119 - T112. Halo-Dash: The Deep and Shallow History of Aquatic Life's Passages between Marine and Freshwater Habitats

Monday, 10 October 2022
1:30 PM - 5:30 PM

119-5: COMPARATIVE GENOMICS OF ALEWIFE: INSIGHTS INTO THE GENETIC BASIS OF DIADROMY

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Abstract

Throughout evolutionary history, transitions into novel habitats have generated phenotypic novelty and biodiversity, as they subject organisms to altered landscapes of natural selection. Transitions between saltwater and freshwater habitats, for example, have led to major diversification events across animals and have helped shaped the current distribution of species on this planet. Among the fishes, salinity habitat transitions are deeply rooted in the evolutionary history of this group. An important evolutionary step in the transition between salinity zones is the evolution of diadromy, characterized by migration between fresh- or salt-water during particular life stages. Although it is rare, diadromy is distributed broadly across taxa; it has potentiated diversification, either by acting as an evolutionary link between fresh- and salt-water, or by itself as a unique ecological niche leading to adaptive radiation. Despite the importance to diadromy to biodiversity, there has been almost no research into the genetic changes that underlie its evolution. To help address this gap, we report on the first high-quality reference genome assembly (long-read sequencing with Oxford Nanopore) of the Alewife (*Alosa pseudoharengus*), a diadromous clupeid (family *Clupeidae*) that breeds in freshwater along the coastal United States and spends its adult life at sea. Using analyses of natural selection (*dN*/*dS*) and gene family expansion-contraction (CAFÉ), we conducted a comparative genomic analysis between Alewife and previously published marine, non-diadromous species. Combined, these analyses identified a set of genetic loci that evolved uniquely in the branch leading to Alewife, representing a set of genes that may contribute to the evolution of diadromy.

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