

Comparison of Even- and Odd-Year Broodlines of Pink Salmon Using Genotyping by Sequencing

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Pink salmon represent a critically important component of the North Pacific and Bering Sea ecosystem. They are the most numerous salmon species in the North Pacific Ocean and Bering Sea and are unique among Pacific salmon with an obligate two-year life history resulting in two genetically distinct lineages (even- or odd-year) that largely overlap in range. In North America, odd-year broods predominate in the south, with even-year pink salmon predominating in more northerly latitudes. In many streams, even- and odd-year lineages occupy the same habitat, but experience no gene flow providing for a naturally-occurring replicate experiment to test for genomic signals of adaptation. We present next-generation sequence results using restriction site associated DNA (RAD tags) to compare three paired populations of even- and odd-year pink salmon. Our population pairs originate from widely-separated locations in North America and include Norton Sound in Northwest Alaska, Prince William Sound in Southcentral Alaska, and Puget Sound in Washington State. We compare sequence divergence and identify outlier loci between population pairs, as well as within and between the lineages, and test for signals of neutral and adaptive markers across the genomes.