



Population genetics and migration

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PURPOSE

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

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 that suggest that Pacific halibut residing in the Aleutian Islands may be genetically distinct from other regions. Current genetic approaches provide an improved level of resolution that may be instrumental in establishing the genetic structure of the Pacific halibut population. By studying the genetic characteristics of spawning populations, genetic signatures of geographic origin can be established and, consequently, could be used to assign Pacific halibut to their spawning origin and, therefore, inform on movement and distribution of Pacific halibut.

DISCUSSION

The main purpose of the proposed studies is to incorporate genetic analyses into migration-related research in order to improve our understanding of Pacific halibut movement and dispersal and of the genetic structure of the Pacific halibut population. The IPHC Secretariat is proposing three specific topics for investigation.

- 1. Analysis of genetic variability among juvenile Pacific halibut in the Bering Sea and the Gulf of Alaska.** The aim of this study is to evaluate the genetic variability among juvenile Pacific halibut in a given ocean basin in order to infer information on the potential contribution from fish spawned in different areas to that particular ocean basin. We hypothesize that genetic variability among juvenile Pacific halibut captured in one particular ocean basin (e.g., eastern Bering Sea) may be indicative of mixing of individuals originating in different spawning grounds and, therefore, of movement. By comparing the genetic variability of fish between two ocean basins (i.e., eastern Bering Sea and Gulf of Alaska), we will be able to evaluate the extent of the potential contribution from different sources (e.g., spawning groups) in each of the ocean basins and provide indications of relative movement of fish to these two different ocean basins (Figure 1). The use of genetic samples from juvenile Pacific halibut collected in the NMFS trawl survey in the eastern Bering Sea and in the Gulf of Alaska, aged directly or indirectly through the length-age key, will allow us to provide genetic information from fish that are at or near their settlement or nursery grounds.

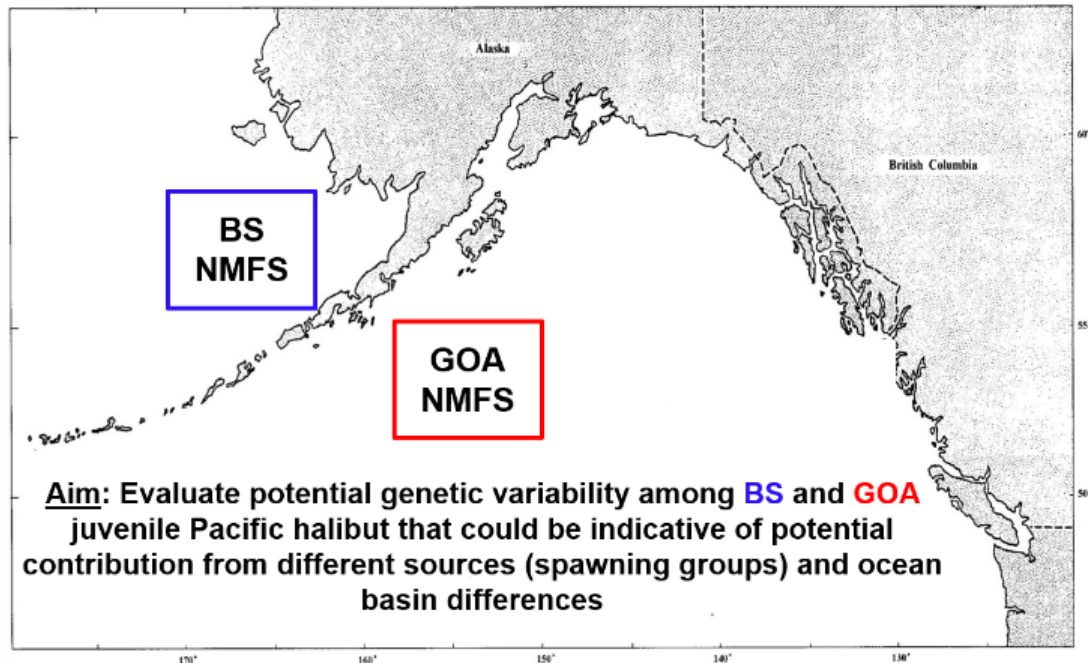


Figure 1. Map of the Northeastern Pacific Ocean where sampling for genetic analyses will take place in order to evaluate the potential genetic variability of Pacific halibut in different ocean basins.

2. **Analysis of genetic population structure in IPHC Regulatory Area 4B.** Recent studies have reported significant genetic population structure on the basis of microsatellites that suggest that 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 is indicated, suggesting a possible basis for separating IPHC Regulatory Area 4B into two management subareas. However, in order to evaluate that possibility it is advisable to re-assess those conclusions using samples specifically collected to evaluate the implied stock delineation. In particular, the existing analyses employed summer-collected (i.e., non-spawning season) samples west of Amchitka Pass and may or may not be representative of the local spawning population. Although unlikely, we cannot exclude the possibility that the observed differentiation in the Aleutian Islands may be representative of differentiation caused by dilution of the west-Aleutian sample by individuals from some other region. The proposed work would sample the local population on either side of Amchitka Pass during the spawning season so as to best characterize spawning structure and provide management advice regarding the relative justifiability for considering the western Aleutians as a genetically-distinct substock. Subsequently, genetic analyses will be conducted to evaluate the level of genetic differentiation between the two sampled areas. Sample collection will take place west and east of Amchitka Pass during the winter of 2020 in order to collect fish during the spawning season (Figure 2). A commercial fishing vessels has been chartered specifically for the purpose of collecting fin clip samples from 60 mature males and 60 mature females from each region.

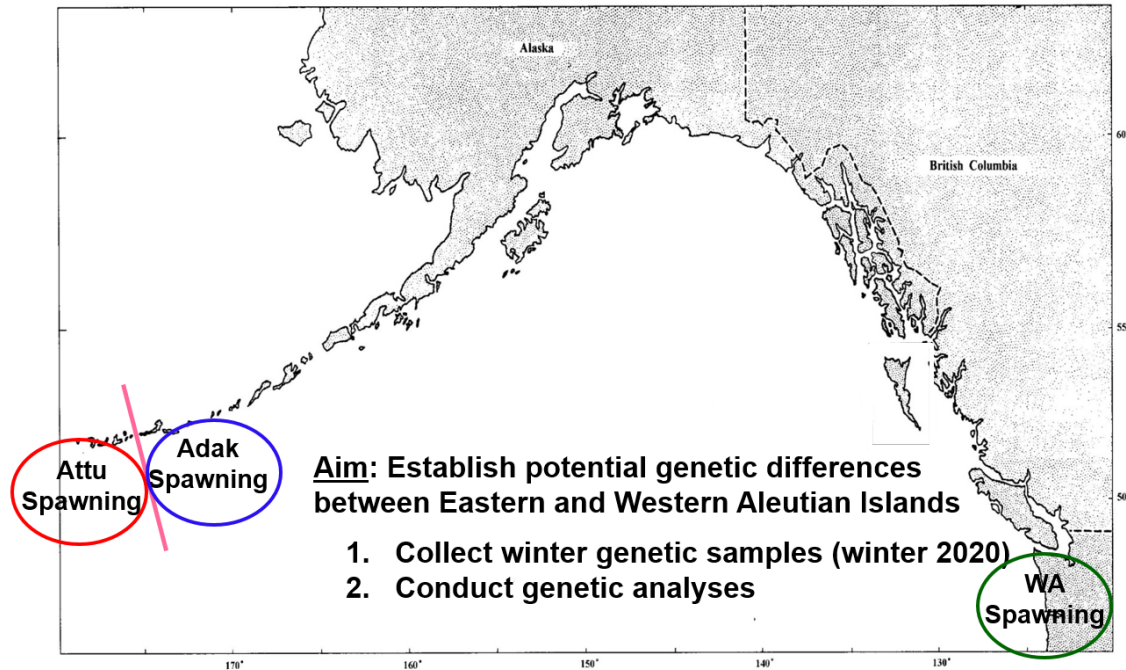


Figure 2. Map of the Northeastern Pacific Ocean where sampling for genetic analyses will take place in order to evaluate the potential genetic differences between fish spawned in the Western (Attu) and Central (Adak) Aleutian Islands.

- 3. Identification of potential genetic signatures of origin or spawning groups to revise population structure.** In order to expand our proposed studies evaluating the Pacific halibut population genetic structure to the entire northeast Pacific Ocean covering the IPHC Convention Area, a broader genetic study is proposed that aims at establishing genetic baselines from known spawning groups throughout the geographic area in question. In addition to the genetic samples that would be collected in the project described above (eastern and western Aleutian Islands), we propose to collect additional winter samples from spawning fish off the Washington coast representing the southernmost spawning groups on the northeast Pacific Ocean. With these genetic samples, together with winter samples collected in the Portlock area (central Gulf of Alaska) in 2018 and in Haida Gwaii in 2004 and in the Bering Sea (Pribilof Canyon) in 2004, we plan to establish genetic signatures of these spawning groups to revise the genetic population structure with up-to-date genetic techniques (Figure 3).

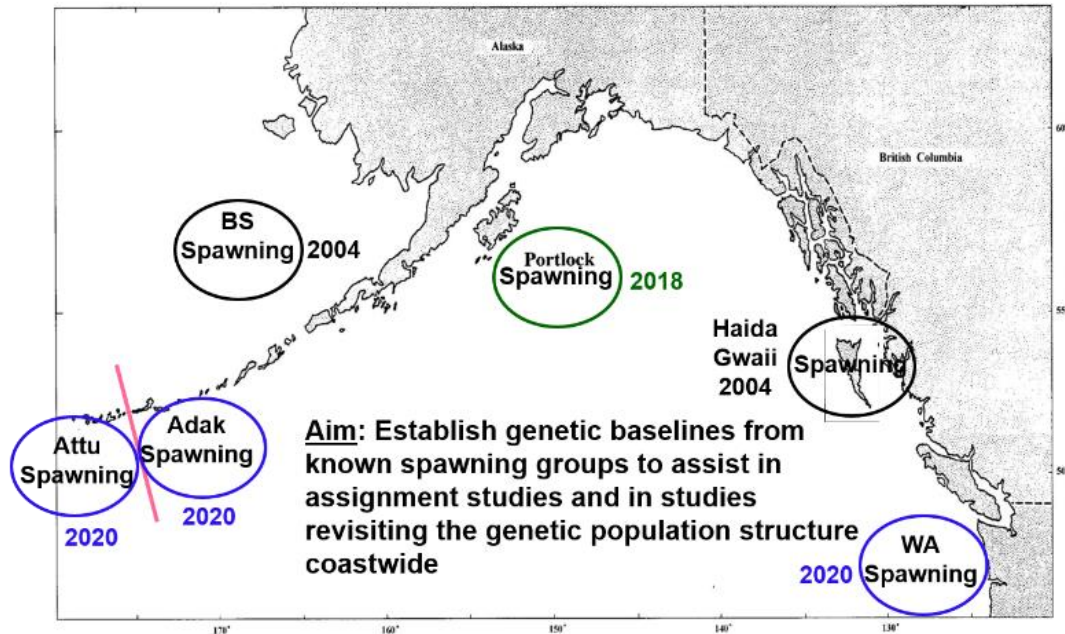


Figure 3. Map of the Northeastern Pacific Ocean where additional sampling, complementing previously collected samples, for genetic analyses will take place in order to establish the genetic characteristics of known spawning groups (genetic baselines).

RECOMMENDATION

That the RAB:

- 1) **NOTE** paper IPHC-2020-RAB021-12, which outlined the studies on population genetics and migration by the IPHC Secretariat.