

Environmental Studies Program: Ongoing Studies

Study Area(s): Cook Inlet

Administered By: Alaska OCS Region

Title: Using Genotyping-by-Sequencing (GBS) Population Genetics Approaches to Determine the Population Structure of Tanner crab (*Chionoecetes bairdi*) in Alaska (AK-13-03-20)

BOEM Information Need(s) to be Addressed: BOEM needs population level information about species that could be affected by oil and gas exploration, development and production. Information from this study will inform NEPA analyses for future lease sales, EPs, and DPPs.

Total BOEM Cost: \$25,000
plus Joint Funding (\$25,000)

Period of Performance: FY 2016-2018

Conducting Organization: CMI, UAF

Principal Investigator(s): Genevieve Johnson

BOEM Contact: [Rick Raymond](#)

Description:

Background: Genetic tools are increasingly being applied to assess population structure and connectivity in marine species, and are in many cases identifying much greater spatial structure than previously assumed by other tools. Understanding the population structure of tanner crabs (*Chionoecetes bairdi*) in the Cook Inlet Planning Area using genetic tools will be important for determining effective management areas and stock boundaries. It is still unknown whether the stocks around Cook Inlet and Shelikof Strait are isolated and distinct or the populations are substantially connected to other populations throughout Alaska. If the former is the case, OCS activities in this area would need to be concerned with the potential of impacting an isolated stock that would not be supplemented by other populations. If the latter is the case, any potential impacts from OCS activities might be lessened by recruits entering affected areas from elsewhere.

Tanner crabs were historically an important commercial species in Alaska, but declines in recent decades led to several fishery closures. The causes of these declines and the lack of substantial recovery are still poorly understood. Improved understanding of the genetic stock structure and exchange between regions may help to inform management practices for this species. Genetic studies of a closely related species, snow crab (*Chionoecetes opilio*), show substantial population connectivity throughout its distribution. However, tanner crabs tend to inhabit warmer, nearshore waters and larvae may not be as exposed to potential agents of dispersal such as ocean currents.

Objectives:

- Test the null hypothesis of genetic homogeneity across all sampled populations using a massively multi-locus genotype dataset generated through the GBS approach. If genetic heterogeneity is detected, test alternative models of population structure.
- Assess whether populations in BOEM special project areas of Cook Inlet and Shelikof Strait are distinct or contiguous with nearby populations and evaluate the extent of their natural genetic variability.
- Test for evidence of extreme population size changes in the extent and nature of observed standing genetic variation.

Methods: Samples of hemolymph (a fluid analogous to vertebrate blood) were collected from approximately 800 tanner crabs caught in trawl and crab pots during ADF&G and NMFS summer surveys. Researchers will conduct genetic analysis by the Genotyping by Sequencing (GBS) technique. Total genomic DNA will be extracted from hemolymph samples using established protocols. The DNA quality will be checked by gel electrophoresis and fluorometry. GBS requires high quality DNA, so only samples that yield large, unbroken molecules will be used. Briefly, genomic DNA from each sample is fragmented using a combination of restriction enzymes to generate pools of variable length fragments flanked by restriction enzyme recognition sites. The restriction enzyme digested pools from each sample are then linked to individual identifying tags as well as other tags specific to the sequencing platform. The tagged genomic fragment pools are then stringently size selected to focus sequencing effort on a well---defined subset of restriction digest fragments. This ensures that the same genomic regions or loci are sequenced from the different individuals being genotyped. The size-selected pools are then sequenced on a platform that generates several million sequences reads for each individual analyzed. Using bioinformatic tools, sequence output is quality controlled and manipulated to generate high quality multi- locus genotype datasets.

Collection data associated with the samples examined in this study will be archived in the ARCTOS database at the University of Alaska Museum. Sequencing output will be deposited in the sequence reads archive (SRA) of the National Center for Biotechnology Information. These sequence reads will be made freely available for public dissemination and use in further studies. Finally, a full dataset consisting of quality filtered multi-locus genotypes from all specimens examined in the study will be published as supplementary information for any research publications resulting from this work.

Current Status: Completed

Final Report Due: December 2017

Publications Completed:

Johnson, G. 2018. Using Genotyping-by-Sequencing (GBS) Population Genetics Approaches to Determine the Population Structure of Tanner Crab (*Chionoectes bairdi*) in Alaska. In: CMI Graduate Student Projects: Volume 1. University of Alaska Coastal Marine Institute, Fairbanks, Alaska. OCS Study BOEM 2018-021.

Affiliated WWW Sites: <http://www.boem.gov/akstudies/>
<http://www.cfos.uaf.edu/cmi/>
<https://marinecadastre.gov/epis/#/search/study/100136>

Revised Date: August 8, 2018