

Genetic population structure of blackspotted rockfish in Alaska using low coverage whole genome sequencing (lcWGS), and its management implications.

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Blackspotted rockfish are dispersed throughout the Gulf of Alaska, Bering Sea, and Aleutian Islands. They co-occur with rougheye rockfish in most Alaskan waters and are managed as a complex, but generally only blackspotted rockfish are found in the Aleutian Islands. This species is long-lived (>100 years) and has a generation time of ~50 years. Blackspotted rockfish larvae are pelagic for weeks to months and juveniles settle in shallower water (200-300 m). Adults move into deeper water (300 - 500 m) and live near the bottom. Movement is hypothesized to be limited, like other rockfish species.

The blackspotted rockfish fishery in the Western Aleutian Islands (Area 543 west of Longitude 177E) has had disproportionately high catch rates as bycatch in the POP fishery over most of the past two decades. This has been an ongoing management issue, and in recent years the Western Aleutian Islands/Central Aleutian Islands subarea Allowable biological catch (ABC) has been partitioned into a “Maximum Subarea Species Satch” or MSSC. Several genetic studies have attempted to characterize stock structure in this species, to inform management of this stock and determine whether further spatial management is warranted, such as replacing the MSSC with a separate quota or TAC. No genetic structure was detected in blackspotted rockfish in a microsatellite analysis presented to the Plan Team in 2014 (12 markers, Godinez and Gharrett, in prep), or in a more recent low coverage whole genome sequencing analysis (lcWGS) (millions of markers, Timm et al. in prep). Because lcWGS provides information on the entire genome, it is considered the most comprehensive and powerful source of genetic information to examine stock structure.

In considering how to interpret these new genetic results in a management context, it is important to note that the primary factors that influence genetic divergence are population size, migration, generation time, and time since colonization. In larger populations, genetic divergence occurs more slowly than in small populations and species with longer generation times diverge more slowly. A lack of genetic structure in blackspotted rockfish is unsurprising given large population sizes, long generation time, and dynamic habitats over evolutionary time since past glaciation events. The habitat of the Aleutian Islands was highly variable over evolutionary time (~10k years+) due to glaciation, leading to unknown patterns of connectivity and colonization. Simulations suggest that migration rates $\geq 1\%$ per generation would homogenize genetic structure in this species, but these rates are much lower than the 10% migration rates considered necessary for demographic independence. In other words, genetic results do not inform the scale of migration because other factors may be responsible for the observed result. The limited power of genetic analyses to identify meaningful demographic connectivity has led to calls to fully consider both genetic and non-genetic information when considering spatial stock units (Waples et al. 2008, Spencer et al. 2010).

Interpretation of management implications of the recent genomic analysis is also aided by a review of how the Plan Team and SSC interpreted 2014 microsatellite analysis. In 2014, the Plan Team and SSC expressed concern regarding stock structure (despite the updated genetic data), based on the low abundance and high exploitation rates in the WAI. Since 2014, the exploitation rates in the WAI has become more disproportionate relative to estimated biomass, prompting both the Plan Team and SSC in 2020 to call for steps for identifying more effective spatial

management tools. Given this non-genetic information on increasing exploitation rates and continued low abundance in the WAI, there is not evidence to alter the recent Plan Team and SSC recommendations that more effective spatial management measures should be identified.

References

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Waples, R.S., A.E. Punt and J.M. Cope. 2008. Integrating genetic data into management of marine resources: how can we do it better? *Fish and Fisheries* 9:423–449.