Computational Analysis of Mobile Elements in Intron-Sequences of Invertebrates

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Mobile Elements (MEs) are DNA regions that can move and replicate within the genome. The high numbers of MEs in genomes (around 40%) raises the question of whether their patterns of presence/absence in orthologous regions of different genomes contain a phylo-genetic signal and can be used as alternative phylogenetic markers in cases where analysis of primary sequence information has not been able to resolve evolutionary divergences. Here we developed an approach for exploring the phylogenetic signal in introns of nine animal taxa with known evolutionary relationships.

Specifically, we screened intron sequences (of all introns in the genome and of orthologous gene families) for MEs in nine organisms (Figure 1). We found that *Branchiostoma* (the only deuterostome included in the study) differs in number and subclass-composition of MEs in comparison to the protostomes. We then determined if the information of ME distribution can be used to reconstruct phylogenetic relationship of the invertebrates.

Under the criterion of maximum parsimony, patterns of ME absence and presence were not able to recover the accepted taxonomic tree. However, mapping ME gain and loss onto the accepted tree resulted in a clear separation between the ME numbers of the Ecdysozoa and the Lophotrochozoa.

Our results indicate that the distribution of ME may be phylogenetically informative in these taxonomic groups, but that alternative analysis methods and/or the inclusion of additional taxa may be required. The annelids were shown to contain a number of informative ME insertions/losses and will be targeted in a future study.
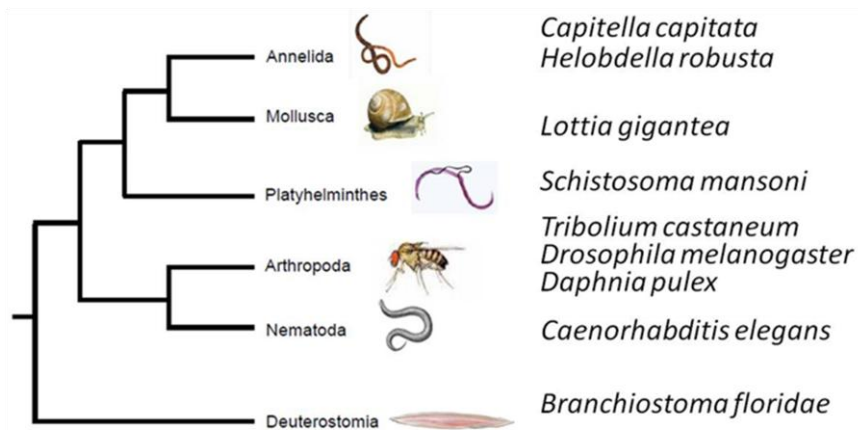

Figure 1: Taxonomic tree of the nine taxa included in the survey.