EBS summary

Low-coverage whole-genome sequencing analysis of 429 samples of Pacific cod from known spawning regions during spawning season indicates 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 2.1), the pattern of population structure mostly resembles isolation-by-distance (IBD), 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 2.1), and was supported by previous research that highlighted the zona pellucida gene region (Spies et al. 2019). Notably, there was not a significant break in genetic structure between the eastern Bering Sea (Unimak) and the western Gulf of Alaska (Shumagins and Kodiak).

A new finding from the lcWGS data was the identification of a new genetic group in the Bering Sea represented by samples from Russia along the western Bering Sea shelf. We refer to this as a northern Bering Sea ‘type’. 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 2.1 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 2.1 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 a strong genetic break with the northern Bering Sea type. 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 2.2). These adaptive differences provide further support for the Aleutian Island management unit that was established as distinct from the Bering Sea in 2013. Overall, the presence of a distinct northern Bering Sea type, a distinct eastern Gulf of Alaska type, and a mixed eastern Bering Sea/western Gulf of Alaska stock indicate that there may be opportunities to restructure management units for Pacific cod in those regions. More research is needed to fully understand how the types of cod are distributed during non-spawning seasons.

GOA summary

Recent research funded by the Pacific States Cod Disaster Fund includes evidence for distinct genetic differences among some juveniles found in the western Gulf of Alaska, which may be the result of differential spawn timing. In addition, we found mixing between eastern GOA and western GOA juvenile cod, indicating transport not only by the prevailing currents moving eGOA cod westward, but also eddies that likely move wGOA eastward (S. Schaal pers. comm.). The fate of juvenile cod transported long distances is unknown; however, it is unlikely they remain and successfully spawn in a new location because of the large genetic differentiation observed between eastern and western GOA spawning cod populations. Several transcriptomics experiments on age-0 and juvenile cod investigated mechanisms of mortality under increased temperatures and co-occurring acidification (S. Spencer pers. comm.). Results indicated heightened immune response paired with lipid dysregulated under warming-associated mortality. Acidification slowed/impaired digestion, which may also contribute to larval condition. Finally, investigations are underway to evaluate whether there is a genetic difference between cod tagged in the western GOA that migrate into the EBS during summer months vs. those that remain stationary (L. Timm pers. comm.).