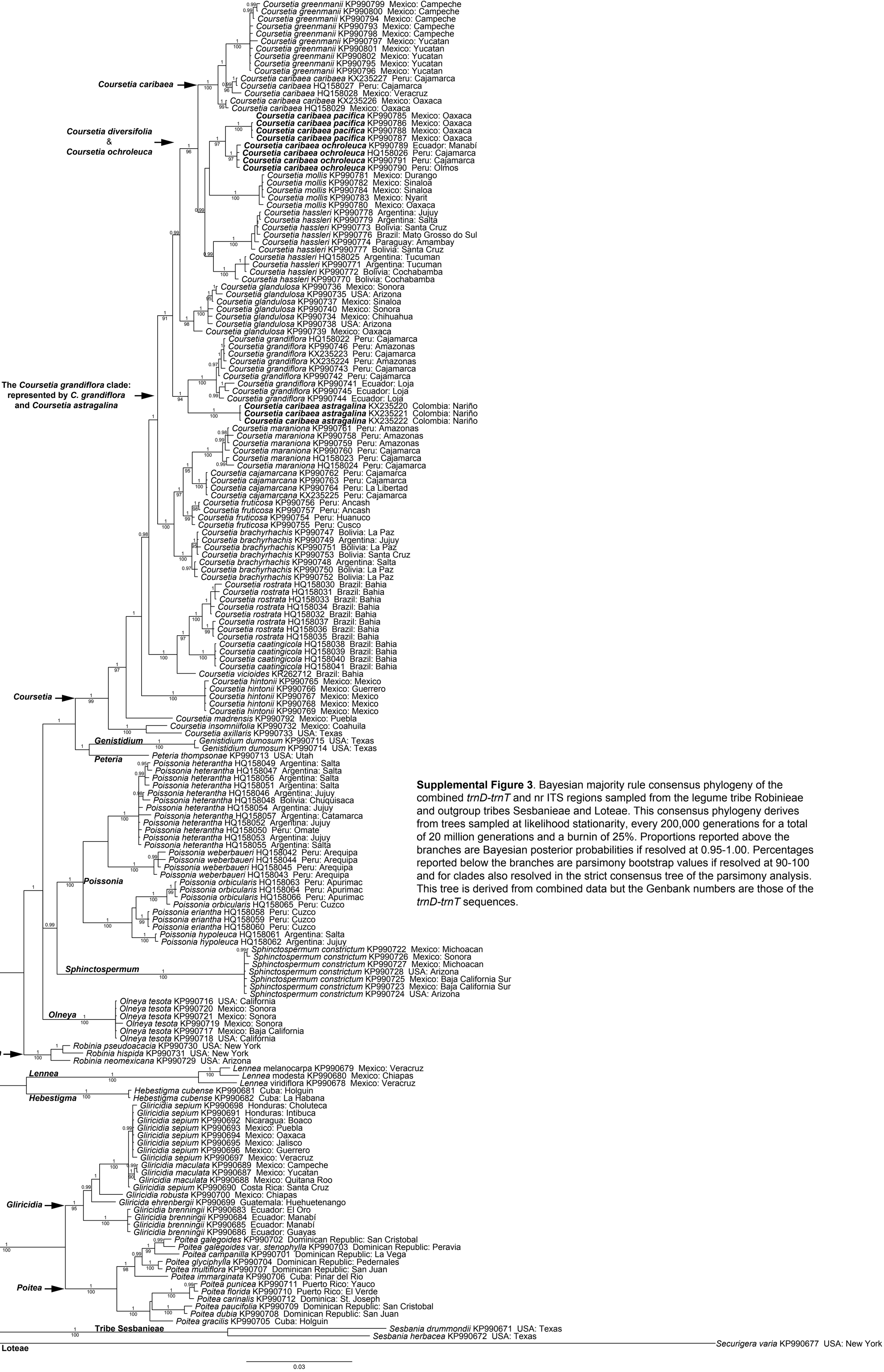


Supplemental Figure 3. Bayesian majority rule consensus phylogeny of the combined *trnD-trnT* and nr ITS regions sampled from the legume tribe Robinieae and outgroup tribes Sesbanieae and Loteae. This consensus phylogeny derives from trees sampled at likelihood stationarity, every 200,000 generations for a total of 20 million generations and a burnin of 25%. Proportions reported above the branches are Bayesian posterior probabilities if resolved at 0.95-1.00. Percentages reported below the branches are parsimony bootstrap values if resolved at 90-100 and for clades also resolved in the strict consensus tree of the parsimony analysis. This tree is derived from combined data but the Genbank numbers are those of the *trnD-trnT* sequences.