

Hox and ParaHox gene expression in the zebra mussel, *Dreissena polymorpha*

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Mollusca constitutes the second most speciose animal group after Arthropoda. The great diversity of its representatives is reflected not only in species number, but, more importantly, in the wide range of morphological plasticity they exhibit. This plasticity of homologous structures (e.g., radula, shell, foot, neuromuscular systems) raises questions concerning the molecular basis that underlies morphological variation in molluscan representatives. Hox and ParaHox genes are commonly recognized as key players in establishing the anterior-posterior body axis of bilaterian animals. In many bilaterian animals, Hox genes show an orchestrated expression that is temporally and spatially correlated with the arrangement of the individual genes on the genome (collinear mode of expression). In mollusks, Hox genes show such a mode of expression in polyplacophorans, while in representatives of the conchiferan clades Gastropoda and Cephalopoda this collinearity has been lost, whereby the Hox genes most likely evolved lineage-specific novel functions. However, a broad comparison throughout the conchiferans is yet hampered by the lack of Hox expression data on crucial clades including Scaphopoda, Monoplacophora, and Bivalvia. To partially fill this gap and to contribute to the question concerning the putative role of Hox genes in molluscan body plan diversification, Hox gene expression will be analysed in the bivalve *Dreissena polymorpha*. To this end, an initial characterization of gene expression domains by in-situ hybridization will be performed for the expected 11 Hox and 3 ParaHox genes that are commonly known in mollusks. This will help to reconstruct scenarios of morphological evolution based on molluscan phylogeny and at the same time will provide insights into putative novel and conserved functions of Hox and ParaHox genes in this diverse lophotrochozoan phylum.