



mandibles. The terminal-instar larvae of all studied species are for the first time thoroughly described and illustrated with SEM pictures; diagnostic characters for the family and the studied genera are provided. A key for the identification of the Torymid larvae, at genus and species level, associated with cynipid galls is also given. Information, including new rearing records, is given on the larval biology of each torymid species. Most studied torymid larvae are solitary monophagous parasitoids of the host cynipid larvae.

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### Phylogeny of the Chalcidoidea (Hymenoptera)

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Economically and ecologically, Chalcidoidea are one of the most important groups of insects. With an estimated 375-400K species thought to exist, they are also among the most diverse groups of insects. The current classification includes 19 families and from 80-90 subfamilies of Chalcidoidea. The monophyly of several groups is suspect, and other groups which are considered monophyletic lack definitive support. The Chalcidoidea TWiG of the Hymenoptera Tree-of-Life project is focused on development of a combined analysis of the relationships at the subfamily level. To date we have sequenced more than 300 taxa for the gene regions 18S-E17-35 and 28S D2-D5. Analyses provide support for the Mymaridae as monophyletic and basal to the remainder of Chalcidoidea. Monophyletic groups include Eucharitidae, Eulophidae, Signiphoridae, Encyrtidae, Tanaostigmatidae, Ormyridae and Trichogrammatidae. Surprisingly, Chalcididae are not monophyletic. In almost all cases, previously recognized subfamily groups are monophyletic. A morphological data set is being developed for Chalcidoidea. Over the past year, a historical list of over 700 characters was evaluated independently and in a workshop format. This list has been reduced to 452 characters, of which 141 require further investigation to assess homology and coding accurately. These characters will be scored initially for a core group of chalcidoid taxa, and then subsequently, an attempt will be made to include all of the molecule-scored taxa, and ultimately to include the important taxa which are missing molecular data. Results will be presented for the molecular analyses across all of the Chalcidoidea.

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### A molecular phylogeny of the Hymenoptera

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There have been several attempts to recover a phylogeny of Hymenoptera based on molecular sequencing data that have focused on either the lower Hymenoptera with an emphasis on the relationships of Symphyta, or across the Apocrita with a more restricted sampling of the Symphyta. These analyses have been based on either single-gene analyses or combined analysis of different nuclear and ribosomal genes. For the Hymenoptera Tree-of-Life project the approach is two fold. An initial focus is to sequence multiple genes for a 'skeleton' set of taxa thought to represent the subordinal diversity of the entire order. For these taxa, we are sequencing all of the nuclear ribosomal genes 18S and 28S (D1-D10), as well as COI, Forkhead, wingless, Ef-1alpha (both copies) and possibly CAD. The second aspect will be to expand this skeleton taxon set based on more 'gene-limited' analyses of taxa within each of the taxonomic working groups (TWiGs). Initial analyses of the skeleton matrix data support previously recognized relationships within Hymenoptera. We will present the results of our skeleton matrix for the 18S and 28S data sets and relate how these compare to previous molecular and morphology-based studies of Hymenoptera.

