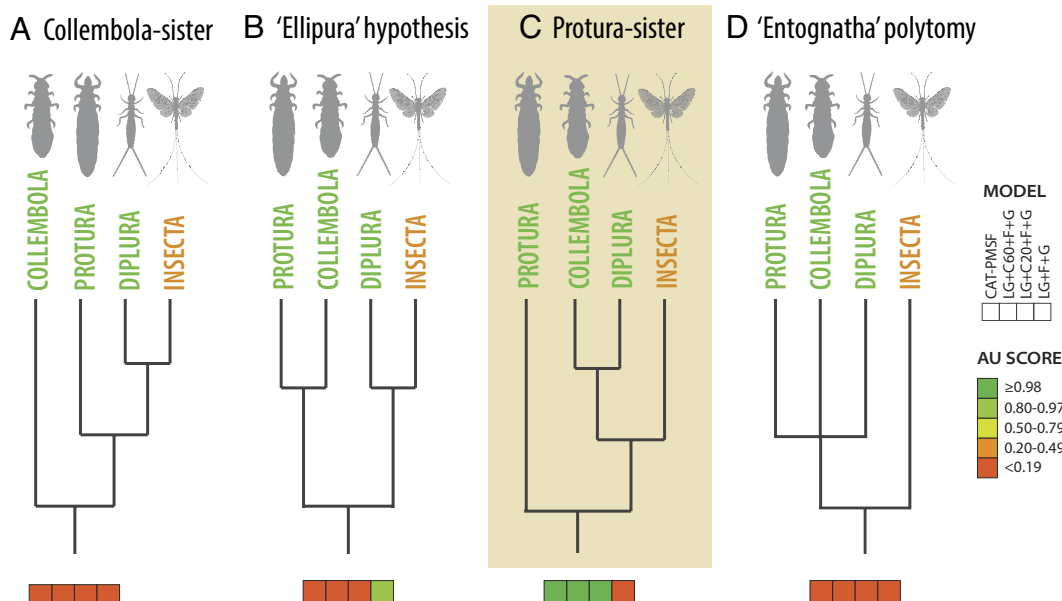


**Fig. 2.** Phylogeny of the noninsect hexapods. Main topology inferred from the Matrix 6 using the Bayesian across-site compositional heterogeneity CAT-GTR model implemented in PhyloBayes. Node supports from all analyses are indicated by the colored squares (The node supports of each phylogenetic tree is shown in [S1 Appendix, Supplementary Appendix B](#)). Only the lowest support values are shown when different matrices or different models produced conflicting results. [H1.guide: Collembola + (Protura + (Diplura + Insecta)); H2.guide: (Collembola + Protura) + (Diplura + Insecta); H3.guide: Protura + ((Collembola + Diplura) + Insecta)]. Collembola + Diplura = original circumscription of Entognatha; Entognatha + Insecta = Holomerentoma (a.k.a. Holomera).

groups in the third hypothesis [H3: “Protura-sister” hypothesis, i.e., Protura + ((Collembola + Diplura) + Insecta)], or the Protura + the Holomerentoma of Prell (76).

The most complex site-heterogeneous models, PMSF(C60) and CAT-GTR, supported the “Protura-sister” hypothesis when all supermatrices were analyzed (except for the Matrix 2, which



**Fig. 3.** Four different topological hypotheses analyzed in this study. (A) Collembola + (Protura + (Diplura + Insecta)) (“Collembola-sister” hypothesis). (B) (Collembola + Protura) + (Diplura + Insecta) (the “Ellipura” hypothesis) (8). (C) Protura + ((Collembola + Diplura) + Insecta) (“Protura-sister” hypothesis). (D) unresolved polytomy corresponding to the “Entognatha” hypothesis (14, 44). Topology test *P*-value (AU score) from Matrix 6 under CAT-PMSF, LG+C60+F+G, LG+C20+F+G, and LG+F+G models are indicated by the colored squares.