

Using integrative phylogenetics to clarify evolutionary relationships in Adephaga: Characterization of targeted genomic loci

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The use of phylogenetic data generated with high-throughput sequencing has revealed fascinating biographic and evolutionary histories while resolving historically intractable phylogenetic relationships. The second largest beetle suborder, Adephaga (Coleoptera), has been studied in depth in recent years. Consisting of over 45,000 species and found world wide, this suborder includes important predators in terrestrial and aquatic ecosystems. However, limited taxonomic sampling in important clades muddles our understanding of the diversification and systematic relationships in this group. To test recent hypotheses of lineage relationships in the suborder, we will integrate multiple genomic data-collection strategies that have been used and produce the most complete phylogeny of Adephaga to date. Previously used methods including anchored hybrid enrichment of exons (AHE), whole genomes, transcriptomes, and ultra-conserved elements (UCEs). Recently some UCE datasets have been described to target more than one loci on the same gene and are composed of off-target loci (e.g., fungi or bacteria). This fundamentally alters interpretations of phylogenetic relationships and complicates investigations of evolutionary history. Because of these pitfalls, it is necessary to characterize and identify the genetic composition of genomic-data used in phylogenetic analyses. Preliminary analyses using two different UCE kits suited to Adephaga phylogenetics suggests that multiple UCE loci are found on the same gene. Additionally, there is evidence these UCE loci may have been generated using contaminated genomes. Preliminary phylogenetic results indicate that all data-collection strategies can be successfully integrated. Further bioinformatic work characterizing the genomic loci used will improve phylogenetic models and future evolutionary investigations.