A Differential Transcriptomic Approach to Compare Target Genes of Homologous Transcription Factors in Echinoderm Species

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Abstract Embryonic development is controlled by differential gene expression throughout developmental time. The ParaHox genes, *Cdx* and *Xlox* have been shown to be involved in the formation of the properly functioning gut in the sea urchin *Strongylocentrotus purpuratus* and the sea star *Patiria miniata*. Several genes involved in the gene regulatory network (GRN) are known, however, the network is still incomplete. With the current state of sequencing technology, we are now able to expand the network and gain further insight into the process of gut development on a more global scale. Through the use of high-throughput sequencing technology and knockdown experiments we have further characterized the effects of *Cdx* and *Xlox* on the GRN involved in gut development at different developmental stages. Additionally, we have conducted a cross-species comparison to identify genes that are more likely to be evolutionarily important for the development of the echinoderm gut. Within those genes we found a number of transcription factors that could potentially have important roles in the formation of the echinoderm gut. Using both RNA-seq and gene homology, we have set the foundation for further studies of echinoderm gut and the ParaHox GRN downstream of *Xlox* and *Cdx*.

Keywords Differential transcriptomics • Gene regulatory network

1 Introduction

The developmental program of an organism and its phenotypic features are encoded into its DNA. The binding of transcription factors to specific DNA, which controls the expression of genes and ultimately the development of the embryo, is known as a gene regulatory network (GRN). Evolutionary conservation has provided us

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