# Dynamic genomes of Hydra reveal anciently active repetitive elements of animal chromosomes

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## Abstract

Animal genomes are characterized by highly conserved chromosomal homologies that pre-date the ancient origin of this clade. Despite such deep conservation, the mechanisms behind the retention, expansion, and contraction of chromosomal elements and the long-term (macro-evolutionary) functional implication of these processes remain to be elucidated. Here we present a comprehensive stem-cell resolved genomic and transcriptomic study of the fresh-water cnidarian *Hydra vulgaris*, an animal characterized by its high regenerative ability, the capacity to propagate clonally, and an apparent lack of senescence. Utilizing newly generated single haplotype telomere-to-telomere genome assemblies of the two recently diverged hydra strains, we show how the macro-evolutionary history of its chromosomal elements are shaped by ancient and recent transposable element (TE) expansions, which, combined with the distinct strain-specific preference for either sexual or asexual reproduction, is forming divergent evolutionary trajectories in these genomes. By comparing the individual genomes of hydra's three types of stem cell lineages, we show that distinct TE families are actively and preferentially inserting in the genomes of each of the lineages. In whole transcriptomes, over 14,000 transcripts were composed of nearly complete TE sequences, and finer classification into families, subfamilies, and individual loci reveals an increased detection of cell type-specific expressions of TEs. The active TEs include elements that differentially contribute to the changes in the genome size as well as persistent structural variants around loci associated with cell population proliferation. Our study reveals a core set of 14 TE families including 11 DNA elements, 2 LINE elements, and one LTR element that act in this role. The evolutionary analysis of these elements suggests an ancient role in maintaining the evolutionary topology of animal chromosomes.

**Keywords:** Hydra, Genome expansion, Haplotype resolved telomere to telomere genome assemblies, Stem cell genomes, Anciently active transposable elements

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