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How have all the diversity and complexity of life forms around us evolved? The tales of evolution continues to be developed as we venture deeper and deeper into decoding the secrets hidden in the genetic code of life, a seemingly simple language comprising four basic letters A, T, G, and C, organized and functioning in the most sophisticated ways. Unravelling how genes and genomes evolve structurally and functionally provides a basis to understand the incredible complexity and diversity of life that we see around us every day. The rapid advances in DNA sequencing and the consequent boom in genomic data continues to reveal to us some of the answers to what kind of genomic variations shape the lineage- and species-specific evolutionary innovations. Fish genomes provide a particularly interesting system to study evolution of vertebrate genomes, given the incredible diversity in life histories and adaptations they exhibit. In her thesis, Srinidhi Varadharajan contributes the assemblies of two fish genomes, namely the European grayling and the nine-spined stickleback, providing insights into evolution of genome architecture and function.

One of the most common routes to generation of new genetic material is by duplicating existing genes. A more extreme type of such a mutation is the doubling of the entire genome (whole genome duplication, WGD). Multiple WGD events have played a vital role in the evolution of vertebrate genomes, as the resulting functional redundancy is believed to provide raw material for evolution of new functions. Salmonid fishes, owing to their evolutionarily young WGD event, provide an ideal system to investigate consequences of such large-scale events. The work by Varadharajan provides and utilizes the genome assembly of European grayling in a comparative framework with the genome of Atlantic salmon to show the vital role of selection in shaping gene expression regulation post WGD and highlights potential differences in selective pressures on distinct biological functions. In addition, the results also show distinctly different selective pressures on a key gene involved in chloride ion homeostasis between the freshwater European grayling and the anadromous Atlantic salmon.

The nine-spined stickleback is a member of a family explored extensively in ecological and evolutionary studies. The comparative analysis with the closely related three-spined stickleback provides insights into differences in repetitive content among the two species and describes a recent duplication in the hemoglobin gene cluster in the nine-spined stickleback and potential copy number variations among closely related populations.

Lastly, chromosome-level genome assemblies for both grayling and nine-spined stickleback presented in the thesis provide examples of large-scale rearrangements that can lead to substantial differences in the number and morphology of chromosomes even between closely related species. Overall, this thesis shows the utility of comparative genomics to understand consequences of genome evolution.