



# Population Structure of Black Rockfish in the Gulf of Alaska

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## Introduction

Black rockfish (*Sebastes melanops*) stocks are harvested extensively in Alaska by both commercial and sport fisheries, and like rockfishes throughout the North Pacific, they are easily overharvested and slow to rebuild. Schools of adults often aggregate over shallow rocky areas making them particularly susceptible to fishing.

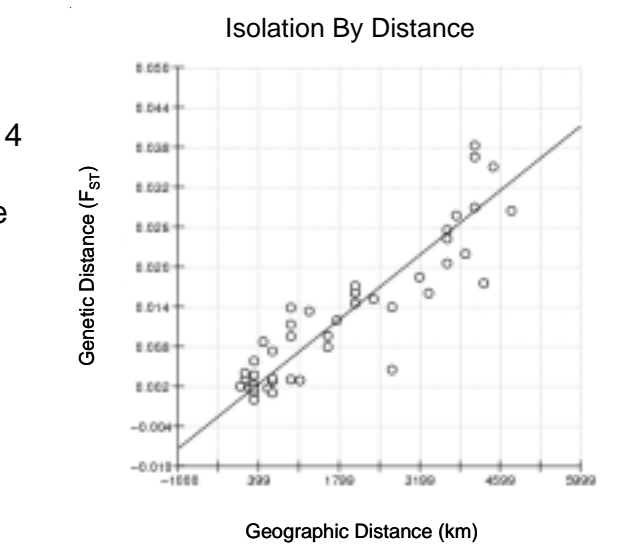
The understanding of the genetic structure of discrete stocks and the biological significance of local depletions is a central feature of conservation and restoration of commercially exploited fisheries resources. Marine organisms represent unusual challenges in the study of population genetics. Adult marine organisms may make extensive migrations over huge distances and have highly dispersive larval and early life history stages. In this study, we surveyed the population structure of 11 populations of black rockfish ranging from the Alaska Peninsula across the Gulf of Alaska to the Pacific Northwest using a suite of 10 microsatellite loci.



Mondragon Photography

## Results (continue)

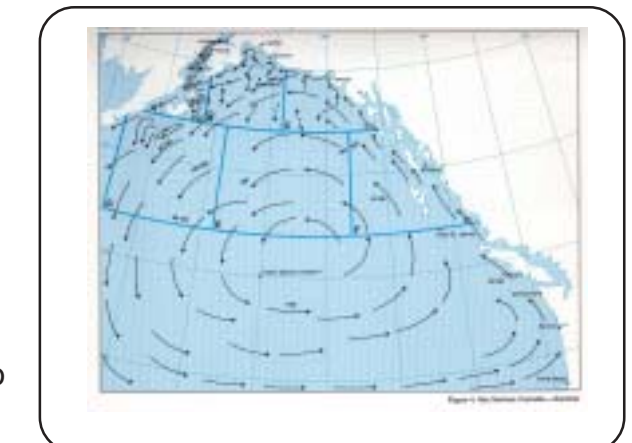
An isolation by distance analysis was conducted resulting in an estimated positive correlation ( $R^2 = 0.814$ ) between genetic distance ( $F_{ST}$ ) and geographic distance (km).



## Discussion

Black rockfish exhibit low but significant population structure across the range. This low level of structure is consistent with previous studies of genus over broad geographic ranges based on microsatellite and allozyme loci. There was little divergence, despite broad geographic separation, among the Alaska Peninsula and western Gulf of Alaska populations ranging from Akutan to Valdez. In general, the population structure fits an *isolation by drift* model.

However, we did find significant divergence between western Gulf of Alaska and Southeast Alaska populations as indicated by differences between collections from Valdez and those from Yakutat. We also observed significantly higher number of alleles in the Southeast Alaska and Pacific Northwest populations. These results support the existence of a zoogeographic discontinuity between the western Gulf of Alaska and Southeast Alaska. In this area, there are interruptions to the northward flowing Alaska Current as a result of deepwater troughs (Wise and Leslie 1988). Flow is diverted shoreward with easterly flow occasionally occurring in the areas from Yakutat to Kayak Island at the entrance to Prince William Sound. These features may have a significant effect on patterns of larval drift and may be reflected in the observed discontinuities.



From Wise and Leslie 1988

Southeast Alaska populations differed significantly from those of the Pacific Northwest, a possible reflection of the splitting of the northward flowing Alaska Current from the southward flowing California Current along the British Columbia coast. A thorough investigation of populations from the more southern portions of the range will provide a more complete picture of the full range of the genetic structure and the observed discontinuities.

Literature Cited  
Wimberger, P., J. Burr, A. Gray, A. Lopez, and P. Bentzen. 1999. Isolation and characterization of twelve microsatellite loci for rockfish (*Sebastes*). *Marine Biotechnology* 1: 311-315.

Wise, J. L. and L. D. Leslie. 1988. Section I: Selected topics in marine and coastal climatology. Pages 1-1 - 131 in William A. Brower, Jr., Ronald G. Baldwin, Claude N. Williams, Jr., James L. Wise, Lynn D. Leslie. *Climatic atlas of the outer continental shelf waters and coastal regions of Alaska*. Volume 1 Gulf of Alaska, Anchorage: AEIDC, University of Alaska, 1988.

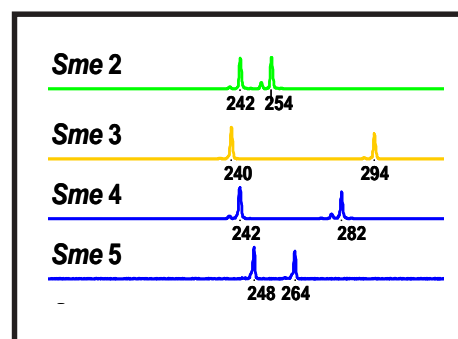
## Acknowledgements

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## Methods

Black rockfish were collected either by hook and line or were sampled from commercial and sport fish catches. Hook and line sampling was generally non-lethal as sampling was within 10 m of the surface. Sample sizes were set at 100, but realized sample sizes varied from 24 to 130 individuals. Fin clips from individual fish were excised, placed in ethanol, and shipped to the laboratory for analysis.

DNA was extracted using a rapid precipitation method; all microsatellite analyses were conducted on an ABI 377 automated sequencer. Individuals were analyzed for 10 microsatellite loci including tri- and tetranucleotide loci cloned from black rockfish (*Sme 2, 3, 4, 5, 8, 9, 11, 14*; Alaska Department of Fish and Game, unpublished, primer sequences available upon request) and dinucleotide loci from quillback rockfish *S. maliger* (*Sma 1,3*; Wimberger et al. 2000).



## Results

A wide range of variation was observed at the 10 loci with number of alleles per locus varying from nine to 50. Overall, 240 alleles were observed across all loci and populations. Population structure and relationships among collections were evaluated using multiple approaches.  $F_{ST}$  was calculated among all collections as well as pairwise between collections using *FSTAT* version 2.9.3. Significant population structure was detected with an overall value of  $F_{ST}$  of 0.011 ( $P < 0.001$ ). A trend of increasing allelic richness was observed with the Southeast Alaska and Pacific Northwest populations having significantly greater allelic richness than those in the western Gulf of Alaska group ( $P = 0.02$ ).

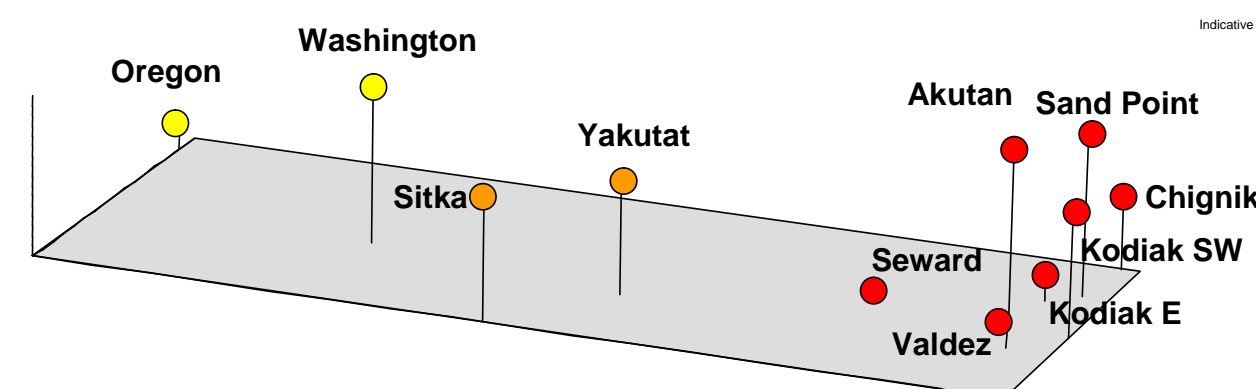
Pairwise tests for population differentiation among all populations (excluding those with < 30 individuals; Seward and Westport) show a consistent pattern of non-significant tests among all of the western Gulf of Alaska group (Akutan to Valdez). However, significant test statistics were observed between all the western Gulf of Alaska group and every Southeast Alaska and Pacific Northwest population.

A matrix of pairwise  $F_{ST}$  values between all pairs of populations was also computed and used to visualize population structure using multidimensional scaling (MDS). The MDS shows a large cluster of closely related populations from the Alaska Peninsula through the central Gulf of Alaska. The populations from Yakutat and Sitka from Southeast Alaska fall between the large western cluster and those from the Pacific Northwest.

## Pairwise Tests of Population Differentiation

	Sand Point	Chignik	Kodiak--Southwest	Kodiak--East	Valdez	Yakutat	Sitka	Oregon
Akutan	NS	NS	NS	NS	NS	**	**	**
Sand Point		NS	NS	NS	NS	**	**	**
Chignik			NS	NS	NS	**	**	**
Kodiak--Southwest				NS	NS	**	**	**
Kodiak--East					NS	**	**	**
Valdez						**	**	**
Yakutat							NS	**
Sitka								**

Indicative adjusted nominal level (5%) for multiple comparisons is: 0.001



Multidimensional scaling of pairwise  $F_{ST}$  values. Color of points correspond to collections on the map above.

