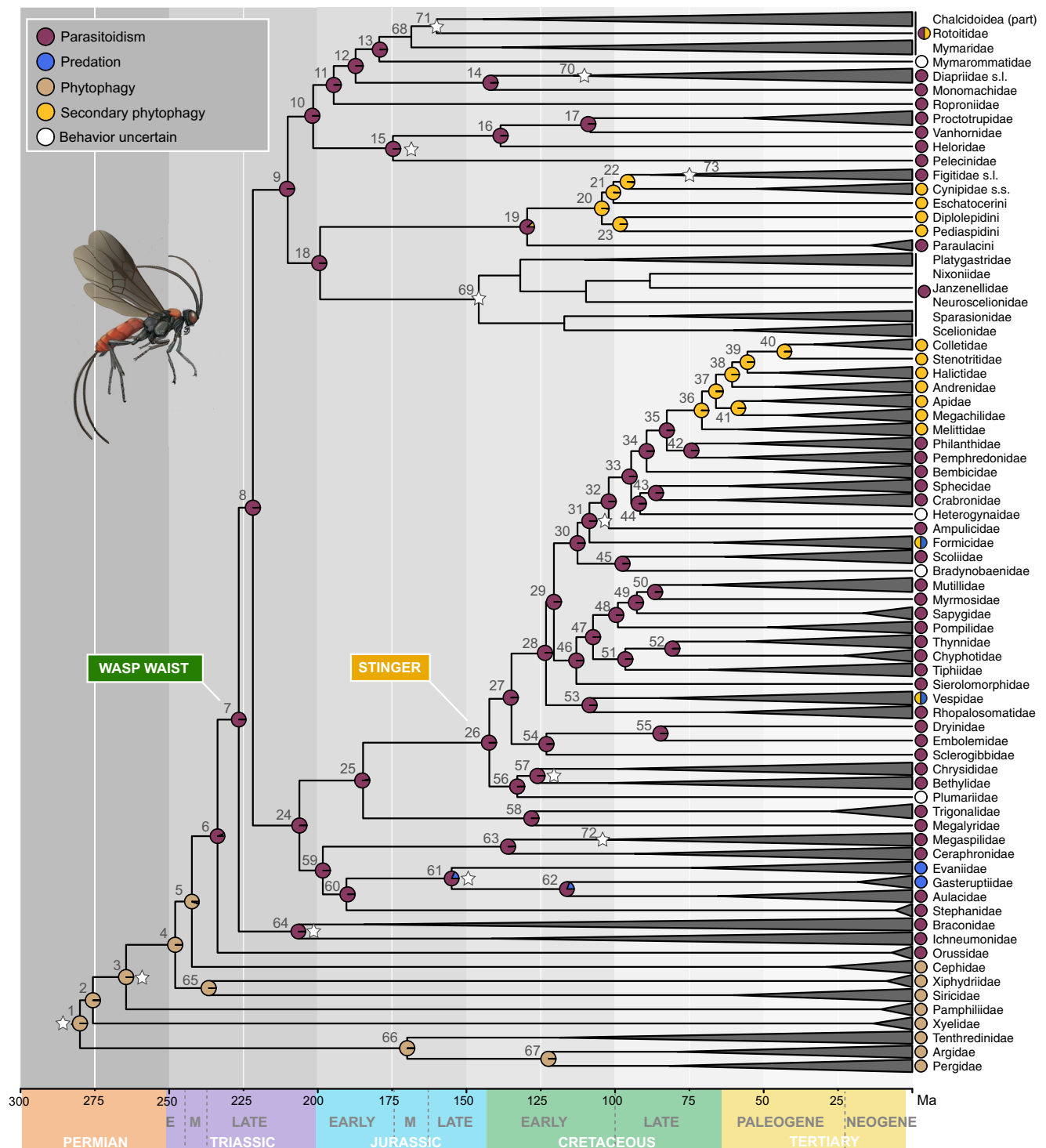


**Fig. 1 | Family-level phylogeny of Hymenoptera.** Phylogeny shows relationships between hymenopteran families as estimated from 446 UCE loci in the nuc-70%-SWSC analysis. This data set was partitioned using the Sliding-Window Site Characteristics Entropy (SWSC-EN) algorithm<sup>106</sup> and PartitionFinder2<sup>107</sup> in combination with the r cluster algorithm<sup>108</sup> and analyzed using Maximum Likelihood (ML) best-tree and ultrafast bootstrap searches in IQ-TREE v1.6.10<sup>109</sup>. This result is referred to as topology C-1 (topC-1) throughout the text and the remaining figures and tables.

Various nodes have been collapsed for clarity of display, with numbers of species subtended by the respective branches included in brackets. Ultrafast bootstrap (ufBS) support values are indicated by colored squares on respective nodes: dark blue = 100%, light blue = 91–99%, and yellow = 70–90%. Support values lower than ufBS = 70 are not shown. Scalebar represents substitutions/bp. Source data for this figure can be found in the Dryad repository at <https://doi.org/10.5061/dryad.08kpr54m> (folder 2.1.7).



**Fig. 2 | Timeline and evolution of parasitoidism in Hymenoptera.** Chronogram estimated using approximate likelihood in MCMCTREE with the PAMLv4.9 package<sup>13</sup> from the nuc-70% matrix and topology C-1. All outgroups were pruned from the tree and alignment prior to divergence time estimation. Twelve calibration points were used, which are indicated by a white star. Terminals have been collapsed down to family or clade-level post analysis. Families of Platygastroidea are shown in the chronogram, but were lumped at the superfamily level for ancestral state reconstructions; therefore, pies are absent in this clade. Ancestral state reconstructions with corHMM were estimated from topology C-1 and

mapped in pie format onto the chronogram; states for terminals are indicated beside terminal branches. Divergence estimates and ancestral state probabilities can be accessed in Supplementary Data 6 and 8, referring to numbers beside nodes. Pie states are red = parasitoid, blue = predatory, brown = phytophagous, yellow = secondarily phytophagous, and white = behavior unknown. For detailed information on methodology and results, also refer to the main text and the Supplementary Methods. Source data for this figure can be found in the Dryad repository at <https://doi.org/10.5061/dryad.08kpr54m> (folder 2.2.2).