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## 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

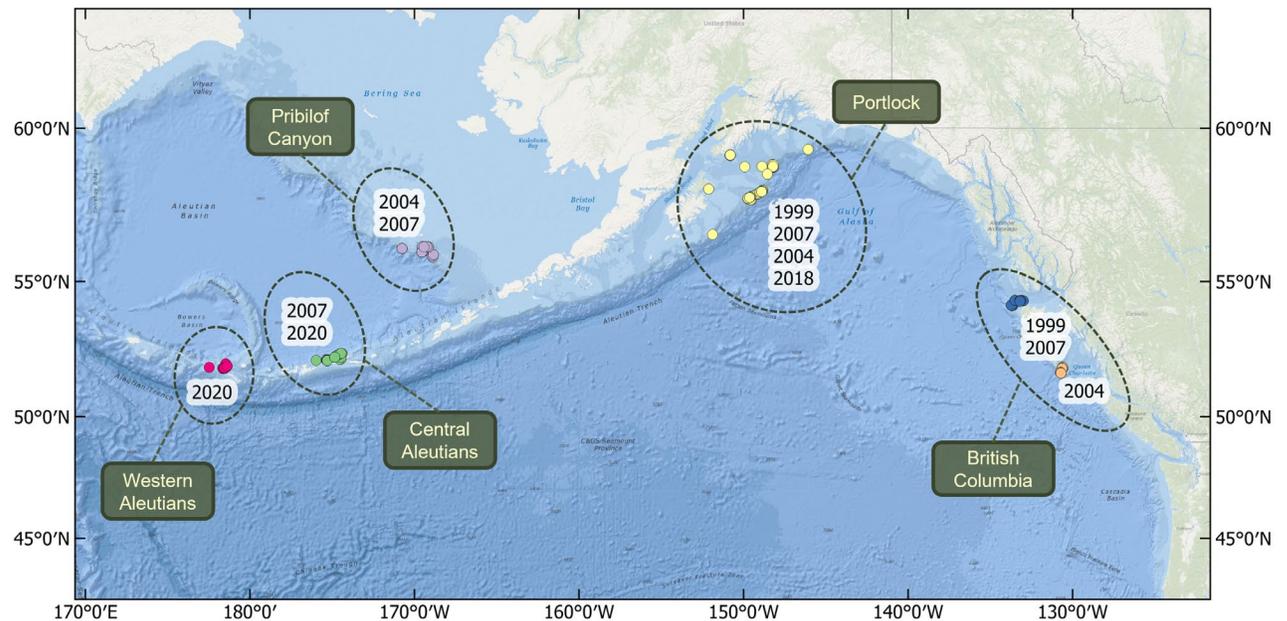
Understanding population structure is imperative for sound management and conservation of natural resources. Pacific halibut in US and Canadian waters are managed as a single, panmictic population on the basis of tagging studies and historical (pre-2010) analyses of genetic population structure that failed to demonstrate significant differentiation in the eastern Pacific. However, two studies published within this decade have reported significant genetic population structure suggesting that Pacific halibut residing in the Aleutian Islands may be genetically distinct from other regions. Recent 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 (~10-100), whole-genome scale approaches can now be conducted with lower cost and provide orders of magnitude more data (millions of markers). 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 on population genomics is to conduct an analysis of Pacific halibut population structure in IPHC Convention waters using 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. In particular, 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. In particular, previous 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 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. Given that the IPHC Secretariat completed the sequencing of the Pacific halibut genome in 2020, low-coverage whole-genome resequencing (lcWGR) will be used to obtain genomic sequences from 600 Pacific halibut (50 per collection). lcWGR 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, identify potentially adaptive regions of the genome, and used in other management applications. For example, a panel of SNPs could be developed to estimate the contribution of different spawning groups to a mixed sample or identify the geographic origin of individual Pacific halibut.



**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-2021-RAB022-13, which outlined the studies on population genomics by the IPHC Secretariat.