Microchemical techniques to evaluate priority contaminant sources along the migration routes of Chinook (Oncorhynchus tshawytscha) and Coho Salmon (Oncorhynchus kisutch) Micah Quindazzi^a, Tanya Brown^b and Francis Juanes^a





Fisheries and Oceans Canada



Introduction

Tracking the marine migrations of salmon is important for understanding marine survival and contaminant profiles^{1,2,3}. These considerations are important both for the health of salmon populations^{4,5}, as well as their predators^{1,6,7}. Current methods of tracking these migrations are constrained by costs, methods of retrieval, and need to individually tag salmon. Intrinsic tags can overcome these problems^{8,9}.

Questions and Hypotheses

- Is otolith microchemistry an effective way of tracking marine migrations of Chinook and Coho Salmon? hypothesize that this method will be effective due to overall differences in water chemistry and physiological conditions between regions.
- Does early marine growth determine the marine migration life history displayed by the individual? hypothesize that faster growing fish will more likely become residents.

Methods

- Coho baselines captured from Strait of Georgia (SoG) and West Coast Vancouver Island (WCVI) in 2018
- Coho collected from hatchery facilities across Southern BC (Big Qualicum, Chilliwack, and Quinsam)
- Conducted laser ablation inductively coupled plasma mass spectrometry (LA-ICP-MS) to collect element and trace element data
- N=20 per baseline region; N=52 for BQ; N=68 for CH; N=58 for Q
- Scale circuli spacing measured for first 10 circuli post marine check for early marine growth measurement

Statistical Analysis

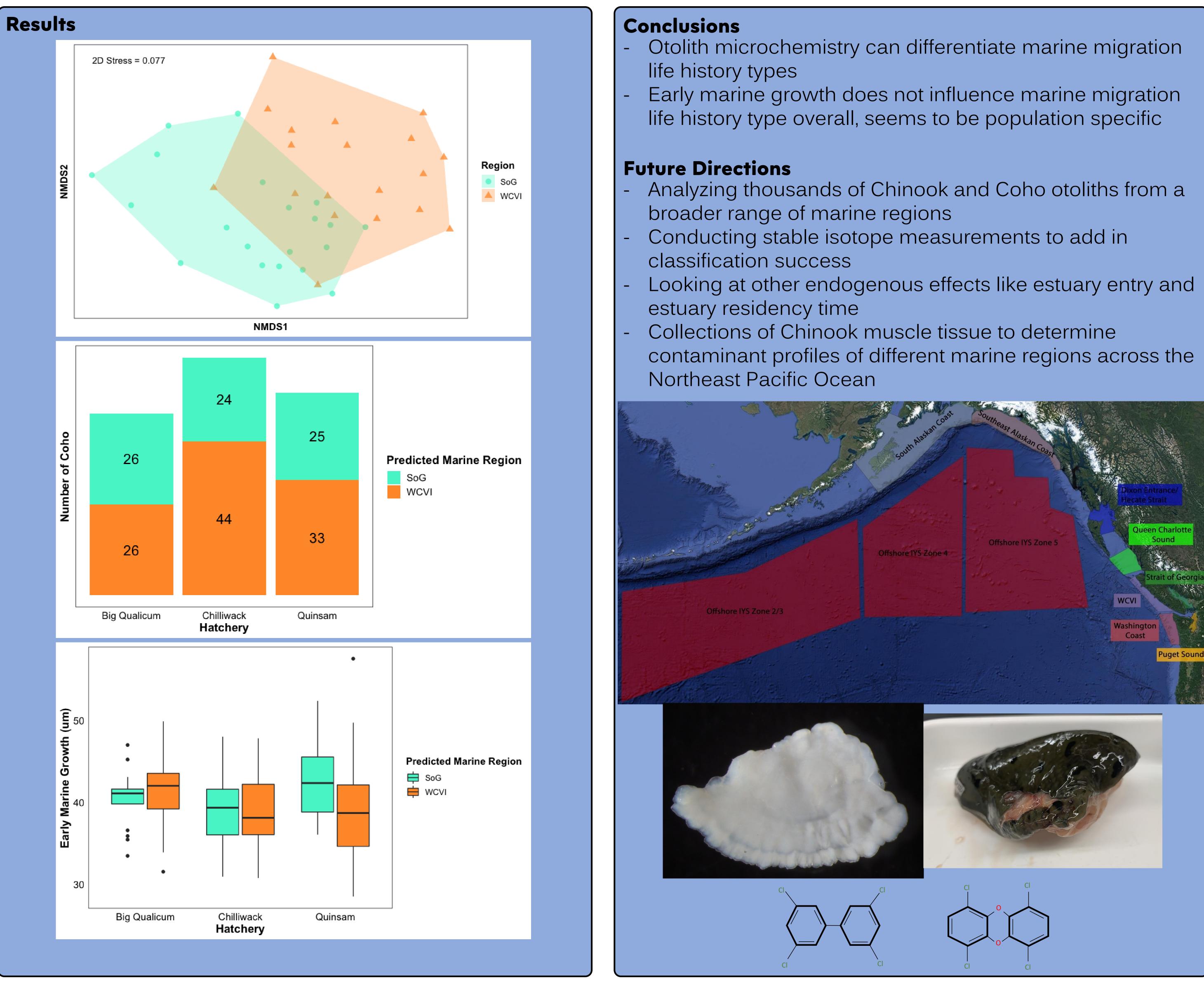
- Utilized Random Forest (RF) models to assign salmon to different marine regions
- Created PERMANOVA model to compare marine migration life history type against early marine growth rate, population, origin, and sex

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a. University of Victoria b. Department of Fisheries and Oceans

