

Parallel evolution of germline epigenetic poising and somatic development in metazoa

The evolutionary history of gene regulatory states in developing germ cells can provide critical insight into mechanisms of reproduction and development. Recently, I have examined the poised (H3K4me3/H3K27me3 bivalent) epigenetic state in male and female germ cells during mouse development, and in male germ cells of five species spanning 175 million years of mammalian evolution. These studies identified a set of genes that is stably marked by the poised state throughout germ cell development, and revealed that epigenetic poising is also conserved at several hundred genes in male germ cells throughout the mammalian lineage. Genes at which poising is conserved are ancient regulators of morphogenesis that sit at the top of transcriptional hierarchies controlling somatic tissue development. In contrast, genes that gain poising in germ cells of individual species acquire species-specific functions downstream of conserved poised genes. I propose that critical regulators of animal development gained an epigenetically privileged state in germ cells early in metazoan evolution, manifested in mammals by H3K4me3/H3K27me3 poising.