

Genetic population structure of blackspotted rockfish in Alaska

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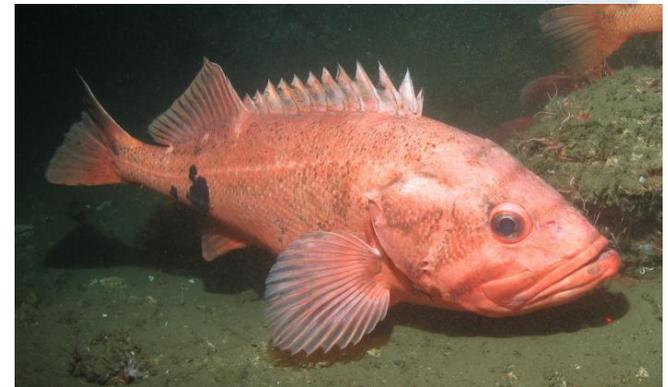
Special thanks to Tony Gharrett, Alex Godinez, and Paul Spencer

1

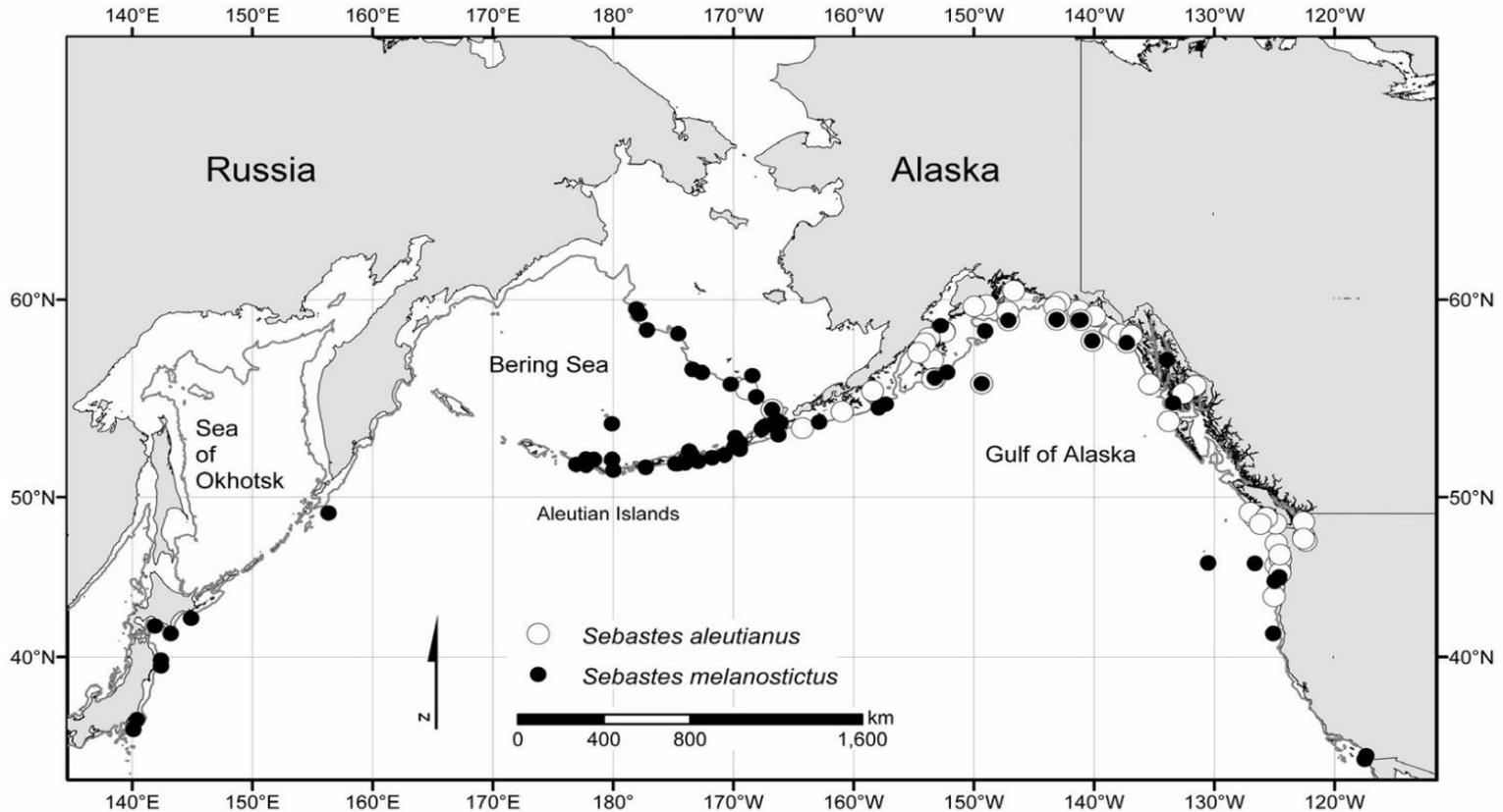


Blackspotted rockfish (*Sebastes melanostictus*) biology

- Long lived, can live > 100 years, generation time ~50 years
- Larvae disperse with currents for weeks to months, juveniles settle in shallower water (200-300 m)
- Adults move deeper (300 - 500 m) and live near the bottom
- Limited movement of adults (hypothesized)
- Blackspotted previously managed with rougheye in a complex and before that with other rockfish including shortraker
- Most blackspotted caught as bycatch in other fisheries (e.g. POP)



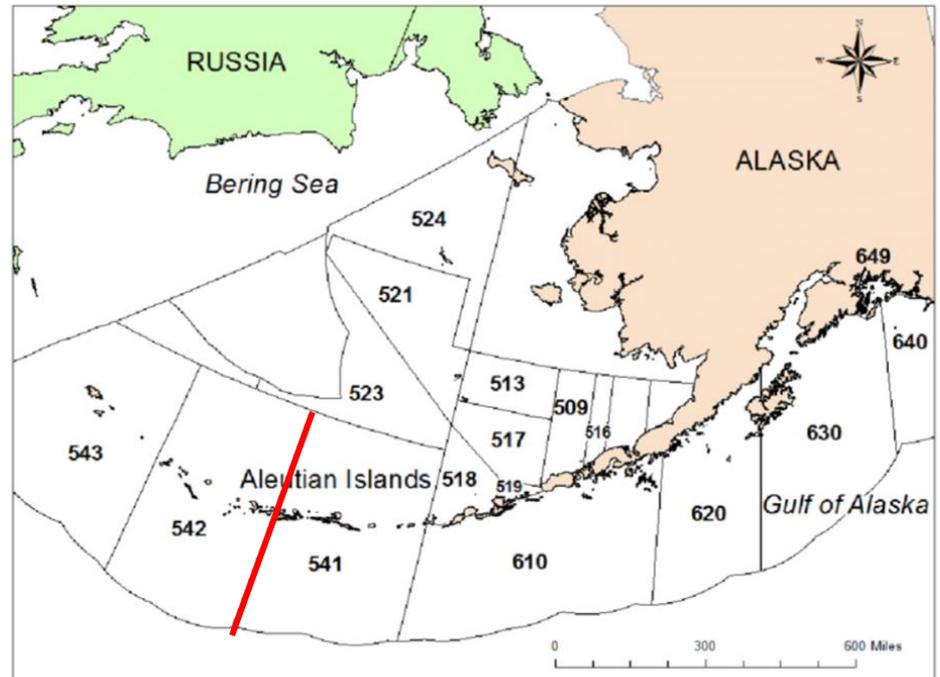
Spatial distribution of rougheye/blackspotted complex



Blackspotted rockfish much more common in western Aleutians

Spatial management and harvest

Two management areas in the Aleutians: (1) Eastern Aleutians and Eastern Bering Sea (EAI/EBS) which includes 541 and (2) central and western Aleutians (CAI/WAI) which includes 542 and 543



Concern of high exploitation in western Aleutians

Concern over high exploitation resulted in assessment including a maximum subarea species catch (MSSC), which has been exceeded

Year	WAI	MSSC	WAI Catch	Catch/MSSC
2015		46	67	1.46
2016		58	38	0.65
2017		29	34	1.17
2018		35	66	1.89
2019		37	100	2.70
2020		48	155	3.23

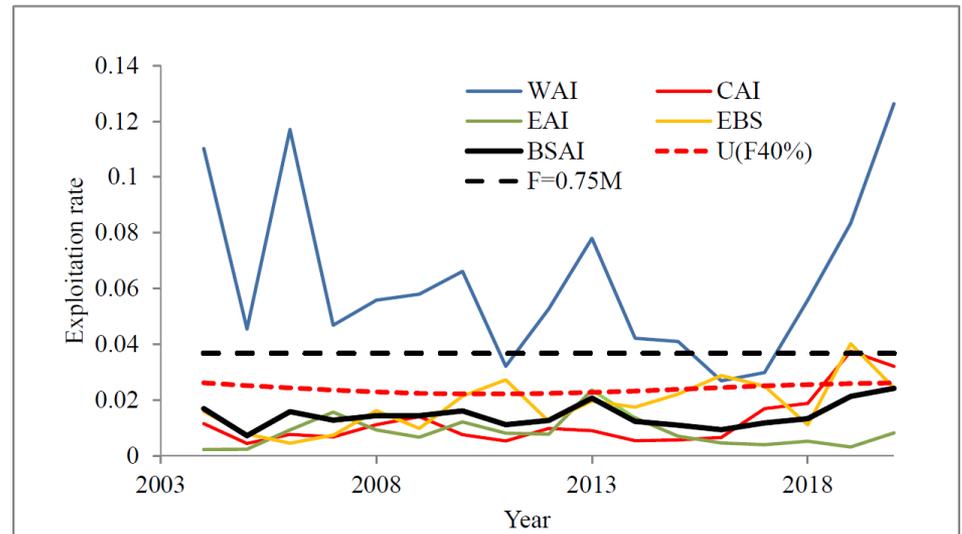
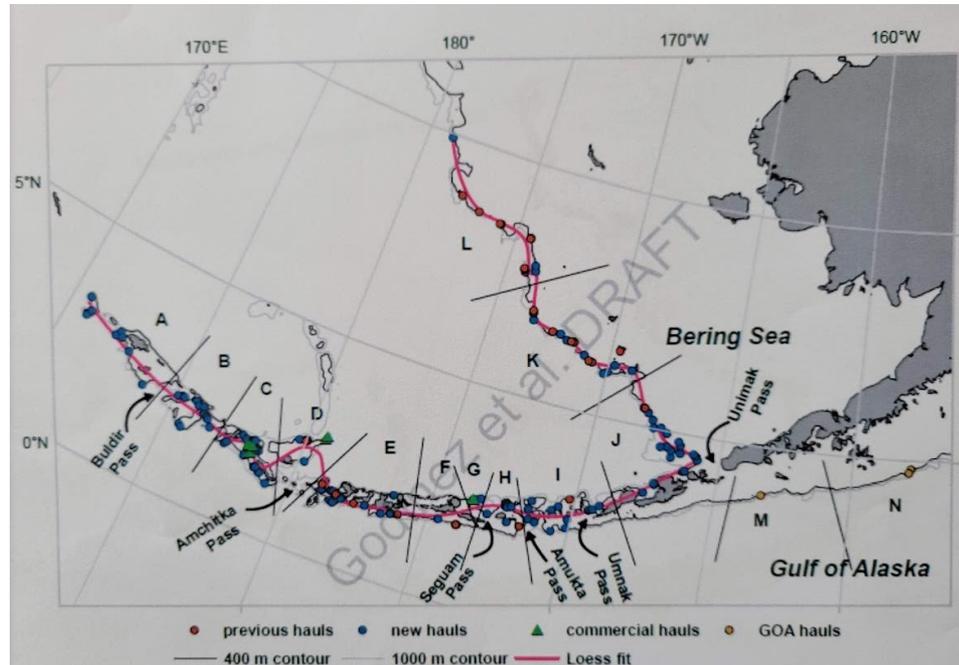


Figure 14A.1. Exploitation rates within BSAI subareas for blackspotted/rougeye rockfish, with reference exploitation rates of $0.75 * M$ and $U_{F40\%}$.

- 1) If overexploitation is occurring in the CAI/WAI, can fish from proximate stocks replenish this area?
- 2) Does genetic data indicate spatial population structure suggesting low connectivity on evolutionary timescales?

Genetic population structure of blackspotted rockfish with microsatellites



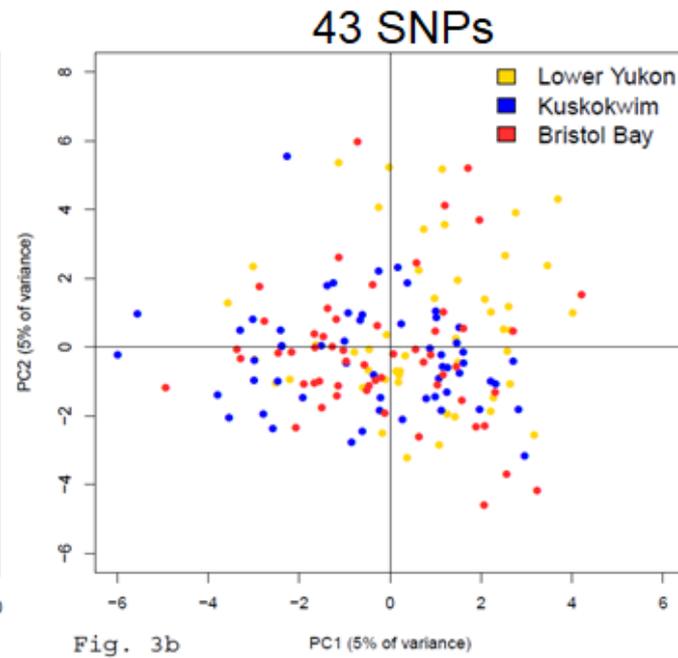
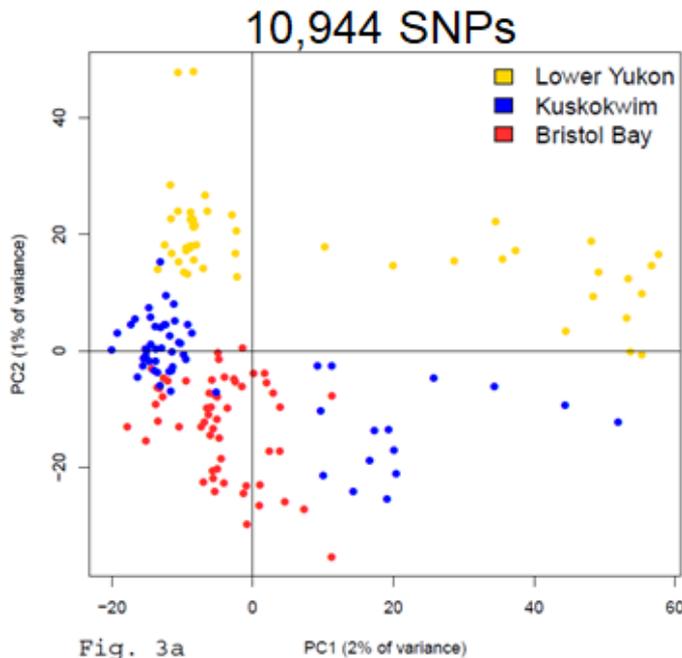
Most comprehensive study to date conducted by Godinez et al. (in prep), who analyzed 1,013 samples from 165 hauls at 12 microsatellite loci

No detectable population structure with microsatellites

Description	Sample size	Number of loci	<i>P</i> -value for IBD relationship
Original samples from 2010 study, rescored data	168	6	0.0074
Updated dataset, same loci and areas sampled in 2010 study	692	6	0.0637
Updated dataset and loci, same areas sampled in 2010 study	692	12	0.1035
Original samples from 2010 study, rescored data, only new loci	168	6	0.1645
Updated dataset and loci	942	12	0.1126

- Previous studies with fewer markers suggested subtle signals of structure, but more comprehensive analyses including more markers indicated no structure (negative slope of isolation by distance line and non-significant *p*-value)
- Both the change in the sample size and number of markers examined contribute to the difference between the two studies, with additional markers contributing more to that difference (T. Gharrett personal communication)
- Put simply, the substantially more robust dataset detects no structure

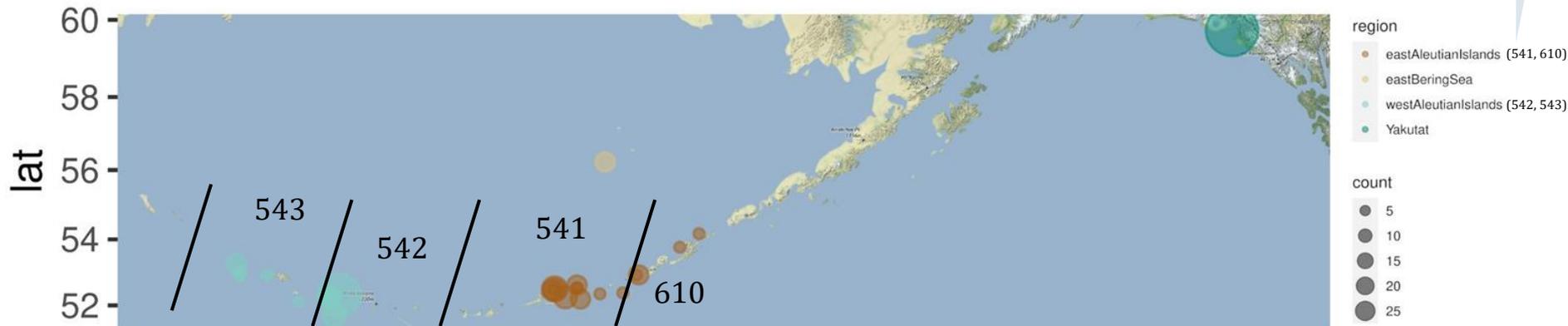
Transition to genomics: Can we detect structure with millions of genetic markers?



Larson et al. 2014

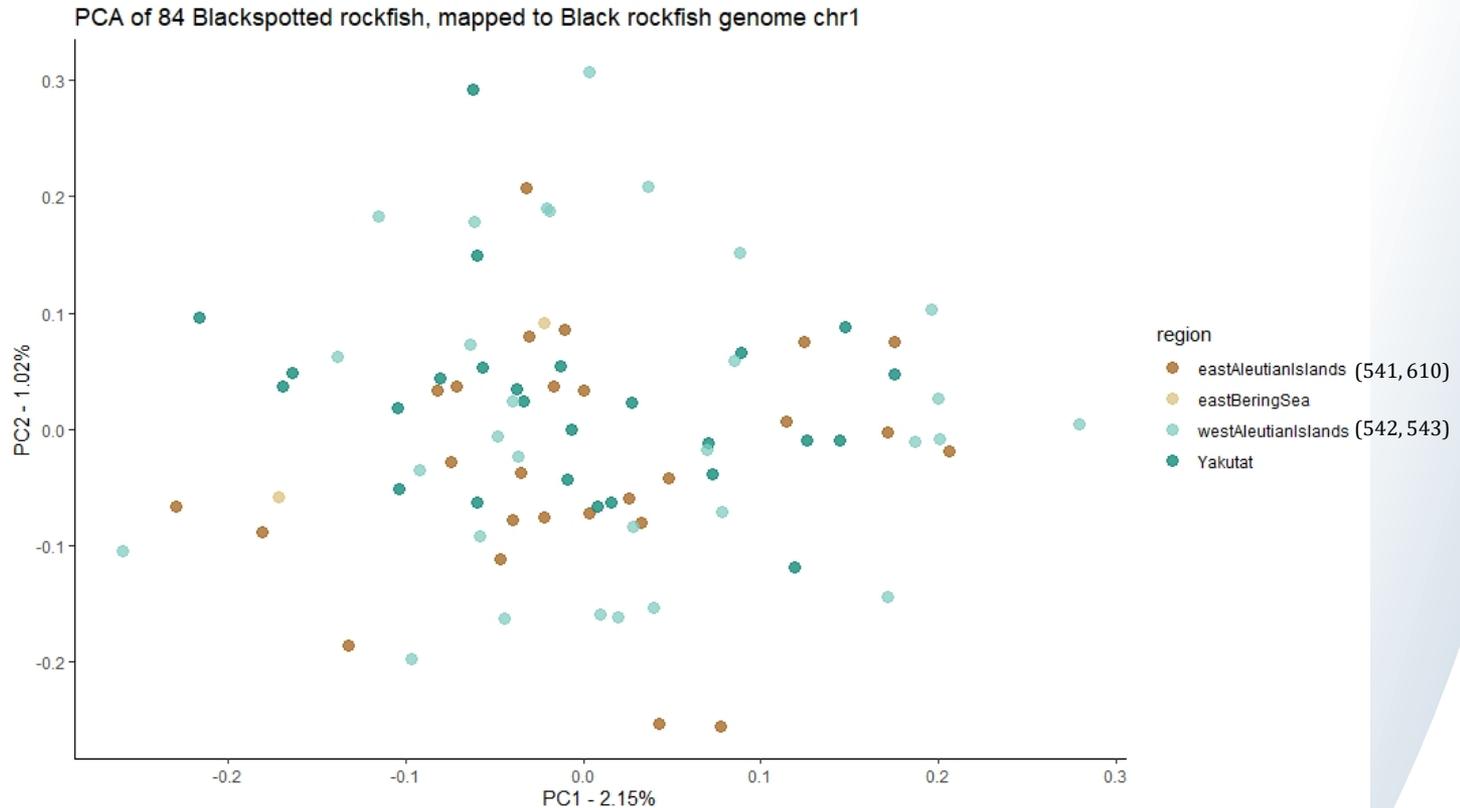
Whole genome sequencing of blackspotted rockfish

Blackspotted rockfish: 84 samples collected for whole genome resequencing



- 84 individuals from AI, GOA, and BS, fewer individuals than microsatellites due to cost
- 5.4 million single nucleotide polymorphisms (SNPs)

No detectable structure at 5.4 million SNPs



Does a lack of genetic population structure indicate demographic connectivity relevant for fisheries management?



What influences genetic population structure?

- Population size: larger populations genetically diverge more slowly
- Generation time: species with longer generation times diverge more slowly
- Migration rates: species with high migration rates diverge more slowly
- Time since establishment: species that recolonized more recently are less diverged

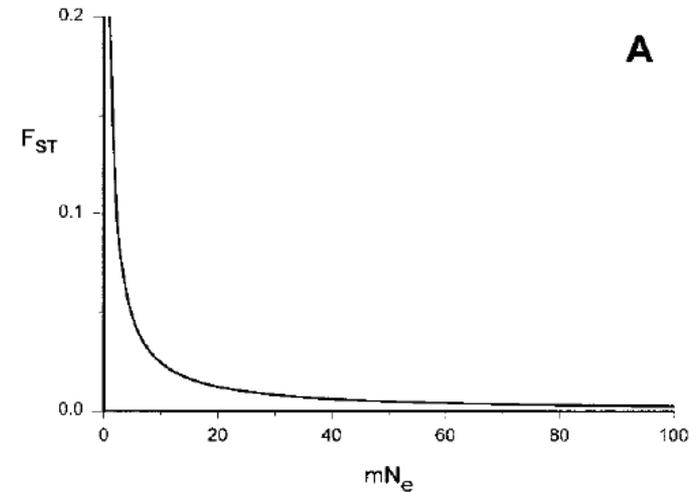
Relevant parameters for genetic structure in blackspotted rockfish

- Population sizes of blackspotted rockfish are large (in the millions)
- Generation time of blackspotted rockfish is long (~50 years)
- Habitat around the Aleutians was highly variable over evolutionary time (~10k years+) due to Glaciation, leading to unknown patterns of connectivity and colonization
- Larval dispersal during the pelagic phase may indicate potential connectivity

These factors suggest that genetic population structure of blackspotted rockfish will be low as empirical evidence indicates, and they may diverge over (evolutionary) time.

Migration and genetic structure

- FST is a common metric to estimate genetic structure
- Genetic structure is generally detectable at an FST of ~ 0.002
- Large marine populations can fall below this limit even if migration is relatively low
- For example a population with an $N_e=10,000$ and $m=0.01$ would fall well below this threshold (100 on graph)



Waples 1998

For populations with large N_e , “it is a very challenging task to use genetic data to distinguish between migration rates that do and do not lead to demographic independence.” (Waples et al. 2008)

Simple simulations for blackspotted rockfish

Parameter	Estimate
Generation time	50 years
# of generations	200 (~10,000 years)
Effective population size (N_e)	20,000 (likely underestimate)
Migration rates (m)	0, 0.001, 0.01

- We conducted simple simulations to investigate genetic structure between two populations with variable migration rates. At $m=0$ $F_{ST}=0.0047$, at $m=0.001$ $F_{ST}=0.0036$, at $m=0.01$ $F_{ST}=0.0008$
- Population structure may have been detectable at migration rates of 0 and 0.001 but not at 0.01 therefore any migration above 1% should be more than adequate to homogenize structure in blackspotted rockfish



Genetic versus demographic connectivity

- Very small levels of migration ($< 1\%$) are sufficient to homogenize genetic structure of blackspotted rockfish
- But demographic connectivity occurs at much higher rates of migration likely around 10% (Hastings 1993)
- Thus, even though we observe genetic connectivity in blackspotted rockfish, it is possible and likely that these populations are somewhat demographically independent given other assessment data



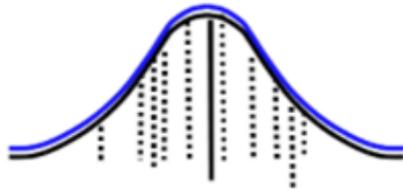
Genetic versus demographic connectivity

- We emphasize that lack of genetic structure should not be used as justification to adopt less conservative spatial management and that this decision should be based on assessment data
- In summary, detection of genetic structure likely indicates demographic independence, but lack of genetic structure does not indicate demographic connectivity

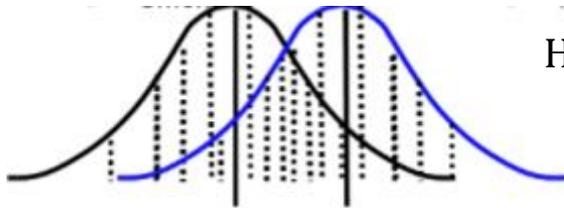


Absence of evidence is not evidence of absence.

Research question: Is demographic movement in blackspotted rockfish sufficient to replace WAI stocks subject to high fishing mortality rates?



H_0 : Allele frequencies do not differ among NMFS areas.



H_A : Allele frequencies differ among NMFS areas.

We did not reject the null hypothesis using highly powerful genetic techniques. Do we now have sufficient information to inform our research question? No.

In this case, genetics was not a tool that can answer the question. Other tools such as tagging may be more useful.

Conclusions

- No genetic structure was detected in blackspotted rockfish using microsatellites (12 markers) or whole genome sequencing (millions of markers)
- Lack of genetic structure in this species is unsurprising given large population sizes, long generation time, and dynamic habitats over evolutionary time due to glaciation
- Simulations suggest that migration rates $<1\%$ would homogenize genetic structure in this species, but these rates are much lower than the 10% migration rates likely necessary for demographic independence

Management implications

- In 2014, the Plan Team and SSC expressed concern regarding stock structure (despite the updated genetic data), based on low abundance and high exploitation rates in the WAI:

The SSC agrees with the Plan Team that the blackspotted/rougheye rockfish remain at the concern level in the WAI, and notes that concern is now heightened, given the high catch and exploitation in 2013 and 2014. (SSC minutes, Oct 2014)

- Since 2014, exploitation rates in the WAI area have become more disproportionate relative to estimated biomass, prompting both the Plan Team and SSC in 2020 to call for steps for identifying more effective spatial management tools (i.e., either a white paper and/or a workshop)
- Although the whole genome analysis is consistent with the 2014 microsatellite analysis, the non-genetic information on disproportionate harvesting (and other factors) does not provide evidence to alter the recent Plan Team and SSC recommendations that more effective spatial management measures should be identified