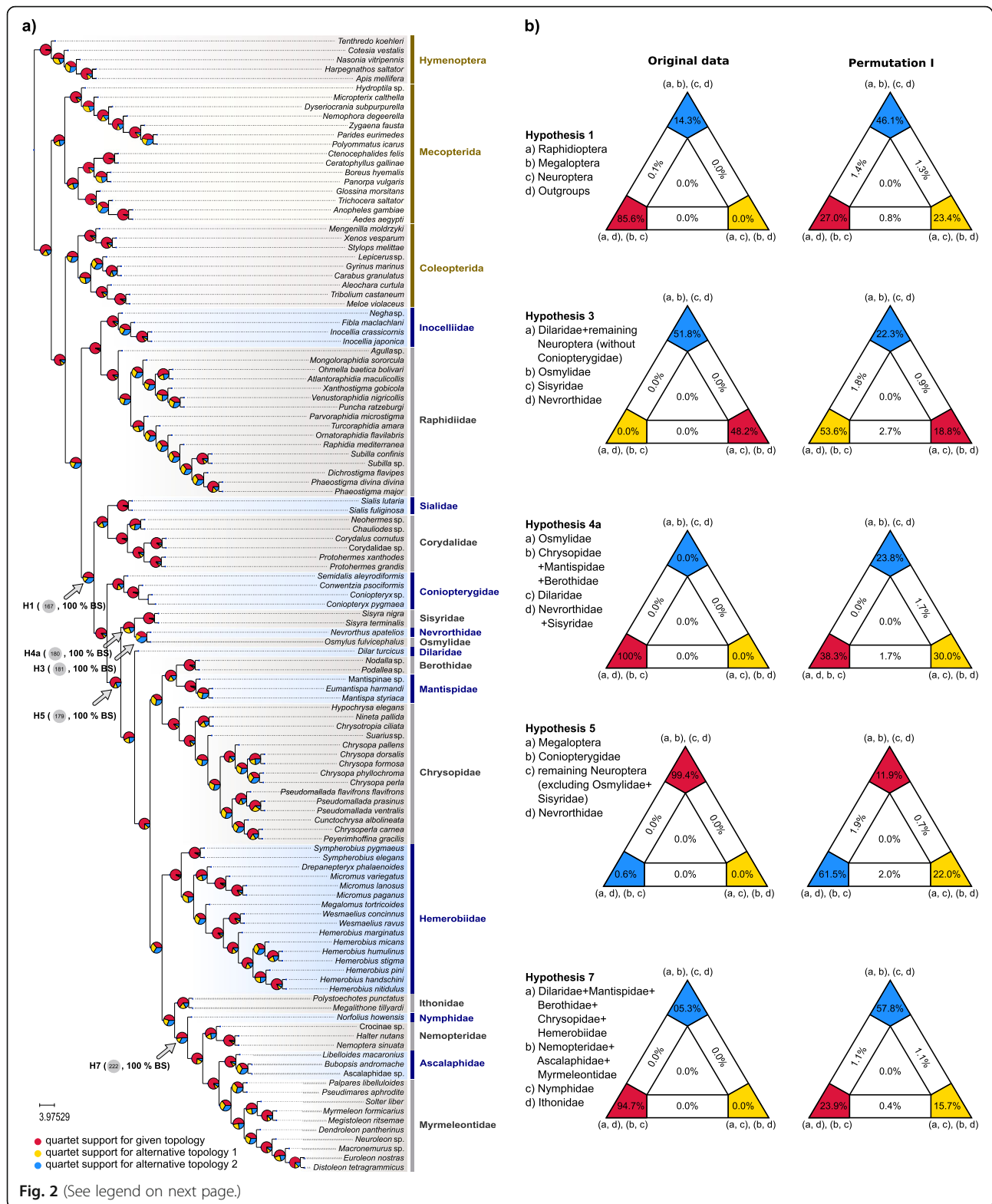


Fig. 1 (See legend on next page.)



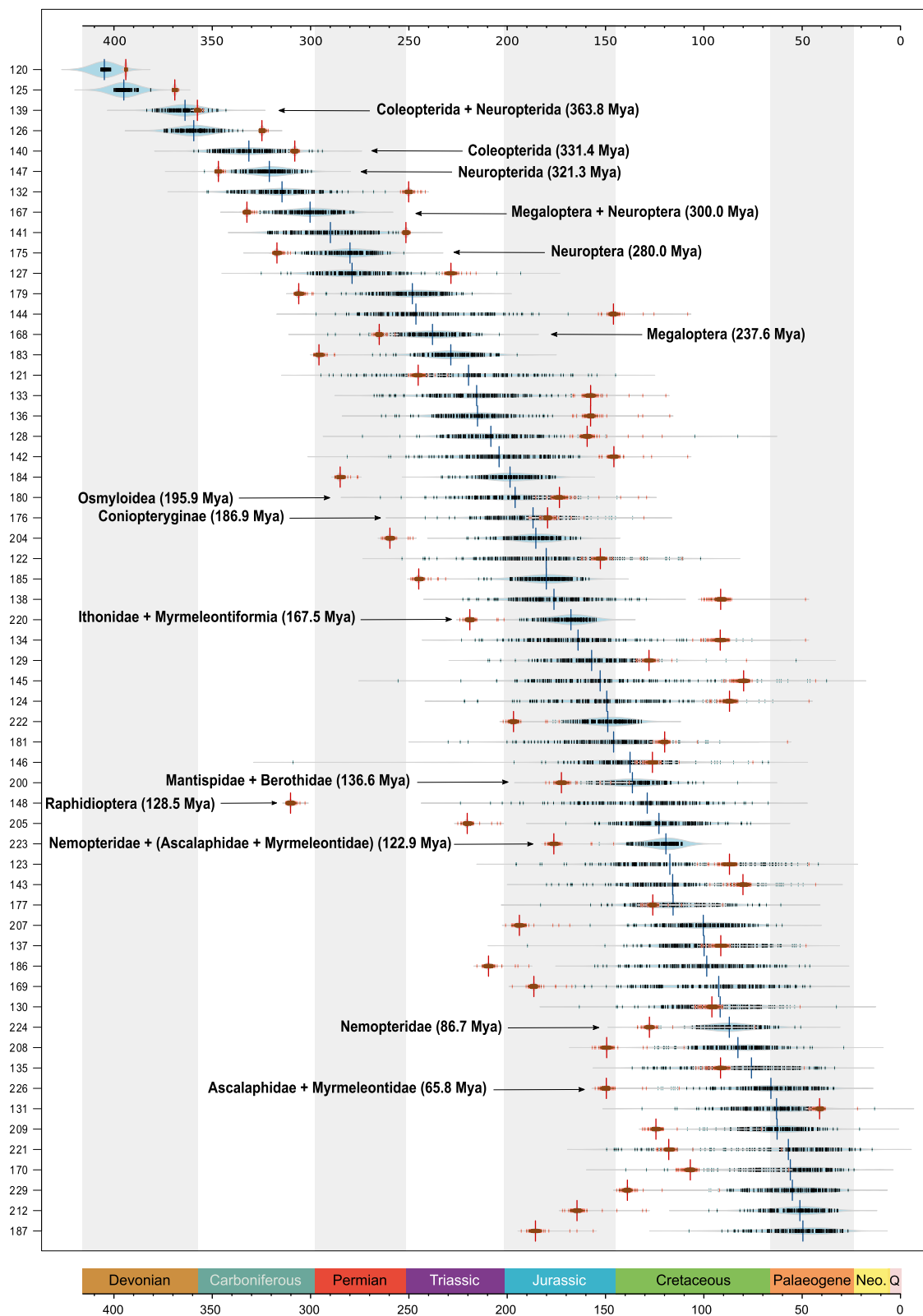
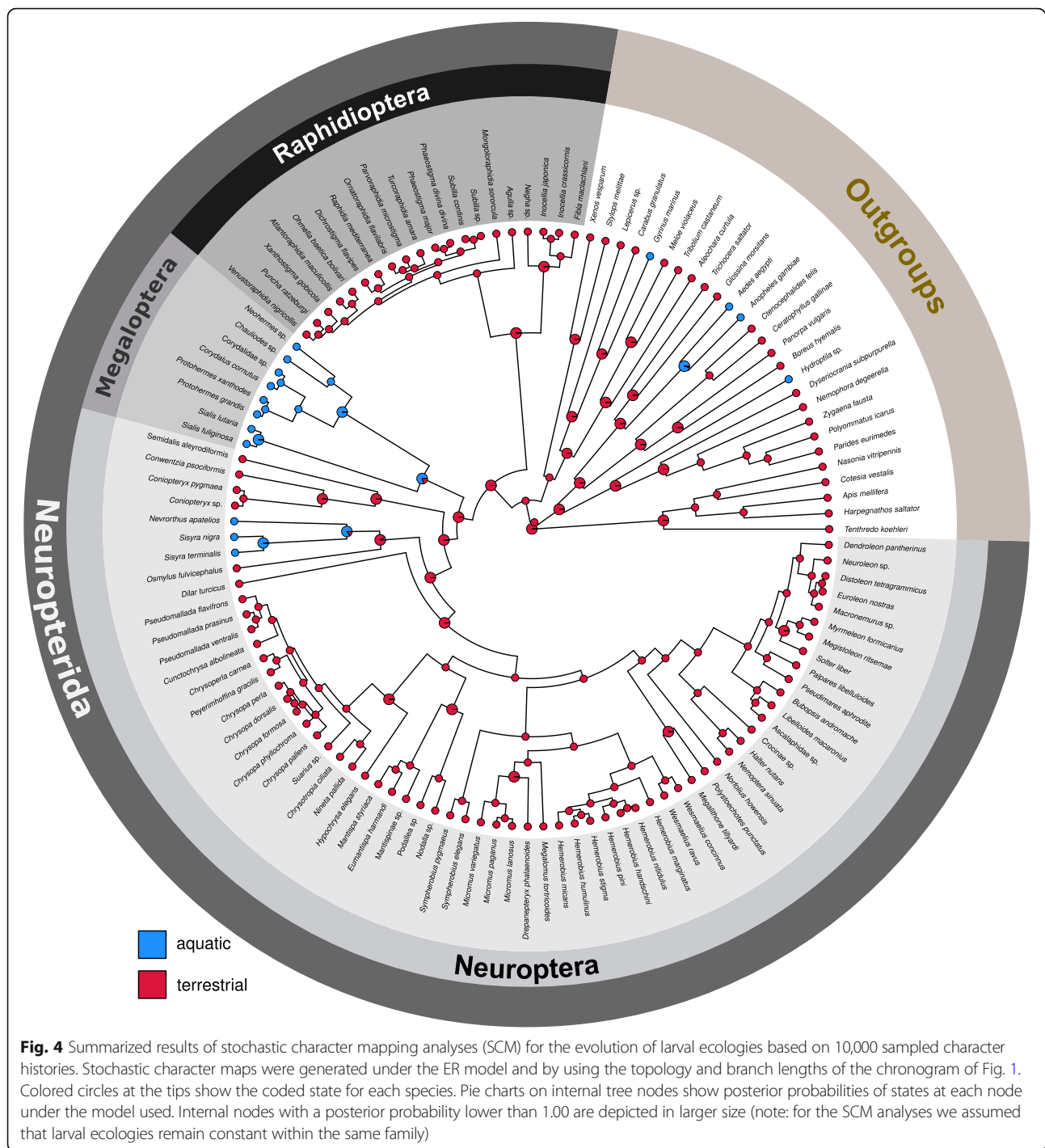


Fig. 3 (See legend on next page.)



relationships within Neuropterida, we have used a combination of gene tree-based and concatenation-based quartet methods and compared results with those of the classical non-parametric bootstrapping approach and with those of the newly described bootstrap by transfer support measure (TBE). We observed that a few seemingly well supported phylogenetic relationships assessed by bootstrapping are in fact inflated due to potentially confounding factors in

the data. In most instances, concatenation-based and gene tree-based quartet methods deliver congruent pictures, that are in several cases in stark contrast to the classical resampling approaches. We conclude from these observations that at least parts of the backbone tree of Neuropterida should still not be considered robustly resolved. Below we discuss two examples from the backbone tree of Neuroptera that do not receive unequivocal support from our quartet analyses: