

## Improved Genetic Stock Identification of Chum Salmon Through the PacSNP Collaboration

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Understanding the distributions of chum salmon in the oceanic and near-shore waters of the North Pacific Ocean and Bering Sea has become increasingly useful for studying the effects of climate change, large-scale hatchery production, and bycatch in offshore fisheries. For more than two decades, genetics data have been used as a key tool for studying the migratory routes of the species based on extensive sets of data from spawning populations originating from across the species' range. During this period the genetic markers applied continually improved with advances in technology. With the collaborative development of the PacSNP baseline among North American and Asian researchers, single nucleotide polymorphisms (SNPs) were demonstrated as particularly amenable for multinational applications because they are easily shared, require little inter-laboratory standardization, and can be assayed through increasingly efficient technologies. The PacSNP baseline is focused on the continued development of the database and applying it to problems of international interest. We present improvements to the PacSNP baseline to provide a more comprehensive representation of populations and greater resolution through the addition of more informative markers.