

Mining developmental origins of germline stem cells in early eumetazoa

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Stem cells differentiate into different lineages during animal development. Among bilaterian model organisms, such as mouse, zebrafish, fly and nematode worms, specialized germline stem cell fates are distinguished during embryogenesis and maintained in adulthood. However, how primordial germ cells differentiate during development in the pre-bilaterian animals, like sponge and hydra, is still unknown. Because of hardly-accessible pre-bilaterian embryos, most previous studies focus on their multifunctional adult stem cells, which can give rise to soma and germ cells. To demonstrate pre-bilaterian germline development and the underlying mechanism, we introduce an emerging Cnidarian model, *Nematostella vectensis*, featuring with tractable developmental process and distinct adult gonad. In this project, we specifically aim to interrogate the functions of conserved germline genes and to search for novel germline regulators. First, *vasa* and *nanos* homologs were characterized in developing *N. vectensis* germline; however, whether they are necessary or sufficient in this process is yet confirmed. With the advent of well-developed CRISPR/Cas9 genome editing tool in *N. vectensis*, we will manipulate germline genes by knocking them out. Second, because *vasa* and *nanos* homologs are not exclusive germline landmarks, but also expressed in some *N. vectensis* somatic cells, other germline markers are required for tracking germline development. Therefore, we will compare gonad RNA expression profiles with different tissues to characterize specific germline genes. Then, we plan to confirm their specificity by *in situ* hybridization to test if they are expressed in certain germ cell differentiation stage or in the gonad “niche”. Through these methods, *N. vectensis* germline research will provide insights into eumetazoan (i. e. Cnidarian and bilaterian) germline segregation evolution.