

Evolutionary and Developmental analysis of germline formation in simple chordate embryos

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In sexually reproducing animals, correct specification of the germ cell lineage during development is critical for transmission of the genetic information over generations. Previous studies demonstrated that, in contrast to conserved molecules and mechanisms for somatic cell development, the primordial germ cell (PGC) segregation from somatic cells is governed in part by non-homolog molecules across various species[1]. In particular, it is of interest to understand how and why genes responsible for keeping the PGC identity during early development through regulation of analogous transcriptional repression, such as PEM in *Halocynthia roretzi*, Pgc in *Drosophila*, and PIE-1 in *C. elegans*, can be easily replaced in evolution[2-4].

In our current study, we are interested in studying the specification of PGC in two closely-related ascidian species, *Halocynthia roretzi* and *Ciona savignyi*, as their PEM genes may harbor certain unpredictable divergences in terms of function or functional domains, according to the previous studies. Specifically, we are focusing on comparing the mechanisms and functional domain applied by the germline transcriptional repressor PEM from these two representative ascidian species. Here, we are also keen on working with a basal Urochordate animal *Oikopleura dioica*, in which PEM is not present in its genome and also the process of germ cell specification remains unclear. We are examining the molecular mechanisms by which *Oikopleura dioica* mediates germline formation. Thus, our study aims to provide more comparative information to pinpoint whether and how the mechanisms for PGC specification might be different even within closely-related Tunicata lineages.

References

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