Paper No. 200-7
*Presentation Time: 3:30 PM*

# GENOMIC-SCALE DATA SETS RESOLVE THE ECDYSOZOAN PHYLOGENY AND PROVIDE NEW INSIGHT ON THE ORIGIN AND EARLY EVOLUTION OF ARTHROPODA

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Ecdysozoa, the group including Nematoda (roundorms) and the Arthropoda, has dominated Earth's habitats since the Cambrian, and includes the largest majority of the extant animal biodiversity and biomass. The monophyly of this group as long been debated and has only recently been confirmed by the analyses of complete animal genomes. However, the relationships within the Ecdysozoa remain uncertain. We assembled large-scale phylogenomic data sets, and identified the nearly complete microRNA repertoire for a representative sample of ecdysozoan species. These independent genomic-scale data sets were analysed and the relationships among the Ecdysoza resolved by means of congruence. We were able to show that of the two generally accepted ecdysozoan clades (the Panarthropoda and the Cycloneuralians) only the first, which includes the Arthropoda, the Tardigrada (water bears) and the Onychophora (velvet worms), is monophyletic. The second, Cycloneuralia, most likely represents a paraphyletic assemblage of phyla. We were also able to show that within Panarthropoda, the velvet worms represent the sister group of the Arthropoda with the water bears representing the sister group of the Arthropoda plus Onychophora. In addition, we assembled the largest set of arthropod calibration points to date and used all currently available genomic-scale data sets, to generate a detailed molecular timescale of Ecdysozoan evolution. Our results show that the Ediacaran was the cradle of the Ecdysozoa, but that individual ecdysozoan phyla radiated in the Cambrian or later. Finally, our results provide important clues improving our understanding of how this important group colonised the continents. Overall, our results substantially clarify the relationships among the Ecdysozoa and provide an invaluable framework to understand evolutionary patterns within this group.

Session No. 200
**T145. The Origins of Arthropod Diversity: Phylogenetic Insights from the Living and the Dead II**
*Tuesday, 6 November 2012: 1:30 PM-5:30 PM*

*Charlotte Convention Center 217BC*
Geological Society of America *Abstracts with Programs.* Vol. 44, No. 7, p.478



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