

**Annual Progress Report to:**

**Pollock Conservation Cooperative  
Research Center  
School of Fisheries and Ocean Sciences  
University of Alaska Fairbanks  
Fairbanks, AK 99775-7220**

**for Project:**

**Combining genetics and population dynamics to improve management  
of Pacific ocean perch (*Sebastes alutus*).**

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**Summary of Work from 1 January 2011 to 31 October 2011.**

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## **Abstract**

Pacific ocean perch (POP) are the most abundant *Sebastes* rockfish species in Alaskan waters in both biomass and catch. An assumption made for many marine species, such as POP, which have pelagic larvae and apparently mobile adults, is that their population structures extend over very broad reaches, possibly including much of the natural range. Genetic studies of POP population structure have demonstrated that relatively strong divergence occurs between collections that were sampled at locations spaced about 400 km apart along the Gulf of Alaska (GOA) and Bering Sea (BS) continental slopes (Palof et al. 2011). The degree of divergence suggests that, although population structure is not a consequence of geographic or oceanographic boundaries, the limited net dispersal that occurs in both pelagic larvae and adults restricts the spatial scale of POP production to areas that are related to the average distance moved between birth and reproduction called neighborhoods. The spatial scale of neighborhoods (productivity units) is the geographic scale on which management should focus. Incorporating demographic information from our genetic studies requires an evaluation of the current POP survey and fishery data. In this study we plan to develop a robust estimate of neighborhood size, determine if there is natural spatial variability that can be detected in current population modeling, and incorporate spatial structure into population dynamics and harvest models for POP.

## **Introduction**

In this PCCRC project, we are developing and applying quantitative models to the GOA POP population to examine the influence of population subdivision on population dynamics models that are used to evaluate sustained production of exploited resources. The project arose because an assumption made for POP and many other marine species, which have pelagic larvae and apparently mobile adults, is that their populations extend over very broad reaches, possibly including much of their natural ranges. However, this may often not be the case.

From the results of research conducted in our laboratory, we have preliminary estimates of the extent of substantial dispersal and of neighborhood size. The questions that we will address are the effects that harvest patterns exert on the production and genetic structure of POP and, by extension, other species for which limited dispersal results in a neighborhood models for population structure, and for which the neighborhoods are much smaller than the management areas. To evaluate these effects, we plan to develop quantitative models that include information

about dispersal, population dynamics, and exploitation; and to test with simulations the effects of different spatially-based harvesting strategies, which will range from harvesting over the entire management area to harvests in a few limited locations within the area.

Since our last report to PCCRC in January 2011, we have made substantial progress in developing our quantitative modeling approach, refining our estimates of neighborhood size, and investigating spatial variability in the current population dynamics model for POP. Our current exploration of regional population dynamics models for POP have some interesting preliminary results but more robust evaluations are underway to determine model variability versus data variability.

## **Approach**

### *Data Quality*

Although assessment of the quality of our genetic data was a subobjective for this project, it was vital to move forward with our modeling objectives with quality population structure parameter estimates. In our previous annual reports, we thoroughly explained the theoretical role of null alleles, and we used simulations to determine their influence on population genetic calculations. In the lab we designed new PCR primer pairs and reanalyzed the homozygotes in our POP samples in order to determine the incidence of null alleles. Addressing the presence of null alleles is important to the robustness of our genetic data and the models into which we incorporate these data. We also used SNP technology to verify that all of the samples analyzed in this study were Pacific ocean perch, because occasional misidentifications do occur during sample collection at sea.

### *Modeling*

We have established, using genetic information, that the geographic scale of the management areas is probably much larger than the scale of the productivity units. We need to further evaluate how the composition of these productivity units, or neighborhoods, is affected by a range of harvest plans. The methods of harvesting can vary spatially as fish distributions change and as management areas expand or shrink and can also vary with respect to fishing pressure and the number of fish removed from an area. We do not know how these processes influence the genetic components of a population, which may be important for long-term abundances.

We began by determining if there were natural geographic breaks in the GOA POP population that are detectable from the survey and catch data. Based on estimates of neighborhood size from the genetic data, we established levels of spatial groupings – regional, statistical area, and smaller neighborhood size areas – to examine the variability present. The results of this analysis assisted us in determining the spatial scale at which further analyses should be focused. While variation in growth parameters was detected at all levels, further analyses will focus on the regional scale due to data quantity and availability.

We then developed regional models based on the current ADMB (Automatic Differentiation Model Builder) model for the GOA POP population, which is used to estimate population dynamic parameters for GOA POP. Running these models on a regional and then a statistical area level will determine the detectability of differences in the biologically important parameter estimates. Additionally, this analysis will provide insight the ability to manage POP on a smaller spatial scale given the current knowledge of the species.

Before moving on to simulations we plan on extracting as much demographic information as possible from our genetic data. Estimates of lifetime dispersal, “neighborhood size”, and genetic connectivity were obtained from the genetic population structure study conducted in Palof et al. 2011. A sensitivity analysis, performed on a range of effective densities using Rousset’s method for estimating neighborhood size, yielded rough estimates between 70 and 140km. Questions have arisen as to the validity of the dispersal distribution implored by this method for POP. We plan on determining if other dispersal distributions can and should be evaluated. We also plan on investigating more recent developments in estimating neighborhood size from genetic data.

We plan to use the program AgeNe (Waples et al. per comm.) to investigate the relationship between effective population size ( $N_e$ ) and census size ( $N$ ). The output from our age structured models will be used to evaluate this relationship for varying POP spatial groupings. This will provide some insight into the relationship between our population dynamics models and genetics.

We will then generally look at the interactions between harvest rates, spatial distributions, and population dynamics. Spatial models are described in depth in Quinn and Deriso (1999, chapter 10). An application of a spatial model to fishery harvest policy (Heifetz and Quinn 1998) described the necessary model features and showed that spatial considerations can alter the optimal harvest policy. Simple simulations will allow us to determine how population structure

and movement influence population productivity. These simulations will be established in Excel, and then moved, as they increase in complexity, to a statistical program such as R. These extensive simulations will provide basic information as to how the variables interact without introducing specific parameters.

After the many aspects of the complex interactions and processes are fully explored, we plan to use this knowledge on POP. We hope to use routine dispersal models to estimate POP abundance and apply both varying spatial and harvest considerations based on our initial explorations and simulations. Spatial considerations for our model will be established using previous knowledge of the species (Hanselman et al. 2003, Hanselman and Quinn 2004), which included two years of scientific surveys. Information from regular AFSC surveys will also be synthesized.

Once the background of a spatial model is developed, the proportional density of POP will be measured under a constant spatial harvest model, where fishing mortality the same for all spatial areas, and a patchy harvest model, where fishing mortality is higher in some areas than in others. The goal of these models will be to see how the concentration of fishing effort, through mortality, affects the density of the species, specifically at varying spatial scales. The models that will be used here are similar to those used in research for marine protective areas with respect to spatial considerations, but do not necessarily make all of the assumptions of marine reserves such as perfect management and zero harvest in the reserve (Rodwell and Roberts 2004, Hart 2006).

## **Results**

### *Previous accomplishments*

Our previous reports summarized the data quality portion of this project. We concluded, from the results of our simulations and laboratory observations, that our data has very low frequencies of null alleles at most of the loci that we applied and that null alleles have had little influence on our analyses of population genetics structure or on the estimation of parameters derived from the data. Therefore, we conclude that our genetic data is of high quality and it can be relied upon to estimate demographic parameters. We also used SNP technology to positively ID 994 of our sample individuals as POP. The other 4 individuals resulted in failed reactions.

Our previous reports also summarized our data explorations of the POP survey data, specifically growth characteristics such as length, age, and weight. We established preliminary levels of spatial scales and determined which levels have statistical importance for the survey data. The three spatial scales chosen are based on broad geographic areas, statistical reporting areas, and areas similar in size to the estimated neighborhood size for POP (Figure 1). Exploratory analysis of these spatial regions has shown variation but due to data quality and availability the regional spatial scale was initially chosen for further analysis (Figure 2). For our initial analyses the transitional area in Figure 1 lumped with the Eastern region due to the confidentiality of the fishery data. Also, the transitional area in Figure 1 will be revisited when the spatial model is applied at the scale of statistical areas, since the transitional area encompasses statistical area 640. This data exploration detected differences in length, age, and weight but none of the 3 spatial scales exhibited substantially more variation than the others, therefore we chose, initially, to do further analyses using the regional model.

#### *Current accomplishments*

We developed regional models based on the current ADMB (Automatic Differentiation Model Builder) model for the GOA POP population. Dana Hanselman, the POP stock assessment scientist at the Alaska Fisheries Science Center, provided the current ADMB model, which is used to estimate population dynamic parameters for GOA POP. This model incorporates both survey and fishery data over time in a complex estimation of life history and population dynamic parameters, such as overall biomass, recruitment, age structure, survey selectivity, and many other useful parameters. We used this model to estimate parameters based on the regional groupings in Figure 2 of East, Central and West. This model assumes there is no movement to other regions after fish recruitment.

Preliminary results suggest that there are region-specific differences in some parameter estimates, such as recruitment (Figure 3). The results of further robust testing are currently being compiled. These include testing for interplay between mortality estimates and fishery selectivity, and fixing natural mortality between the regions. The results of these should be completed by January 2012. Additionally, if variation on a regional level holds true we plan to break down the model to statistical areas, which would divide the central and eastern areas into two (Figure 2).

Once the data can be efficiently separated by statistical area these models will be run at this spatial level, we expect this to be underway or completed by January also.

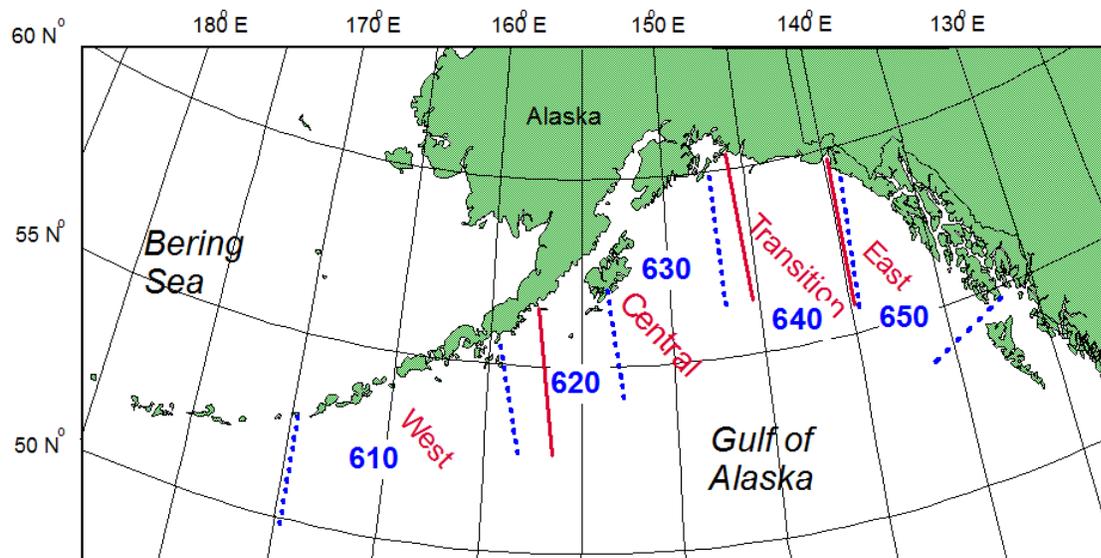
We are currently working on regional models that include area specific growth relationships to maximize area variation in model parameters. Although these regional growth relationships are not expected to be significantly different, variation will allow for differential estimation of other important parameters by region.

The initial setup of our basic simulations to understand the interaction between structured populations, movement, and harvest strategies was extensively fleshed out during this reporting period. Ms. Palof is currently working on translating these into computer simulations using Excel and R.

Ms. Palof, the doctoral student on this project, completed her coursework and plans to take her comprehensive exams this spring. She spent this fall as a teaching assistant for UAF's Modern Applied Statistics class as part of her professional development.

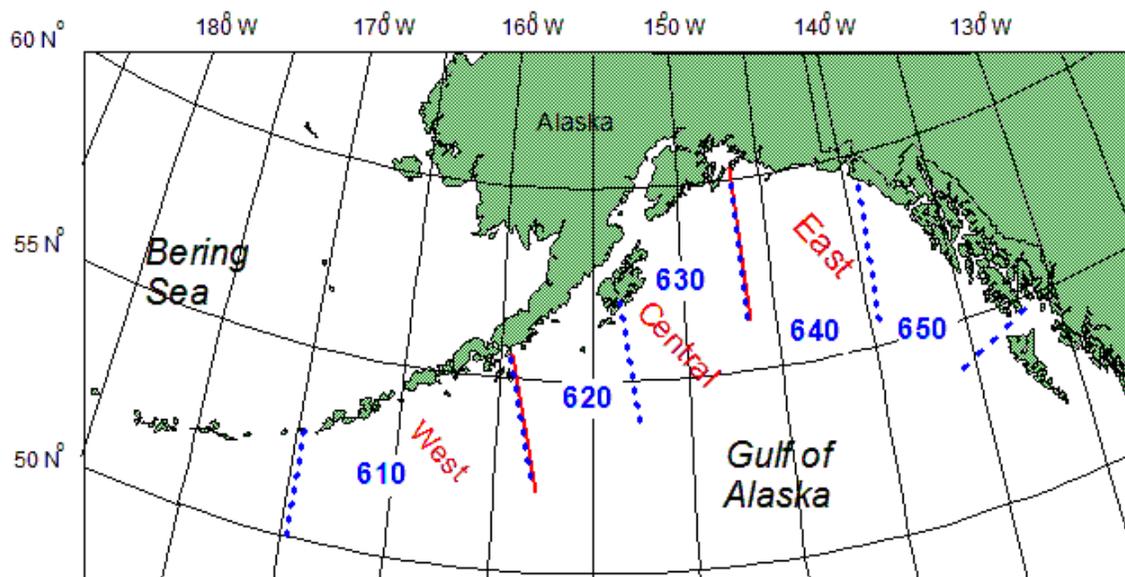
### **Future plans**

We plan on finishing up our robust testing of the regional ADMB models, which will include adding the statistical area spatial level. We will also consider a suite of linked regional models, in which recruitment may be a function of spawning stock in multiple regions. One of our future priorities will be to initialize the simulations on the interactions of population structure, movement, and harvest.



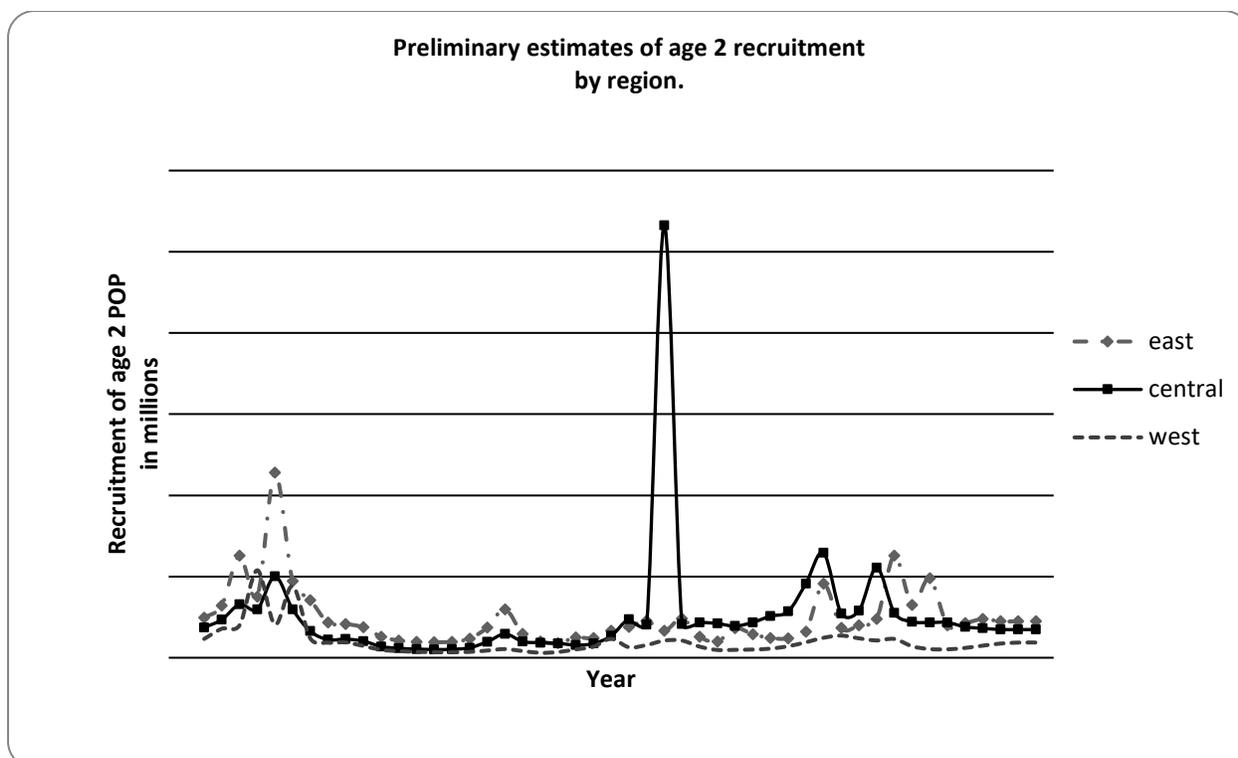
**Figure 1.**

Map of the Gulf of Alaska with spatial groupings. The red boundaries and red labels (East, Transition, Central, and West) refer to the regions, the largest spatial groups. The blue boundaries and blue labels (650, 640, 630, 620, 610) refer to the statistical reporting areas, which is the second spatial grouping. The third spatial grouping groups by intervals of two lines of longitude starting at 133E, these are not shown but intervals of longitude by 5 degrees are labeled in black.



**Figure 2.**

Map of the Gulf of Alaska with regional (solid red lines) and statistical area (dashed blue lines) groupings.



**Figure 3.**

Estimates of age 2 recruitment in millions at the regional level over time.

Recruitment is a highly variable parameter that has large amounts of error associated with it; these estimates are preliminary and should be taken with caution.

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