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Phylogenomics of the Hemipteroid Insect Orders

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The hemipteroid orders (Psocodea, Thysanoptera, and Hemiptera) are a highly diverse group among the insects. The relationships among these orders and to other insect groups has remained problematic. Using Illumina sequence technology, two types of phylogenomic data have been generated for these insects. The first is a dataset of assembled transcriptomes for around 200 species. Second, genome sequencing data sets have been produced for around 100 species of this group for which fresh material for RNA sequencing is not available. A procedure using the automated Target Restricted Assembly Method (aTRAM) to assemble 1:1 single copy ortholog protein coding genes from these data is illustrated. Trees from these data sets are well resolved and solve some key issues on the phylogeny among the major lineages of hemipteroid insects. From transcriptome data, Coleorrhyncha is placed as the sister taxon of Auchenorrhyncha. Within Auchenorrhyncha, Fulgoromorpha is resolved as the sister taxon of Cicadomorpha. There is high support for monophyly of the four superfamilies: Fulgoroidea, Cicadoidea, Cercopoidea, and Membracoidea. Within Membracoidea, Myerslopiidae is the sister taxon of all other leafhoppers and treehoppers, with the latter being strongly supported as derived from within leafhoppers.