



Population genomics

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PURPOSE

To provide the RAB with a description of the studies conducted by IPHC Secretariat on population genomics.

BACKGROUND

Understanding population structure is imperative for sound management and conservation of natural resources. Pacific halibut in US and Canadian waters are managed as a single, panmictic population on the basis of tagging studies and historical (pre-2010) analyses of genetic population structure that failed to demonstrate significant differentiation in the eastern Pacific Ocean. However, more recent studies have reported significant genetic population structure suggesting that Pacific halibut residing in the Aleutian Islands may be genetically distinct from other regions. Advances in genomic technology now enable researchers to examine entire genomes at unprecedented resolution. While genetic techniques previously employed in fisheries management have generally used a small number of markers (i.e. microsatellites, ~10-100), whole-genome scale approaches can now be conducted with lower cost and provide orders of magnitude more data (millions of markers). Using low-coverage whole genome resequencing we have the capability to examine genetic structure of Pacific halibut in IPHC Convention Waters with unprecedented resolution. By studying the genomic structure of spawning populations, genetic signatures of geographic origin can be established and, consequently, could be used to identify the geographic origin of individual Pacific halibut and, therefore, inform on the movement and distribution of Pacific halibut.

DISCUSSION

The main purpose of the present study is to conduct an analysis of Pacific halibut population structure in IPHC Convention waters using modern high-resolution genomic techniques. Recent studies have reported significant genetic population structure that suggest Pacific halibut residing in the Aleutian Islands may be genetically distinct from other regions. Genetic differentiation of the population on either side of Amchitka Pass was indicated, suggesting a possible basis for separating IPHC Regulatory Area 4B into two management subareas. However, these results were confounded by (1) the use of a small number of genetic markers and (2) the use of samples collected outside of the spawning season (i.e. winter) in some areas. These analyses employed summer-collected (i.e., non-spawning season) samples west of Amchitka Pass which may not be representative of the local spawning population, but rather a mixture of spawning groups on the feeding grounds. Therefore, it is advisable to re-assess those conclusions using samples collected during the spawning season and modern, high-resolution genomic techniques.

In January and February of 2020, the IPHC Secretariat conducted genetic sample collections on either side of Amchitka Pass (IPHC Regulatory Area 4B) during the spawning season to address the limitations of previous studies. These samples, in combination with previous samples collected during the spawning season (i.e. Bering Sea, Central Gulf of Alaska and waters off

British Columbia) (Figure 1) will be used to re-evaluate stock structure of Pacific halibut in IPHC Convention waters. The temporal replicates at many of these locations will enable the IPHC Secretariat to evaluate the stability of genetic structure over time, ensuring confidence in the results. The IPHC Secretariat has recently produced a high-quality reference genome and has generated genomic sequences from 610 individual Pacific halibut collected from five geographic areas (Figure 1) using low-coverage whole-genome resequencing (lcWGR). The lcWGR approach offers a cost-effective way to develop a large number (~millions) of single nucleotide polymorphisms (SNPs) that can be used as genetic markers to evaluate population structure with very high resolution. Using this method, we are working to establish a baseline of genetic diversity using sample collections made during the spawning season and have received funding (NPRB Project No. 2110) to use this data set to develop genomic tools (i.e. genetic marker panels) that can be used to conduct mixed stock analysis and identify the population of origin for samples collected outside of the spawning season. The utility of these tools will then be tested in two proof of concept applications comparing the stock composition of a) commercial fishery landings, and b) Pacific halibut collected at the latitudinal extremes of the species' range in the northeast Pacific Ocean (e.g. northern Bering Sea and northern California).

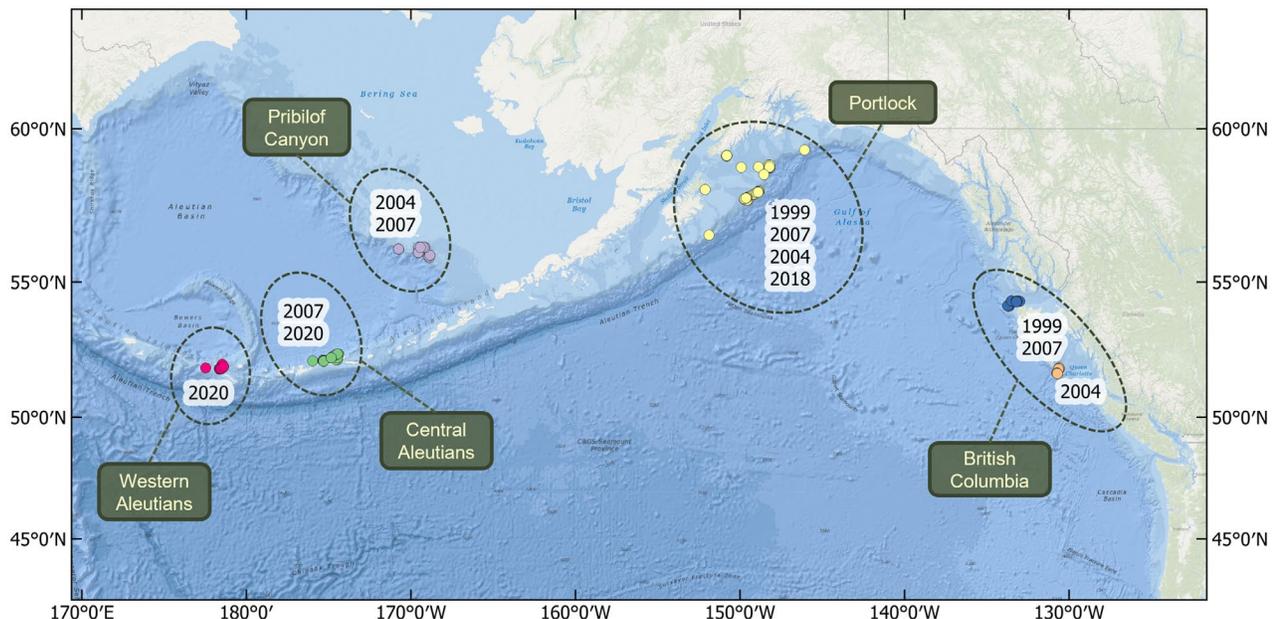


Figure 1. Map of sample collections made during the spawning season used for genomic analysis of population structure in Pacific halibut in the northeast Pacific Ocean.

RECOMMENDATION

That the RAB:

- 1) **NOTE** paper IPHC-2022-RAB023-12, which outlined the studies on population genomics by the IPHC Secretariat.