Exploration of Depth Differentiation of Two Closely Related Rockfish Species Identified through Genetic Analysis

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This project details the habitat preferences of the rougheye rockfish complex. These long-lived and late-maturing fishes are highly vulnerable to overfishing. This commercially harvested complex was identified as two distinct species in 2008, Sebastes aleutianus, and Sebastes melanostictus, that has yet to be split into two distinct management stocks. The purpose of this study was to determine whether or not the two closely related rockfish species occupy different depth habitats. To answer this question I first used genetic techniques to identify 96 frozen rockfish fin clippings that I received from the NOAA Ted Stevens Marine Research Institute in Juneau, Alaska. This procedure involved lysing the fin cells, filtering out pure DNA, and running a polymerase chain reaction (PCR) on the DNA with a Sebastes species microsatellite locus uSma6. The product was then passed through a 3730xl DNA ANALYZER which allowed me to analyze microsatellite sizes and assign each sample a positive species identification. Using this identification data, I then calculated the field identification accuracy for the two stocks to be 82%. Applying a two-sample t-test, I found that the data strongly supported the alternate hypothesis that the mean habitat depths are different ($p<0.001$) between the two species, with the mean depth of blackspotted rockfish (267m) being deeper than that for the roughety rockfish (236m). Currently, blackspotted and rougheye rockfish are being managed as a single population. The findings of this research suggest that that might not be the best management style and may lead to fishing of one species disproportionately to the other, possibly leading to overfishing.

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