Genomics Activity Plan GOAL: Population genetics of all AFSC managed stocks by 2030

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Guidelines for determination of spatial management units for exploited populations in Alaskan groundfish fishery management plans

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Stock structure template

Fishing mortality, spatial concentration of fishery relative to abundance, population trends, generation time, physical limitations (sessile organism), growth differences, age/size structure differences, spawning time differences, maturity at age differences, morphometrics, meristics, spawning site fidelity, mark-recapture data, natural tags (otolith microchemistry), genetics.

HARVEST AND TRENDS								
Factor and criterion	Justification							
Fishing mortality	If this value is low, then conservation concern is low							
(5-year average percent of Fabr or Foft)								
Spatial concentration of fishery relative to	If fishing is focused on very small areas due to patchiness or							
abundance (Fishing is focused in areas <<	convenience, localized depletion could be a problem.							
management areas)								
Population trends (Different areas show	Differing population trends reflect demographic independence that							
different trend directions)	could be caused by different productivities, adaptive selection, differing							
	fishing pressure, or better recruitment conditions							
Ва	rriers and phenotypic characters							
Generation time	If generation time is long, the population recovery from overharvest							
(e.g., >10 years)	will be increased.							
Physical limitations (Clear physical	Sessile organism; physical barriers to dispersal such as strong							
inhibitors to movement)	oceanographic currents or fjord stocks							
Growth differences	Temporally stable differences in growth could be a result of either short							
(Significantly different LAA, WAA, or	term genetic selection from fishing, local environmental influences, or							
LW parameters)	longer-term adaptive genetic change.							
Age/size-structure	Differing recruitment by area could manifest in different age/size							
(Significantly different size/age	compositions. This could be caused by different spawning times, local							
compositions)	conditions, or a phenotypic response to genetic adaptation.							
Spawning time differences (Significantly	Differences in spawning time could be a result of local environmental							
different mean time of spawning)	conditions, but indicate isolated spawning stocks.							
Maturity-at-age/length differences	Temporally stable differences in maturity-at-age could be a result of							
(Significantly different mean maturity-at-	fishing mortality, environmental conditions, or adaptive genetic							
age/ length)	change.							
Morphometrics (Field identifiable	Identifiable physical attributes may indicate underlying genotypic							
characters)	variation or adaptive selection. Mixed stocks w/ different reproductive							
	timing would need to be field identified to quantify abundance and							
	catch							

Meristics (Minimally overlapping	Differences in counts such as gillrakers suggest different environments							
differences in counts)	during early life stages.							
Behavior & movement								
Spawning site fidelity (Spawning	Primary indicator of limited dispersal or homing							
individuals occur in same location								
consistently)								
Mark-recapture data (Tagging data may	If tag returns indicate large movements and spawning of fish among							
show limited movement)	spawning grounds, this would suggest panmixia							
Natural tags (Acquired tags may show	Otolith microchemistry and parasites can indicate natal origins,							
movement smaller than management	showing amount of dispersal							
areas)								
Genetics								
Isolation by distance	Indicator of limited dispersal within a continuous population							
(Significant regression)								
Dispersal distance (< <management areas)<="" td=""><td>Genetic data can be used to corroborate or refute movement from</td></management>	Genetic data can be used to corroborate or refute movement from							
	tagging data. If conflicting, resolution between sources is needed.							
Pairwise genetic differences (Significant	Indicates reproductive isolation.							
differences between geographically								
distinct collections)								

Stock structure template work plan

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Stock Stru	cture work	k plan									
# of BSAI	left	13									
# of GOA	left	15								Proposed	
	Complete	Stock	Lead Author		2010	2011	2012	2013	2014	2015	2016
		Bering S	ea-Aleutian Islands								
	Yes	Eastern Be	ring Sea pollock	Ianelli						Х	
	No	Bogoslof Is	sland Pollock	Ianelli							
	Yes	Aleutian Islands pollock		Barbeaux				Х			
	No	AI Pacific	cod	Thompson							
	Yes	BS Pacific	cod	Thompson	X						
	No	Sablefish		Hanselman							
	Yes	Yellowfin s	sole	Wilderbuer			X				
	No	Greenland '	Turbot	Barbeaux							
	Yes	Arrowtooth	ı flounder	Spies					Х		
	No	Kamchatka	flounder	Wilderbuer							
	No	Northern R	ock sole	Wilderbuer							
	Yes	Flathead sole		McGilliard						Х	
	No	Alaska plai	ce	Wilderbuer							
	No	Other flatfi	sh	Wilderbuer							
	No	Pacific oce	an perch	Spencer							

Genomics AP

Prioritization of genetic stock structure (year of initiation listed):

- Pacific cod, walleye pollock (currently underway).
- 2020: Sleeper shark, blackspotted rockfish.
- 2021: Red king crab, greenland turbot, shortspine thornyhead.
- 2022: arrowtooth flounder, yellowfin sole.

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- Pollock: JISAO Post-doc, cooperative research.
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