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Author

Boore, Jeffrey

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Mitochondrial gene order versus sequence data in heterobranch gastropods

Mónica Medina^{1,2}, Yvonne Vallès², Terrence Gosliner², H. Mathew Fourcade and Jeffrey Boore¹

¹DOE Joint Genome Institute, Walnut Creek CA, USA
²California Academy of Sciences, Golden Gate Park, San Francisco CA, USA
M_Medina@lbl.gov

Crown gastropods exhibit remarkable evolutionary trends such as convergent body plan evolution, as well as adaptations to new environments (e.g. freshwater and land). They also show interesting patterns of evolution at the molecular level. In the particular case of their mitochondrial DNA, and based on the few genomes available, heterobranch gastropods (i.e. hetrostrophan snails, pulmonates and opisthobranchs) are found to have small genomes compared to other invertebrate taxa. More importantly, they present major gene rearrangements that have occurred multiple times throughout the evolutionary history of this clade. We are obtaining complete mtDNA sequences from additional key taxa, which already show that rearrangements are rather common in this group. Having a detailed phylogenetic reconstruction of multiple genomes should help us identify when and how these rearrangements started taking place in gastropod evolution. We will be comparing the gene order data with phylogenetic trees obtained with amino acide and nucleotide for the complete genomes. Additionally, we also have a more complete data set (large taxon sampling) for the mitochondrial large ribosomal subunit (16S), and we will be assessing how these different types of phylogenetic characters complement each other.