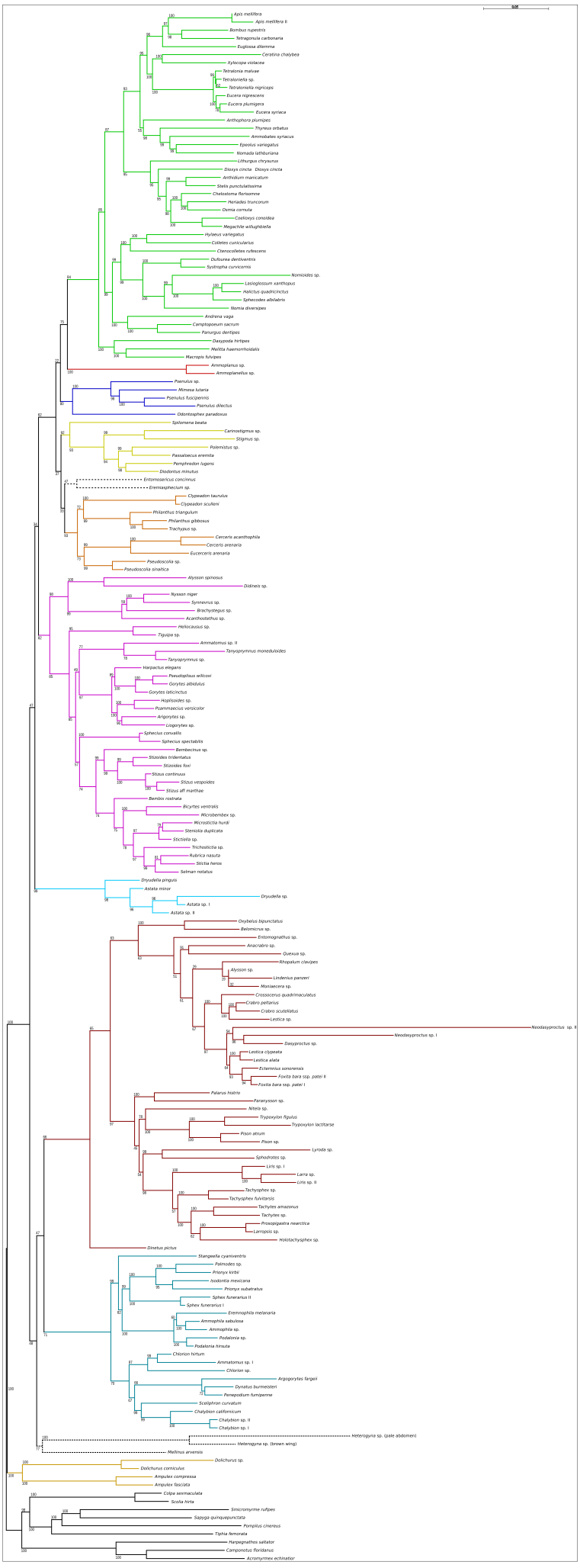

Figure S4: Best ML phylogenetic tree inferred from re-analysing the concatenated amino acid dataset (sm-aa). The phylogenetic tree was inferred from analysing 96,110 amino acid sites comprising 194 single-copy genes with IQTree. The data matrix was analysed with partition-specific substitution models selected by IQTree. Bootstrap convergence was achieved after 200 bootstrap replicates. Taxa are colour-coded according to their potential taxonomic grouping.