

**GUT PATTERNING  
IN DEVELOPMENT AND EVOLUTION  
A COMPARATIVE DIFFERENTIAL  
TRANSCRIPTOMICS APPROACH**

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by

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# ABSTRACT

All bilaterians share a common kit of transcription factors and cis-regulatory elements that compose the Gene Regulatory Network (GRN) essential for the development of the body plan. Modifications within the elements of the GRN determine the evolution of animal forms. In this study, the GRN for embryonic gut specification in two echinoderm species, the sea urchin *Strongylocentrotus purpuratus* and the sea star *Patiria miniata*, has been studied with the purpose of acquiring further knowledge on the process of gut patterning in the sea urchin larva and to compare it with the sea star embryo, focusing on the role that Xlox and Cdx transcription factors have in this process in both echinoderm species. In fact, despite the fact the GRN for endomesoderm specification in *S. purpuratus* has been well studied, however, the molecular mechanisms leading a primitive undifferentiated gut to become a highly specialized structure are still partially unknown for both *S. purpuratus* and *P. miniata*; for the latter the GRN is mostly unrevealed. Taking advantage of genome-wide approaches and modern high-throughput technologies, a partial reconstruction of the sea urchin GRN around Xlox and Cdx transcription factors, known for their key role to start the gut specification process, has been achieved leading to describe the putative interactions of the TFs in the network. An important novel node of the sea urchin GRN featuring the interaction between *Sp-Meis*, an homeobox gene, and Sp-Lox protein has been revealed and the occupancy of Sp-Lox protein on *Sp-Meis* regulatory region has been demonstrated by ChIP-PCR. The comparison of the differentially expressed genes after Xlox and Cdx perturbation in both sea urchin and sea star embryos has revealed that, although the absence of these two proteins affects some digestive functions and developmental processes related to its specification, however many of the regulatory genes involved in these mechanisms are not the same in the two species. This result suggests a phenomenon of rewiring of the gut GRN in *S. purpuratus* and *P. miniata* that, although belonging to the same phylum Echinodermata, are distant million years in term of evolutionary time, as recorded by fossil records.

Further studies aimed to reconstructing the sea star gut GRN will lead to a best comprehension of the gut specification mechanisms also in this animal. A comparative/divergence analysis with the reconstructed sea urchin gut GRN will help to identify the kernel elements that did not change during evolution with a key role in gut formation and patterning, as well as the intrinsic differences in the GRN accumulated during the evolution of both lineages.