**Genomics for Aleutian Islands, Gulf of Alaska, and eastern Bering Sea Pacific cod stock assessments 2022 (Sara Schaal, Wes Larson, Ingrid Spies)**

The most recent genomic analysis of Pacific cod includes a new publication that used pooled whole genome sequencing (Pool-Seq), as well as a new study conducted during 2021 and 2022 that used low coverage whole genome sequencing (lcWGS). The Pool-Seq manuscript (Spies et al. 2022) is the culmination of several years of effort, while the lcWGS is more recent and provides a more powerful approach to gather individual-based sequence data from the whole genome. Here, we focus on how the two studies contribute to our knowledge of the population structure of Pacific cod throughout Alaskan waters.

Low-coverage whole-genome sequencing analysis of 429 samples of Pacific cod from known spawning regions during spawning season indicated population structure similar to what was previously known, but with finer resolution and greater power owing to the larger number of markers. Using 1,922,927 polymorphic SNPs (Figure 1), the pattern of population structure mostly resembles isolation-by-distance, in which samples from proximate spawning areas are more genetically similar than samples from more distant areas. Isolation-by-distance was observed from western Gulf of Alaska (Kodiak and the Shumagin Islands) through Unimak Pass and the eastern Aleutian Islands. Previous studies have reported an isolation-by-distance pattern in Pacific cod using microsatellite markers (Cunningham et al. 2009 and Spies 2012) and reduced-representation sequencing (Drinan et al. 2018). Within the isolation-by-distance pattern, there were some distinct breaks in the population structure. The most significant genetic break occurs between western and eastern Gulf of Alaska (GOA) spawning samples (Figure 1), and was supported by previous research that highlighted the zona pellucida gene region (Spies et al. 2021).

A new finding from the lcWGS data was the documentation of a genetic break in samples taken from the western Bering Sea shelf, adjacent to Russia, and samples from all other regions. In other words, this study identified a new genetic group in the Bering Sea represented by samples from Russia along the western Bering Sea shelf. In addition, a subset of samples collected from Pervenets Canyon in the eastern Bering Sea appeared genetically similar to the western Bering Sea shelf group (Figure 1 bottom right where light blue points, Pervenets Canyon, mix with dark blue points, Russia). The majority of samples from the eastern Bering Sea were genetically more similar to Aleutian Islands and western Gulf of Alaska samples which was a significant deviation from the isolation-by-distance pattern found with the rest of the samples (Figure 1 center where light blue points mix with green squares, Aleutian Islands, and pink circles, western Gulf of Alaska). This result suggests an unresolved combination of isolation-by-distance and mixing among eastern Bering Sea cod stocks with the Aleutian Islands and western Gulf of Alaska.

Ideally resource management should establish management units that match the spatial extent of the stock or population under consideration (Taylor 1997; Fu and Fanning 2004; Laikre et al. 2005; Spies and Punt 2015), but mismatches are common owing to lack of information on stock structure (e.g. Reiss et al. 2009). While eastern Gulf of Alaska, Aleutian Islands, and western Bering Sea shelf spawning cod appear distinctive, genetic continuity in the form of isolation-by-distance and mixing between eastern Bering Sea through western Gulf of Alaska cod merits some consideration. The genetic break between western and eastern Gulf of Alaska cod indicates that this management unit may consist of two distinct stocks, and future research that investigates the location of the break during summer and winter seasons would benefit management. The genetic break within the eastern Bering Sea and continuity between eastern Bering Sea and western Gulf of Alaska cod also merits consideration of the eastern Bering Sea management unit.

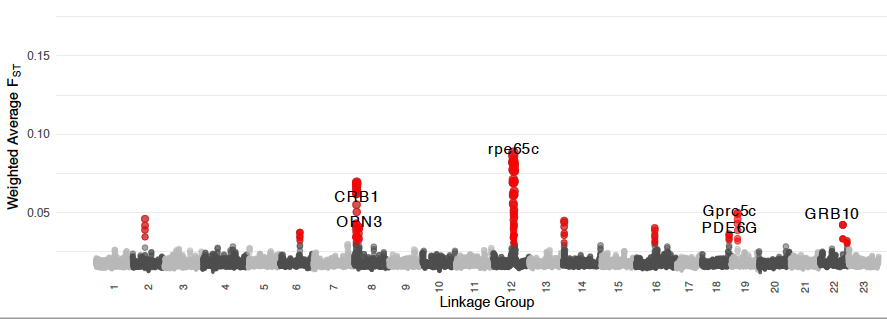
To this point, all the patterns we discussed are present in both neutral and adaptive markers. However, we observed regions of the genome that show evidence for local adaptation within the Aleutian Islands spawning cod using lcWGS and PoolSeq data (Spies et al. 2022, Figure 2). More specifically, at neutral markers Aleutian Island populations seem to follow the subtle IBD pattern documented throughout much of the western GOA. However, Aleutian Island populations are highly diverged at a few genomic regions that we believe are adaptively significant (Spies et al. 2022, Figure 2). These adaptive differences provide further support for the Aleutian Island management unit that was established as distinct from the Bering Sea in 2013.

Taken together, genetic results indicate that a single stock assessment that encompasses eastern Bering Sea and western Gulf of Alaska cod should be explored. All genetic samples were taking during spawning season, in which more than half the fishing takes place on the spawning stock. Satellite tagging is beginning to help us understand cod behavior and migration patterns outside of spawning season, and current and future research should also consider a seasonal stock assessment that accounts for seasonal differences in distribution. Future genetics work will use a GT-seq panel (an informative panel of SNPs that can be screened cheaply) to classify the spawning stock of origin for summer-caught fish to understand how biomass might change seasonally.

The presence of individuals from different genetic groups in the same spawning samples is not completely understood but is also not unprecedented. If these cod were in the spawning area and they were captured in the proportions observed, the populations would rapidly interbreed and soon appear genetically similar. Given that genetic differences consistently appear, however, it is less likely that individuals from different genetically distinct populations are spawning together in these regions. There is a precedent for the observation of genetically distinct individuals captured during spawning season in Pacific cod; a study of Pacific cod taken from the Korean peninsula provided an opportunity to observe this phenomenon (Fisher et al. 2022). In this study spawning populations showed extremely high levels of differentiation and more dispersing individuals were observed than was expected, some of which were immature. Pacific cod have a protracted spawning season of up to three months, which may consist of spawning and migrating to and from the spawning and feeding areas for some individuals. Female Pacific cod release all eggs in a single spawning lasting approximately 20 seconds (Sakurai and Hattori 1996). While males appear to be able to release sperm over a longer period, it is possible that random collections during spawning season of mature Pacific cod may also reflect cod that have moved into a spawning area, but may be feeding and will not spawn there. Similar to the analysis by Fisher et al. (2022), we postulate that the genetic distinctiveness observed among most individuals in a spawning collection would not be present if there were a high effective migration rate. We instead hypothesize that individuals are moving during the spawning season through various spawning grounds on route to where they will spawn or feed subsequent to spawning. This movement pattern within the protracted spawning season may begin to explain some of the unresolved patterns in the lcWGS results (e.g., some western Gulf of Alaska caught individuals being genetically similar to eastern Gulf of Alaska cod). Further research is needed to discriminate among cod that appear to be actively spawning and non-spawning individuals present in spawning areas. In particular, merging genetic results with tagging studies will be a powerful tool for resolving these patterns.

Figure 1. Principal components analysis of 1,922,927 polymorphic SNPs from the lcWGS dataset. 

Figure 2. Regions of the genome that contain outlier loci, due to high *F*ST, a measure of genetic differentiation. Figure based on Pool-Seq data (adapted from Spies et al. 2022)



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