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University of Alaska Fairbanks Proposal

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

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

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Abstract

Pacific ocean perch (POP) are the most abundant *Sebastes* rockfish species in Alaskan waters in both biomass and catch. They are distributed broadly along the Gulf of Alaska (GOA) and Bering Sea (BS) continental slopes. As for most rockfish species, POP do not mature at an early age; and they can live to very old ages. Rockfishes are viviparous; after POP larvae are released they may spend several months in the water column before they settle into more demersal habitats. An assumption made for many marine species, 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. Recently, genetic studies of POP population structure have demonstrated that relatively strong divergence occurs between collections that were sampled at locations spaced about 200 km apart along the GGOAOA and BSBS continental slopes. The degree of divergence suggests that, although population structure is not defined by geographic or oceanographic boundaries, the limited net dispersion that occurs in both pelagic larvae and adults results in restricting 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. We have nearly completed a large scale genetics study of adult POP samples (Palof, thesis research); and a genetics study of young-of-the-year POP juveniles is in progress (L. Kamin, thesis research). From those results we will be able to address questions about the extent of dispersion, and should be able to make preliminary estimates of neighborhood size. The questions we address here are the effects that harvest patterns exert on production and genetic structure of POP and, by extension, other species for which limited dispersion results in a neighborhood model of population structure, and the neighborhoods are much smaller than the management areas. To evaluate these effects, we will develop quantitative models that include information about dispersal, population dynamics, and exploitation and test the effects of different harvesting strategies, which will range from harvesting over the entire management area to harvests in a few limited areas within the area.

Background and relevance to research priorities

Relevance

Conserving and managing fish stocks is often based on geographical areas. In some instances, the boundaries of the areas correspond to the demographic boundaries of the species. For marine species the boundaries may reflect geomorphological or oceanographic features; but for many marine species, demographic boundaries may not be obvious or even discrete. If the spatial scale of the management boundaries is similar to or smaller than demographic boundaries, management will be efficient. However, if management boundaries are much larger than the demographic boundaries, there are risks that both over- and under-fishing may occur and erode the productivity potential of the species. Our recent genetic work with Pacific ocean perch (POP) indicates that the demographic scales of productivity are much smaller than the Gulf of Alaska (GOA) and Bering Sea (BS) management areas. Population genetics data can provide information about both the numbers and spatial sizes of populations, which correspond to demographic productivity units.

We propose to use our genetic data about rockfish population structure to develop quantitative models with which we can evaluate the effect of disparities between the spatial scale of management areas and populations of POP.

This proposal directly responds to PCCRC Research Priority for 2007:

3. Improvements in fishery ... management measures, particularly with regard to
 - a. research which explores a range of management options to protect rockfish from potential overfishing...

The models that we develop will incorporate the life history information that we can deduce. In the following sections is background pertinent to rockfish in general, POP, and the genetic research we have conducted.

*Genus *Sebastes**

Rockfishes (genus *Sebastes*) are an ecologically diverse and economically important group of fishes. Consequently, their conservation is of interest to fisheries managers in the Northeast Pacific. Conservation efforts for many rockfish species are complex because they mature late and are long-lived (Lyubimova 1963, Westrheim 1975, Love et al. 2002). Although the biology of a few species of rockfishes has been well studied, we know little about the life history characteristics of most species. Among the unavailable information that is important for understanding species distribution and life history are timing of release of larvae and mechanisms and distances of larval dispersal (Moser and Boehlert 1991). In the California current system, larvae appear to use the surface waters as prerecruitment habitat; they drift seaward in the summer and shoreward in the winter (Moser and Boehlert 1991). In the Gulf of Alaska, concentrations of *Sebastes* larvae have occasionally been observed over the continental shelf and slope; their distribution varied seasonally (Kendall and Dunn 1985).

All larval and many juvenile rockfishes are difficult to identify to species visually. The only reliable identification method is genetic analysis; and, although some species cannot be completely delineated genetically, the possibilities can be narrowed to groups of two or three species (Rocha-Olivares et al. 2000, Gharrett et al. 2001, Li et al. 2006). We have developed a key for more than 70 *Sebastes* species that is based on mitochondrial variation (Li et al. 2006).

Genetic and biochemical markers have also been used to characterize many aspects of rockfish life history and dispersal patterns. Mitochondrial DNA (mtDNA) has been used to detect intraspecific variation for the rosethorn rockfish (*Sebastes helvomaculatus*, Rocha-

Olivares and Vetter 1999) and to recognize sub-populations of the blue rockfish (*Sebastes mystinus*) along the Pacific coast from Washington to California (Cope 2004). However for many species, mtDNA has too little variation to resolve divergence patterns (Buonaccorsi et al. 2002). Consequently, microsatellite loci, many of which are highly variable, are often used to detect population genetic structure because they often resolve differences that other less variable markers cannot (e.g., Roques et al. 1999, Withler et al. 2001, Roques et al. 2002, Matala et al. 2004ab, Gharrett et al. in press).

Pacific ocean perch life history

Pacific ocean perch are distributed along the Pacific Rim from California to Japan. They are most abundant in Alaskan waters and inhabit both the Gulf of Alaska (GOA) and the Bering Sea (BS) and are the dominant species in the assemblage of slope rockfish. They are slow-growing and long-lived, sometimes reaching ages of more than 100 years. Pacific ocean perch in Alaskan waters have a low rate of natural mortality -- approximately 0.06 -- and a relatively late age at 50% maturity -- about 8 to 10 years (Hanselman et al. 2003). They have been fished heavily throughout their North American range since the 1940's and are a valuable component of the Alaskan groundfish fishery and probably the marine food web.

Many aspects of Pacific ocean perch (POP) life history are still unknown, and what is known is based mostly on observations of populations in the Queen Charlotte Sound (Gunderson 1972, 1974, Hanselman et al. 2005). Like other rockfishes, POP are viviparous, and females release planktonic larvae that are ready to feed. The locations at which insemination (transfer of spermatozoa from males to females), fertilization (fertilization of the ova), and parturition (release of larvae) are unknown, but may be geographically separated. Insemination takes place in the fall and spermatozoa are retained until fertilization occurs in deep water during the winter. Release of the larvae during April and May coincides with plankton blooms in the Gulf of Alaska (Lyubimova 1963, Gunderson 1972, 1977).

Little is known about dispersal and movement after parturition. Juvenile POP are released to a planktonic life history phase, and the larvae probably settle or become demersal within the first year of their lives. Larvae may remain pelagic for only several weeks to a few months (Carlson and Haight 1976), but during that time their movements are influenced by prevailing currents, which may play an important role in the variability of inter-annual recruitment (Ainley et al. 1993). Although little is known about the larval or early juvenile stages, juveniles appear at 1.5 years on the continental shelf off British Columbia; and between one and six years of age, they are commonly observed demersally in coastal fjords in Southeastern Alaska, where they feed mostly on small planktonic or pelagic crustaceans (Carlson and Haight 1976, Leaman 1991). In Southeast Alaska, the segregation of young POP by age, generally corresponds to depth; older POP occur deeper in the water column (Carlson and Haight 1976). By six years, POP have recruited to adult stocks offshore; however, most are not yet sexually mature (Carlson and Haight 1976).

The planktivorous POP are generally semi-demersal, but are pelagic at times (Carlson and Haight 1976). Adult POP occur in waters from 90m to 825m; both sexes are most often found between 200 and 275m in the summer and between 300 and 450m in the winter (Gunderson 1977, Scott 1995). Females, however, may move deeper (500-700m) after insemination, where they remain until their larvae are released (Gunderson 1972, Love et al. 2002).

Pacific ocean perch can live more than 100 years, and the age at 50% maturity for females is 10.5 years in the eastern GOA and in the Bering Sea (Paraketsov 1963, Gunderson 1977, Lunsford 1999, Spencer and Ianelli 2005). Because the method that was used to determine the ages of Bering Sea POP (surface reading) tends to yield lower ages than the method used to estimate GOA ages (break and burn), it is likely that BS POP may take longer to mature (Lunsford 1999, Spencer and Ianelli 2005). Pacific ocean perch recruit into the fishery between ages 7-15, with 50% recruitment at 7-8 years for the GOA, which introduces a lag in the effect of overfishing on the reproductive potential of the parents of these recruits (Gunderson 1977, 1997). Fishing pressure can reduce the reproductive potential of stocks, by reducing the age at maturity. In the northern Washington-Vancouver Island area, ages of POP stocks at 50% maturity were reduced from 10.1 to 8.1 years between 1972 and 1992 (Gunderson 1997).

Population structure and management of POP

Effective management and conservation of a species require knowledge of its population structure. Most populations are composed of numerous, more or less, independent units of productivity, which may be physically separated by geographic or oceanographic features, or effectively separated by life history characteristics such as limited dispersal of individuals. Production by the species as a whole is the sum of the production of each of the units. Declines in production of one or a few units cannot be restored by other units.

Biological indicators of population structure -- Parasite studies of adult POP off the coast of British Columbia are consistent with onshore-offshore movement that is associated with oceanographic currents and feeding but not with long coastwide movements (Leaman and Kabata 1987). Spatial studies of stock responses to fishing pressure support the idea that movement of adults (Gunderson 1997) is limited. The practice of partitioning adults into geographic stocks for management in Canadian waters is also supported by developmental and reproductive differences (Westrheim 1975). Queen Charlotte Island POP appear to form aggregations, which have distinct biological characteristics, such as length and growth parameters (Gunderson 1972). Bathymetric variation in testes development was observed in male POP was off of southeastern Vancouver Island, which suggested the existence of two POP stocks, a shallow water and a deep water stock (Westrheim 1975). Latitudinal differences in POP populations structure was also indicated from differences in female sizes and ages at 50% maturity. A 1975 survey estimated females in the western GOA matured at an average of 28cm and 10 years, as compared to 34 cm and 15 years Southeast Alaska and to 35cm and 11 years near Vancouver Island (Westrheim 1975, Lyubimova 1963, Lunsford 1999).

Species that have late maturation and long lives are often vulnerable to overfishing. In fact during the 1960s and early 1970s, POP were targeted in an intense foreign trawl fishery that was prosecuted mostly by Japanese and Soviet vessels (Ito 1986). The harvest peaked in 1965, when it reached 350,000 metric tons (mt), and POP biomass subsequently fell to levels defined as depleted by North Pacific fisheries management council after its inception in 1977. In 1978 only 8,000 mt were caught (Hanselman et al. 2005, Spencer and Ianelli 2005). During the period of intensive harvesting, POP stocks were reduced from estimates of their virgin biomass by 80% throughout their Alaskan range (Ito 1986); between 1967 to 1969, stocks in the northern Washington-Vancouver Island area were reduced by 85% (Gunderson 1977). The domestic fishery replaced the foreign fleets in 1985, and continued to grow until 1991. From 1991 to 1996, the fishery was restructured; and management practices were changed to encourage the

restoration of the POP stock (Hanselman et al. 2005). Since 1996 catches of POP have increased and there is evidence for good recruitment and increasing biomass.

Because POP are exploited throughout their range, careful management is essential to sustain productivity. At this time, a species-specific ABCs (acceptable biological catch) and TACs (total allowable catch) are assigned to POP in the GOA and BS. In the GOA, the TACs and ABCs are divided among the three geographical management areas (Western, Central, and Eastern GOA) based on the distribution of species biomass; and the BS management area is divided between the BS subarea and the Aleutian Island subarea. In 2005, the ABC's for POP were 13,575 mt for the GOA as a whole, 2,923 mt for the BS subarea, and 11,692 Aleutian Island sub area (Hanselman et al. 2004, Spencer et al. 2004).

Genetics and population structure – For terrestrial and anadromous species, population structure is often generated by geomorphological features that separate segments of a species. Both geographic and oceanographic features can also partition marine species. Substructure within a species generally leads to genetic divergence as a result of reproductive isolation, that is, restrictions on gene flow. Although population structure is often related to geographic and oceanographic features, neither is essential for genetic divergence (and substructure) to develop. If the distance that individuals of a species disperse between birth and reproduction is small relative to the species range, gene flow is restricted and divergence will occur, although discrete, obvious populations may not be apparent. In many instances, the extent of genetic divergence is related to the physical distance separating samples. An important corollary is that the average dispersal distance from a genetics perspective is equivalent to the size of the productivity unit from a population dynamics perspective. Consequently, detection and characterization of population genetic structure provides a means to determine demographic characteristics that are otherwise unavailable.

Modern genetics laboratory methods provide a powerful tool for detecting and evaluating genetic structure. However, population structures of marine species can be challenging to characterize because of their complex life histories. Many marine species have very weak population genetic structure, which has been attributed to demographic and life history characteristics such high abundance (large effective population size) and large dispersal potential as well as to the absence of physical barriers to gene flow (Gold et al. 1994, Palumbi 1994). Although the population structure of marine species may be difficult to define, even weak structure may provide important information about demographic processes and that structure can imply limited demographic exchange or gene flow (Palumbi 2003). These kinds of results suggest that genetic structure should be examined on a scale of mean dispersal distance to best display the genetic structure that exists; and for most marine species dispersal distance is difficult to measure directly, and must be inferred from genetic data. Even where population boundaries are not obvious, erosion of production can occur if the species are managed on a scale much larger than the population structure, because excessive harvests in one portion of the area can reduce overall productivity.

Recent results from characterization of POP population structure

A recent review indicated that there is still little known about the genetic structure of POP in Alaskan waters (Hanselman et al. 2003). Previous research based on allozyme variation showed low levels of population divergence in Alaskan waters (Seeb and Gunderson 1988) and no evidence for interruption of gene flow between the Bering Sea and the western Gulf of

Alaska. However, it was suggested that POP structure cannot be measured by allozyme analysis. Another study of POP in British Columbia waters that was based on microsatellite variation revealed genetically distinct populations within a relatively small area, and the divergence among the populations appeared to be associated with local currents (Withler et al. 2001).

In our laboratory, M.S. student K. Palof conducted a survey of microsatellite variation among GOA and BS collections. Although that work is not yet complete, the available results are consistent with a strong, geographically-based population structure. This work examined variation at 14 microsatellite loci in 12 distinct collections sites that range along the Pacific rim of the GOA from southern Southeast Alaska to the western Aleutian Islands and three areas along the BS continental slope. Pairwise tests (adjusted for multiple testing) between collections indicated that substantial divergence exists among all pairs. In addition, the divergence correlated with geographic separation of the collections and demonstrated an isolation-by-distance pattern (Figure 1). In a subsequent project supported by NPRB, M.S. student L. Kamin has been analyzing many (~2000) young-of-the-year (YOY) POP captured incidentally during juvenile salmon surveys in the GOA and BS. The YOY were captured along several transects, which were sampled in several different years. Preliminary results indicate that the genetic compositions of YOY collected at different sites during the same year differ, but are generally similar to nearby adult collections. Adjacent adult collections, which are separated by about 200 km (Figure 1), differ significantly. The biological and management interpretation of the divergence and the geographic differences among the YOY collections indicates that, even though prevailing currents have the potential to carry larval POP long distances counter clockwise around the eastern GOA, larvae appear to settle close to the area in which genetically similar adults presumably their parents – inhabit and that the combined movements of larvae, juveniles, and adults is much less than 200 km.

These results lead to several conclusions. First, even though the potential for POP dispersal exists, it does not appear to occur. Second as a consequence, the spatial scale on which the adults were sampled exceeded the size of productivity units and more intensive sampling on a smaller scale is needed to understand the scale of population structure of POP. The sampling of several locations on a much finer scale is currently being proposed in a concurrent project to be funded elsewhere. A third conclusion is that the geographic scale of the management areas is probably much larger than the scale of the productivity units.

Objectives/Hypotheses

We will evaluate the effects on productivity of disparities between the geographic scales sizes of management areas and neighborhoods (demographic units) of exploited species. To accomplish that we will develop quantitative models that use population genetics information for POP, although the results will be generally relevant to any species for which the geographic scale of management greatly exceeds the scale of production.

The population genetics data for POP is based on microsatellite variation. The advantage of microsatellite loci is that many have numerous alleles, which can provide excellent resolution among populations. A disadvantage is that microsatellite loci may have non-amplifying or null alleles, which can bias estimates of the frequencies of other alleles. Therefore, one subobjective of this project is to evaluate quantitatively the influence of null alleles on genetic analyses and to determine the extent to which null alleles actually occur in the data we are using to estimate the POP life history parameters, which we use in the harvest models.

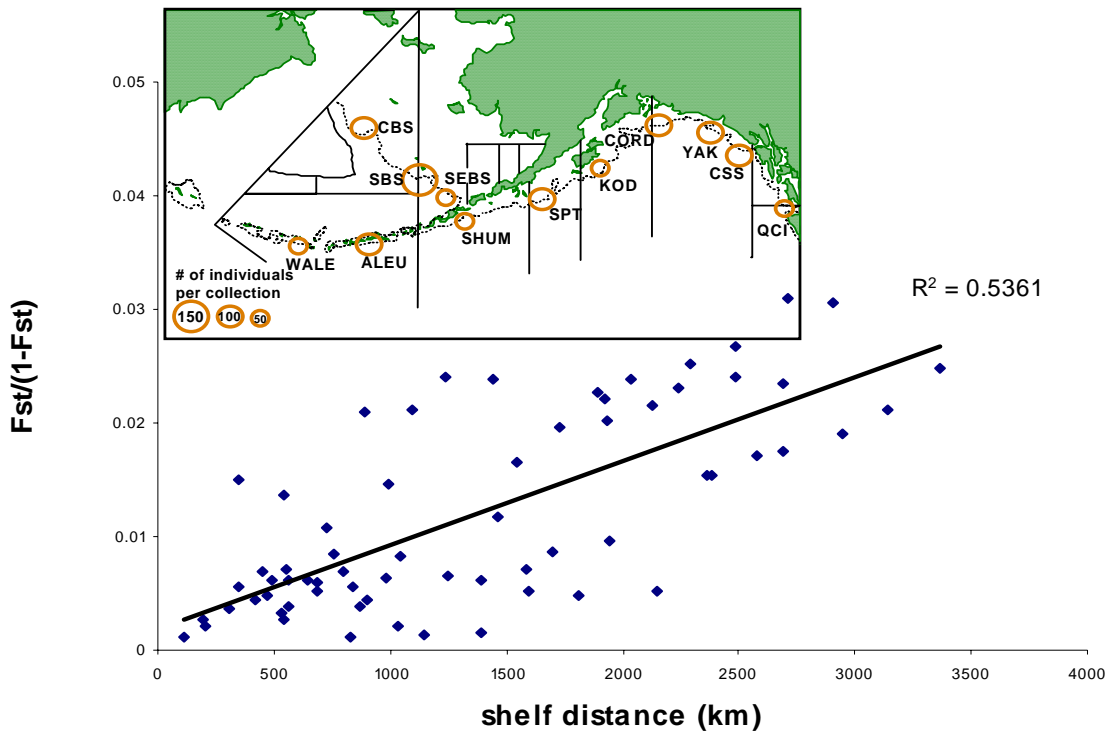


Figure 1. Isolation by distance from distances along the continental shelf line and pairwise F_{ST} . Points represent each population pair.

Methods and analyses

The effect of null alleles

We will test the effect of null alleles on data analysis by conducting simulations that use fabricated allele frequency data. These simulations will evaluate the effects of the magnitude of the null allele frequency on analyses that include normal allele frequencies that vary in magnitude and size. Some of the specific questions we will address are the influence on the estimates of normal allele frequencies, (apparent) Hardy-Weinberg equilibrium, and measures of divergence between populations.

Microsatellite loci are regions in the DNA that include multiple repeats 2 to 6 base pairs – e.g., ACACAC... Allelic differences are the result of different numbers of repeats. Primers for polymerase chain reaction (PCR) amplification of the loci are designed for DNA sequences that flank the repeated nucleotides. Analysis involves amplification of the specific sequence that contains the repeats followed by separating the PCR products by size in order to identify the specific alleles in an individual. Null alleles occur when a mutation occurs in the area that is recognized by a primer, and the primer fails in the amplification process. The result of failed amplification is that only a single allele is amplified; single bands are usually interpreted as homozygotes – two copies of the same allele. Sequences of the regions that include a microsatellite locus are archived in GENBANK. From those sequences, we will design alternative PCR primers with which we will reamplify apparent homozygous individuals (e.g., Matala et al. 2004a). It is unlikely that two different null alleles will appear in an individual.

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 range spatially, as fish distributions change and as management areas expand or shrink, and can also vary with respect to fishing pressure, the number of fish removed from an area. We also do not know how these processes influence the genetic components of a population, which may be important for long-term abundances.

We will begin by generally looking 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 models are needed to identify influential components in processes and to determine the extent of each component's influence. We will use multiple simulations to fully investigate how general productivity units are affected by a range of processes. These simulations will be conducted in Excel, and with programs written in either Fortran or R. These extensive simulations will provide basic information as to how the variables interact without introducing of specific parameters.

We will also use simple models in an attempt to understand how genetics and gene flow are affected by these processes. While 2-dimensional-stepping-stone models have been used to examine gene flow between adjacent demes, we do not believe that they have been coupled with population parameters, such as finite population size and exploitation (Kimura and Weiss 1964). Determining how dispersion (as measured by gene flow) influences the components of the model is also essential to understanding the complex genetic patterns that we may observe (Slatkin and Barton 1989). We plan to spend at least the first year of this project investigating these general ideas as a background for further modeling. The species specific extension of this modeling, described below, depends on the results of this initial simulation period.

After developing a population model, modeling of individuals may also be used to address the impact of life history and fishing efforts on the genetic composition of a member of the population. Individual-based modeling has been used to incorporate the variation that can occur from biotic and abiotic interactions on an individual level, allowing for fish by fish variation that is not seen on a population level (Scheffer et al. 1995, Hinkley et al. 1996, Edwards 2003). In order to do this an individual based model will be developed and used for a number of fish. The number of fish that will need to be included to obtain statistically comparable results will be determined at a later date.

After the many aspects of the complex interactions and processes are fully explored, we plan to use this knowledge on specific species, starting with Pacific ocean perch. We hope to use routine dispersion models to estimate POP abundance applying both varying spatial and harvest considerations. 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 efforts are equally distributed throughout each spatial area, and a patchy harvest model, where efforts will be randomly distributed throughout the spatial areas. The goal of these models will be to see how the concentration of fishing effort affects the genetic composition of the species, specifically the genetically distinct neighborhoods. The models used here will be 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 of our work will be submitted to journals such as the Canadian Journal of Fisheries and Aquatic Sciences. We intend to present our work to scientific and advisory committees of the North Pacific Fishery Management Council.

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Timeline:

Year 1 (Feb 2007 to Jan 2008):

1. Test null allele effect through simulation.
2. Obtain laboratory data from loci that probably have null alleles.
3. Develop hypothetical POP-like population on a fixed grid of say 100 by 100.
 - a. Determine dispersal pattern from genetics
 - b. Synthesize life history information for the model.
 - c. Synthesize spatial information from surveys and fisheries.
 - d. Develop harvest strategies for comparison.
4. Conceptualize individual-based model.
5. Annual written and oral report to PCCRC.

Year 2 (Jan 2008 to Jan 2009)

1. Finalize population model and get results; write manuscript.
2. Develop individual-based model.
3. Investigate stepping-stone model.
4. Annual written and oral report to PCCRC.

Year 3 (Feb 2009 to Jan 2010)

1. Finalize individual-based model; write manuscript.
2. Present results at national scientific meeting.
3. Present results to North Pacific Fishery Management Council bodies.
4. Consider refinements to population model applied to POP.
5. Final written and oral reports to PCCRC.

Timeline:

Year 1 (Feb 2007 to Jan 2008):

6. Test null allele effect through simulation.
7. Obtain laboratory data from loci that probably have null alleles.
8. Develop hypothetical POP-like population on a fixed grid of say 100 by 100.
 - a. Determine dispersal pattern from genetics
 - b. Synthesize life history information for the model.
 - c. Synthesize spatial information from surveys and fisheries.
 - d. Develop harvest strategies for comparison.
9. Conceptualize individual-based model.

Year 2 (Jan 2008 to Jan 2009)

5. Finalize population model and get results; write manuscript.
6. Develop individual-based model.
7. Investigate stepping-stone model.

Year 3 (Feb 2009 to Jan 2010)

6. Finalize individual-based model; write manuscript.
7. Present results at national scientific meeting.
8. Present results to North Pacific Fishery Management Council bodies.
9. Consider refinements to population model applied to POP.



SCHOOL OF FISHERIES AND OCEAN SCIENCES

PROJECT TITLE:
PCCRC

SFOS #:
07-042

PI: Gharrett, A.
START: 1 July 2007
END: 30 June 2010

BANNER #:
8867

						Mos	Year 1	Mos	Year 2	Mos	Year 3	Total Project
A. Senior Personnel:												
PI salaries multiplied by a 4.5% increment per year												
Total Number of Hours												
Gharrett, A.	3.00	Principal Investigator	F9	\$58.93	1.5%	1.00	\$10,876	1.00	\$11,365	1.00	\$11,877	\$34,118
Quinn, T.	3.00	Principal Investigator	F9	\$53.43	1.5%	1.00	\$9,861	1.00	\$10,305	1.00	\$10,768	\$30,934
A. Total Senior Personnel							\$20,737		\$21,670		\$22,645	\$65,052
B. Other Personnel:												
(full time = 174 hours per month)												
Students work part-time during academic year and full-time in summer.												
Graduate student salaries multiplied by a 11.5% increment per year												
Number of Students												
PhD graduate student	1	Grad Student academic yr	GN	\$18.52	0.0%	8.00	\$14,372	8.00	\$16,025	8.00	\$17,868	\$48,265
PhD graduate student	1	Grad Student in summer	GT	\$18.52	0.0%	4.00	\$14,372	4.00	\$16,025	4.00	\$17,868	\$48,265
B. Total Other Personnel							\$28,744		\$32,050		\$35,736	\$96,530
Total Salaries and Wages (A+B)							\$49,481		\$53,720		\$58,381	\$161,582
C. Fringe Benefits												
Faculty Benefits						F9	46.3%	\$9,601	\$10,033	\$10,485	\$30,119	
Grad Student Benefits						GT	8.7%	\$1,250	\$1,394	\$1,555	\$4,199	
FY08 student health costs \$500/semester or \$1500/year							\$1,500	\$1,500	\$1,500	\$4,500		
C. Total Fringe Benefits							\$12,351		\$12,927		\$13,540	\$38,818
Total Salaries and Benefits (A+B+C)							\$61,832		\$66,647		\$71,921	\$200,400
E. Travel												
Travel is incremented by 3% per year for inflation beginning year 2.												
1. Domestic												
2 RT Juneau to Anchorage							\$2,000	\$2,000	\$2,000	\$6,000		
scientific meeting							\$0	\$0	\$1,500	\$1,500		
graduate student							\$0	\$0	\$0	\$0		
E. Total Travel							\$2,000		\$2,000		\$3,500	\$7,500
F. Other/Contractual/Services												
communication costs							\$50	\$50	\$50	\$150		
shipping							\$200	\$200	\$0	\$400		
F. Total Contractual/ Services							\$250		\$250		\$50	\$550
G. Commodities												
project supplies							\$4,500	\$4,500	\$0	\$9,000		
G. Total Commodities							\$4,500		\$4,500		\$0	\$9,000
H. Student Services												
Add a 10% increment to each year												
Number of Students						Tuition	\$ Per Credit	# of Credits	Total			
graduate student	1	In-State Tuition	\$268	18	\$4,824	\$5,306	\$5,837	\$6,421	\$17,564			
H. Total Student Services							\$5,306		\$5,837		\$6,421	\$17,564
I. Total Direct Costs (A-I)							\$73,888		\$79,234		\$81,892	\$235,014
J. Exclusions												
Tuition							\$5,306	\$5,837	\$6,421	\$17,564		
K. Base							\$68,582		\$73,397		\$75,471	\$217,450
L. Total Indirect Costs (F&A)												
2 MTDC						Current Rate:	0.0%	\$0	\$0	\$0	\$0	
M. Total Direct & Indirect (J+M)							\$73,888		\$79,234		\$81,892	\$235,014
Funding Agency Total							\$73,888		\$79,234		\$81,892	\$235,014



University of Alaska Fairbanks Budget Justification

We project that this will be a three-year project, which is the time expected for completion of Ms. Palof's Ph.D.

Salaries:

The funds for this project will be primarily salary support. We request one month each year for PIs Gharrett and Quinn and funding during the academic year (half time) and during the summer (full-time) for Ph.D. student K. Palof.

Benefits:

Staff benefits are applied according to UAF's benefit rates for FY07 negotiated with the Office of Naval Research (ONR). A copy of the rate proposal is available at: http://www.alaska.edu/controller/cost-analysis/downloads/Negotiated/FY07_SB_Neg.pdf. Beginning in FY08 additional student healthcare costs are estimated to be \$500 per semester.

Travel:

Domestic

Travel funds will be needed for travel to the annual PCCRC meeting each year and for Ms. Palof to attend a scientific meeting or symposium in year 3.

Other/Contractual/Services:

Minimal funds are requested to cover communication costs and shipping of samples.

Commodities:

There is a small laboratory component to this project for which we request \$4500 each of the first two years for project supplies.

Student Services (Tuition):

Tuition is requested to support the graduate student per university policy.

Indirect Costs:

No Facilities and Administrative (F&A) Costs are included based on the requirements of the Announcement of Availability of Funds from PCCRC.

Short description of results of previous work funded by PCCRC

PCCRC awarded Gharrett support for two different projects, each of which spanned several years.

The first project: “DNA analysis of the origins of chinook salmon bycatch in Alaskan trawl fisheries”, we analyzed both mtDNA and microsatellite variation in Chinook salmon populations sampled from their natural range, but we emphasized northern populations. The objective was to determine if there was sufficient genetic divergence among them to distinguish origins of fish caught incidentally in Bering Sea trawl fisheries. The results indicated that there was sufficient microsatellite variation to resolve continent and region of origin. In addition, the mtDNA data revealed some unexpected post-glacial colonization patterns.

The second project: “Developing DNA markers for the analysis of chum salmon bycatch in Alaskan trawl fisheries”, is currently developing and analyzing single nucleotide polymorphism (SNP) variation in chum salmon populations that have been sampled throughout the natural range. The focus was SNP variation because Alaska Department of Fish and Game geneticists were reluctant to apply microsatellites. After the project began, we secured another project funded by Bering Sea Fisherman’s Association to examine chum salmon microsatellite variation for mixed stock analysis. We are conducting both projects and using the same samples to develop both data bases. To date, M.S. student M. Garvin has developed more than 20 SNP loci and analyzed more than 4000 chum salmon. With the combined data base, we will be able to identify the broad geographic region from which fish originate and are developing a proposal for submission to the Arctic-Yukon-Kuskokwim Sustainable Fisheries Initiative to analyze BS chum salmon caught in previous years and archived for analysis.

Quinn received PCCRC funding from 2001 to 2005 for the project “Deployment of an acoustic data logger on commercial fishing vessels to evaluate the potential of fishing-induced declines in local pollock abundance,” a collaborative project among UAF, AFSC, UW, and the pollock industry. We received 5 years of funding for a total of about \$250K to deploy data loggers aboard commercial fishing vessels to record hydroacoustic signals all the time while at sea (not just during fishing). In addition, AFSC contributed two years of PhD student funding at a cost of \$72K. This project has demonstrated the feasibility of installing acoustic data loggers on catcher/processors in the EBS pollock fishery to study localized depletion of pollock. In 2001, we developed a prototype data logger that interfaces with the ship’s 38 kHz echo sounder and captures the acoustic backscatter returns. To date, seven PCC vessels, or nearly half the fleet, have been equipped with acoustic data logging systems. Recent work has concentrated on the analysis phase of the project. This work includes classifying the searching behavior of the vessel, integrating the acoustic biomass, identifying pollock aggregations detected while searching, and evaluating what inferences, if any, can be made concerning the rate at which those aggregations are reduced in abundance. The project is moving forward in developing more sophisticated analytical tools for inferring the temporal dynamics of pollock spatial pattern using multiple data sources. This project has become internationally important as one of the most extensive applications of hydroacoustic information in fisheries.

Budget justification/Summary

We project that this will be a three-year project, which is the time expected for completion of Ms. Palof’s Ph.D. The funds for this project will be primarily salary support. We request one

month each year for PI's Gharrett and Quinn and 50% funding during the academic year and full funding during the summer for Ph.D. student K. Palof. There is a small laboratory component to this project for which we request \$4500 each of the first two years. Travel funds will be needed for travel to the annual PCCRC meeting and for Ms. Palof to attend a scientific meeting or symposium once a year.

ANTHONY J. GHARRETT
School of Fisheries and Ocean Sciences
University of Alaska Fairbanks
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(907) 465-6445 ffajg@uaf.edu

Education:

California Institute of Technology	B.S. Biology, 1967
Oregon State University	M.S. Fisheries, 1973
Oregon State University	Ph.D. Genetics, 1975

Experience:

University of Alaska	August 1976 to present
Director, Fisheries Division	July 1994 to June 1998
Professor 1989	
Associate Professor 1980	
Assistant Professor 1976	
Hokkaido University, Fisheries Faculty and	October 1998 to January 1999
Kitasato University, School of Fisheries Sciences	January 1999 to April 1999
Fellow: Japan Society for the Promotion of Science	
NMFS Auke Bay Laboratory	January 1987 to December 1990
Geneticist, Interagency Personnel Act Assignment	
The University of Michigan	January 1985 to December 1986
Visiting Associate Professor	
University of Minnesota	November 1974 to July 1976:
NIH Postdoctoral Trainee	

Research interests:

I am actively engaged in research projects involving:

- Local adaptation, outbreeding depression, and variation in family size in salmonids;
- Heritability and genotype by environmental interaction of development rate in pink salmon;
- Temporal and spatial structure of pink salmon populations;
- Phylogeographic relationships among Alaskan chinook and chum salmon populations based on mitochondrial DNA polymorphisms;
- Comparison of genetic variation in allozymes, mtDNA, and microsatellite loci for use in stock identification in chum, sockeye, and pink salmon.
- Use of mtDNA RFLPs in identification, systematics, and population structure of rockfish (*Sebastes*).
- Population genetics in relationship to the management of Alaskan *Sebastes* rockfishes.

Awards:

The University of Alaska Fairbanks Emil Usibelli Distinguished Research Award 2006.
Stevan Phelps Memorial Award for best genetics publication in an AFS journal in 2005
Stevan Phelps Memorial Award for best genetics publication in an AFS journal in 2003

Selected Publications:

Gharrett, A.J., A.P. Matala, E.L. Peterson, A.K. Gray, Z. Li, and J. Heifetz. In press. Distribution and population genetic structure of sibling species of roughey rockfish. 23rd Lowell Wakefield Symposium, 13-15 September 2005, Anchorage, AK.

Kondzela, C., A. Kendall, Z. Li, D. Clausen, and A. Gharrett. In press. Identity of Pelagic Juvenile Rockfish Collected in the Gulf of Alaska, 1998-2002. 23rd Lowell Wakefield Symposium, 13-15

- September 2005, Anchorage, AK.
- Li, Z., A.K. Gray, M.S. Love, A. Goto, and A. J. Gharrett. In press. Are the subgenera of *Sebastes* monophyletic? 23rd Lowell Wakefield Symposium, 13-15 September 2005, Anchorage, AK.
- Li, Z., M. M. Nishimoto, M.S. Love, and A. J. Gharrett. 2006. Comparing the identification of Southern California juvenile rockfishes (genus *Sebastes* spp.) by restriction site analysis of the mitochondrial ND3/ND4 region and by morphological characteristics. *Fishery Bulletin* 104:376-382.
- Gharrett, A.J., C.W. Mecklenburg, L.W. Seeb, Z. Li, A.P. Matala, A.K. Gray, and J. Heifetz. 2006. Do genetically distinct rougheye rockfish sibling species differ phenotypically? *Transactions of the American Fisheries Society*. 135:792-890.
- Li, Z., A.K. Gray, M.S. Love, A. Goto, T. Asahida, and A.J. Gharrett. 2006. A key to selected rockfishes (*Sebastes* spp.) based on mitochondrial DNA restriction fragment analysis. *Fishery Bulletin* 104(2):182-196.
- Li, Z., A.K. Gray, M.S. Love, T. Asahida, and A.J. Gharrett. 2006. Phylogeny of members of the rockfish (*Sebastes*) subgenus *Pteropodus* and their relatives. *Canadian Journal of Zoology* 84(4):527-536.
- Wang, I.A., E.H. Leder, W.W. Smoker, and A.J. Gharrett. 2006. Timing of development during epiboly in embryos of second-generation crosses and backcrosses between odd- and even-broodyear pink salmon, *Oncorhynchus gorbuscha*. *Environmental Biology of Fishes* 75(3):325-332.
- Gharrett, A.J. 2006. The Genetics of fishes, Chapter 28. Pages 551-597 *In* M. Barton, *Bond's Biology of Fishes*, 3rd edition. Thomson Brooks/Cole Publishers, Belmont, CA.
- Gray, A.K., A.W. Kendall, Jr., B.L. Wing, M.G. Carls, J. Heifetz, Z. Li, A.J. Gharrett. 2006. Identification and first documentation of larval rockfishes (*Sebastes* spp.) in Southeast Alaskan waters was possible using mitochondrial markers but not pigmentation patterns. *Transactions of the American Fisheries Society*. 135(1):1-11.
- Gharrett, A.J., A.P. Matala, E.L. Peterson, A.K. Gray, and J. Heifetz. 2005. Two genetically distinct forms of rougheye rockfish (*Sebastes aleutianus*) are different species. *Transactions of the American Fisheries Society*. 134:242-250.
- Matala, A.P., A.K. Gray, M.S. Love, and A.J. Gharrett. 2004. Microsatellite variation indicates population genetic structure of bocaccio. *North American Journal of Fisheries Management*. 24:1189-1202
- Matala, A.P., A.K. Gray, J. Heifetz, A.J. Gharrett. 2004. Population structure of Alaskan shorttraker rockfish, *Sebastes borealis*, inferred from microsatellite variation. *Environmental Biology of Fishes* 69:201-210.
- Gilk, S.E., I.A. Wang, C.H. Hoover, W.W. Smoker, S.G. Taylor, A.K. Gray, and A.J. Gharrett. 2004. Outbreeding depression in hybrids between spatially separated pink salmon (*Oncorhynchus gorbuscha*) populations: Marine survival, homing ability, and variability in family size. *Environmental Biology of Fishes* 69:287-297.
- Asahida, T., A.K. Gray, and A.J. Gharrett. 2004. Use of microsatellite locus flanking regions for phylogenetic analysis? A preliminary study of *Sebastes* subgenera. *Environmental Biology of Fishes* 69:461-470.
- Churikov, D. and A.J. Gharrett. 2002. Comparative phylogeography of the two pink salmon broodlines: an analysis based on mitochondrial DNA genealogy. *Molecular Ecology* 11:1077-1101.
- Churikov, D. M. Matsuoka, X. Luan, A.K. Gray, V.A. Brykov, and A.J. Gharrett. 2001. Assessment of concordance among genealogical reconstructions from various mtDNA segments in three species of Pacific salmon (genus *Oncorhynchus*). *Molecular Ecology* 10:2329-2339.
- Carney, B.L., A.K. Gray, and A.J. Gharrett. 1997. Mitochondrial DNA restriction site variation within and among five populations of Alaskan coho salmon (*Oncorhynchus kisutch*). *Canadian Journal of Fisheries and Aquatic Science*. 54:940-949.

CURRICULUM VITAE

Terrance J. Quinn II
Professor of Fish Population Dynamics
Juneau Center, School of Fisheries and Ocean Sciences
University of Alaska Fairbanks
Juneau AK 99801-8677
Ph. 907-796-2051
FAX 907-796-2050
E-mail: Terry.Quinn@uaf.edu

Birthdate: October 27, 1952

EDUCATION

Ph.D., Biomathematics, 1980, University of Washington, Seattle WA
M.S., Fisheries, 1977, University of Washington, Seattle WA
B.A., Mathematics, 1973, University of Colorado, Boulder CO

EXPERIENCE

1998- Professor of Fish Population Dynamics, Juneau Center, School of Fisheries and Ocean Sciences, University of Alaska Fairbanks
1985-1997 Associate Professor of Fish Population Dynamics, Juneau Center, School of Fisheries and Ocean Sciences, University of Alaska Fairbanks
1978-1985 Biometrician, International Pacific Halibut Commission

PUBLIC SERVICE

Member since 1986 and former chair of the Statistical and Scientific Committee of the North Pacific Fishery Management Council.
Member of Ocean Studies Board of the National Research Council from 1995 to 1998; served on 5 NRC committees and chaired two of those, all leading to NRC publications.
Associate Editor, Canadian Journal of Fisheries and Aquatic Sciences
Reviewer, several journals in fisheries and statistics, for agencies, for individuals
Editor, three conference proceedings

AWARDS

National Associate of the National Academies of Science, Engineering, and Medicine, December 2001

CONSULTING

National Marine Fisheries Service (stock assessment and fishery management)
Alaska Dept. of Fish and Game (various shortcourses)
Ohio Dept. of Fish and Wildlife (catch-age analysis)
South Atlantic Fishery Management Council (swordfish)
New South Wales Fisheries Research Institute (catch-age analysis)
CSIRO, Australia (catch-age analysis)
Makah Indian Tribe (halibut, groundfish fisheries)
Ministry of Fisheries, New Zealand (hoki stock assessment)
MRAG Americas (North Pacific observer program)
Minnesota Department of Natural Resources (Mille Lacs Lake walleye assessment)
Natural Resources Consultants (independent peer reviewer for assessment of large coastal sharks)

Collaborators

Ram Myers, Paul Fanning, Robert Mohn, Paul Radomski, Jim Bence, Richard Deriso, Hal Geiger, Clive Turnbull, Vidar Westpestad, Gordon Kruse, John Calambokidis, Chris Gabriele, Jan Straley, Sally Mizroch, Joe Niebauer, Steve Hare, Paul Spencer, Jeremy Collie, Jim Ianelli, Martin Dorn, Anne Hollowed, Richard Marasco, Reg Watson, Fritz Funk, Lewis Haldorson, William Smoker, Gary Marty, John Wilcock, Lev Zhivotovsky, Tony Gharrett, Doug McBride, Peggy Merritt, Richard Gates, Jeff Fujioka, Ben van Alen, Pat Livingston, Graeme Parks, Milo Adkison, Robert Small, Carl Safina, Andy Rosenberg, Steve Moffitt

Students

Bonita Nelson, Jack Turnock, Scott Johnson, Bob Lafferty, Scott MacPherson, Nicole Szarzi, Robert Marshall, Lowell Fair, Daniel Bosch, Edgar Jones, Jon Heifetz, Peter Hagen, Randy Ericksen, Lewis Coggins, Erik Williams, Caihong Fu, Matthew Foster, Dana Hanselman, James Savereide, Brian Battaile, Colin Schmitz, Ben Williams, Briana Witteveen, Sara Miller, Kray Van Kirk, Haixue Shen, Peter Hulson, Joe Liddle. (Not chaired but significant involvement: Jie Zheng, Mike Sigler, Peggy Merritt, Ed Farley, Chris Rooper, Michio Fukushima, William Templin)

Books

- Funk, F., T.J. Quinn II, J. Heifetz, J.N. Ianelli, J.E. Powers, J.F. Schweigert, P.J. Sullivan, and C.-I. Zhang (editors). 1998. Fishery Stock Assessment Models. Proc. Symp. Fishery Stock Assess. Models 21st Cent. Alaska Sea Grant College Program, Fairbanks AK, AK-SG-98-01. 1054 p.
- National Research Council. 1998a. Improving Fish Stock Assessments. National Academy Press, Washington DC. 177 p. (co-chair and co-author)
- Quinn, T.J., II, and R.B. Deriso. 1999. Quantitative Fish Dynamics. Oxford University Press, New York. 542 pp.

Selected Articles

1. Battaile, B.C., and Quinn, T.J., II. *In press*. A DeLury depletion estimator for walleye pollock (*Theragra chalcogramma*) in the eastern Bering Sea. *Natural Resources Modeling*.
2. Booth, A.J., and Quinn, T.J., II. 2006. Maximum likelihood and Bayesian approaches to stock assessment when data are questionable. *Fisheries Research* 80:169-181.
3. Marasco, R., Goodman, D., Grimes, C., Lawson, P., Punt, A., and Quinn, T. 2005. Strengthening scientific input and ecosystem-based fishery management for the Pacific and North Pacific Fishery Management Councils. Pacific States Marine Fisheries Commission, Portland OR. 42 p.
4. Quinn, T.J., II, and Collie, J.S. 2005. Sustainability in single-species population models. *Philosophical Transactions of the Royal Society B* 360: 147-162.
5. Radomski, P., Bence, J.R., and Quinn, T.J., II. 2005. Comparison of virtual population analysis and statistical kill-at-age analysis for a recreational, kill-dominated fishery. *Can. J. Fish. Aquat. Sci.* 62:436-452.
6. Safina, C., Rosenberg, A.A., Myers, R.A., Quinn, T.J., II, and Collie, J.S. 2005. U.S. ocean fish recovery: staying the course. *Science* 309: 707-708.
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