

Results

Phylogenetic Analysis. GenBank accessions and voucher specimen information are reported in Supplementary Table 1. PartitionFinder results are summarized in Table 2. Bayesian analysis of the concatenated genetic data separated two major *Neduba* clades (posterior probability = 1) that are subdivided into six Species Groups (all posterior probabilities = 1): Carinata, Propsti, Castanea, Lucubrata, Sierranus, and Sequoia (Fig. 3). The Carinata Group consists of eight lineages, four of which are currently recognized species (*N. carinata*, *N. convexa*, *N. diabolica*, and *N. steindachneri*). The Carinata Group is comprised of two clades (posterior probability = 1): the Carinata Clade and the Convexa Clade. Although Convexa Clade lineages clearly cluster, the interrelationships of those lineages are poorly resolved. The Propsti and Lucubrata Groups contain one lineage each. The Castanea Group consists of reciprocally monophyletic lineages corresponding to *N. castanea* and *N. macneilli*. The Sierranus Group consists of four lineages, with a deep split across *N. sierranus* rendering that species paraphyletic. The Sequoia Group consists of four lineages that are not resolved by concatenated genetic data.

TABLE 2. Partitioning scheme for phylogenetic analysis as selected with PartitionFinder.

Partition	Gene fragment(s) and codon positions	model
1	wg 1st, wg 2nd, 28S	HKY + I
2	wg 3rd	HKY + Γ
3	COI 1st, COI 2nd, COII 1st, COII 2nd	HKY + I + Γ
4	COI 3rd, COII 3rd	GTR + Γ
5	ITS2	HKY + Γ

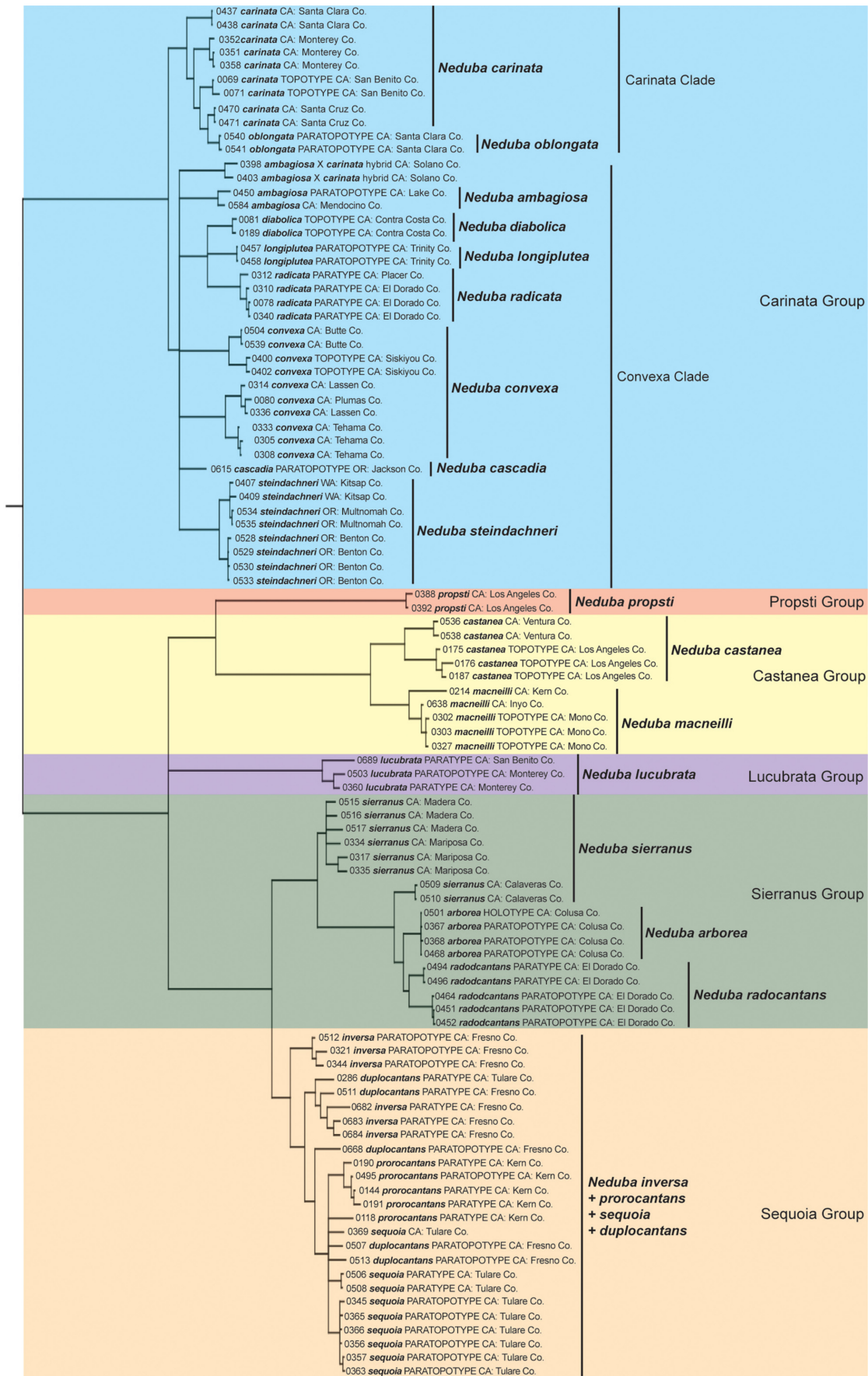


FIGURE 3. Bayesian consensus tree showing species Groups (color coded) and species hypotheses. Nodes with <85% posterior probability are collapsed.

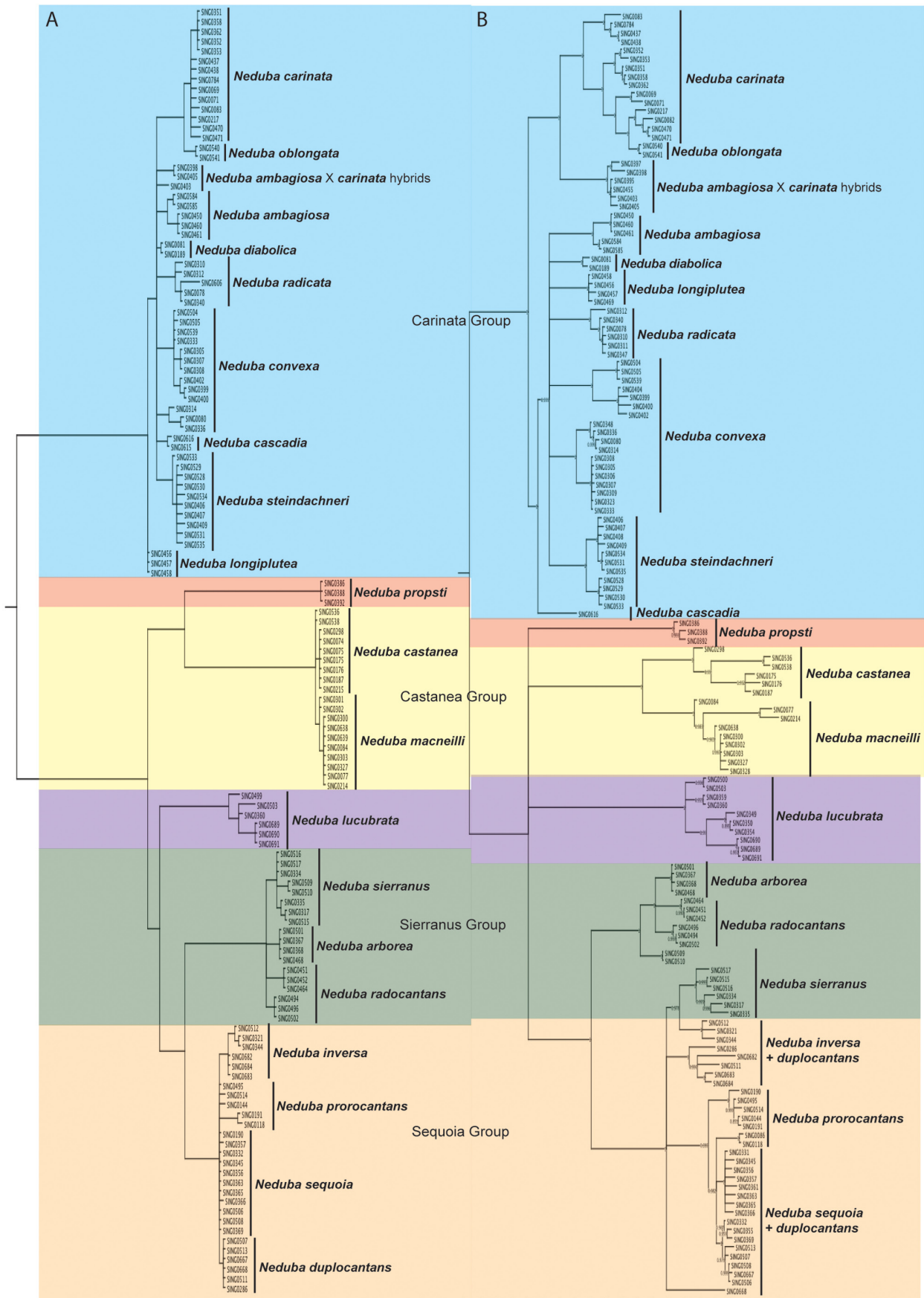


FIGURE 4. Comparison of A. rDNA, and B. mtDNA trees. Nodes with <85% posterior probability are collapsed. Species Groups are color coded.

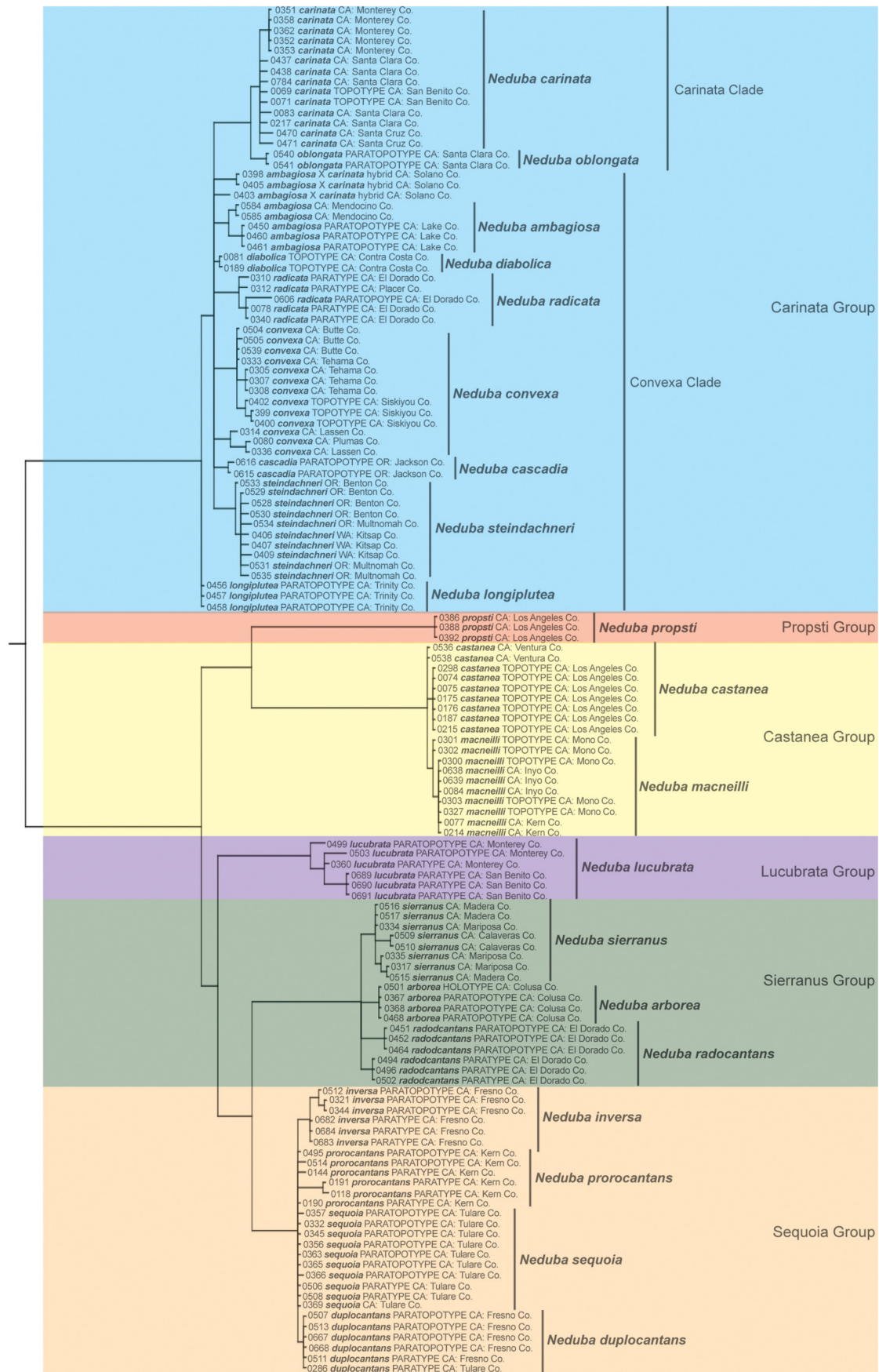


FIGURE 5. rDNA Bayesian consensus tree. Nodes with <85% posterior probability are collapsed. Species Groups are color coded, and species hypotheses are indicated.

Hypotheses resulting from rDNA and mtDNA were incongruent (Fig. 4): the mtDNA consensus tree nested *N. oblongata* within *N. carinata*, and *N. sierranus* collapsed into the poorly resolved Sequoia Group. In both cases, incongruence was due to mtDNA grouping species with adjacent geographic ranges (for a similar pattern in *Aglaothorax* see Cole 2016).

The rDNA consensus tree (Fig. 5) delineates species hypotheses in congruence with morphological, geographical, and bioacoustical character sets. rDNA resolved the lineages of the Sequoia Group, which were obscured in the concatenated dataset by mtDNA introgression.