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Central Issues: Western Alaskan Chum Salmon Runs Decline

WESTERN ALASKA CHUM SALMON CATCH, 1960-2007

YEAR

DRAINAGE
Kotzebue Norton Sound Yukon River Kuskokwim Bristol Bay

NUMBER IN THOUSANDS OF FISH

National Marine Fisheries Service
Central Issues: Bycatch by the BSAI Pollock Fleet

Gisclaire, B R American Fisheries Society
Symposium 70: 799-816, 2009
Tools: Genetics and MSA

Bering Sea pollock bycatch and BASIS samples

AYKSSI Funded Project Between NMFS and UAFSFOS, PI Chris Kondzela
The Nuts and Bolts of MSA
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MSA works better if you have many informative markers

MSA works better if you have data from many populations
The Nuts and Bolts of MSA

mSats = Many different colors at each locus
But scoring and throughput are expensive

SNPs = Less information per marker – use more
But throughput can be millions per day
And data is easily shared and replicated

First you have to find good ones

Currently using a combined SNP/mSat baseline
My PhD is Four Chapters

Chapter 1- SNP Discovery
Collaboration with K. Saitoh, V Brykov, D Churikov

Chapter 2- Chum Baseline Development
Collaboration with J. Pella and M. Masuda TSMRI

Chapter 3 – Focused Genetics of the Kuskokwim River
Collaboration with C. Kondzela TSMRI and W. Templin ADF&G

Chapter 4 – Phylogeography of Chum Salmon
Award from Center for Arctic Research
Chapter 1: Finding Informative SNPs

- Application of single nucleotide polymorphisms to non-model species: a technical review
  M.R. Garvin, K. Saitoh, A. J. Gharrett
  Molecular Ecology Resources 2010 10(8):91-108

- Single nucleotide polymorphisms in chum salmon (Oncorhynchus keta) mitochondrial DNA derived from restriction site haplotype information
  M.R. Garvin, K. Saitoh, V Brykov, D Churikov, and A. J. Gharrett
  Genome 2010 53: 501-507

- Application of SNP markers to chum salmon Oncorhynchus keta: Discovery, genotyping, and linkage phase resolution
  M.R. Garvin and A. J. Gharrett
  J Fish Biology 2010 77(9): 2137-2162

- Diagnostic single nucleotide polymorphisms (SNPs) identify Pacific ocean perch and delineate blackspotted and rougheye rockfish
  M.R. Garvin, R. Marcotte, K Palof, R Riley, L Kamin, and A. J. Gharrett
  Transactions of the American Fisheries Society 2011 In press
Chapter 2 – How Good is the Baseline?

“Mock” Mixture

Baseline

100%

100%

100%

Good

Bad

MSA Algorithm
Chapter 2 – Leave Ten Out Cross Validation: How Good is the Baseline?

10% to create Mixture 1
90% to create Baseline 1

Repeat for all populations

Analyze Mixture 1 with Baseline 1

Ten different sets possible – estimate mean/var of MSA

1. Baseline Population #1
2. Mixture #1
3. Baseline Population #1’
Chapter 2 – Leave Ten Out Cross Validation: How Many SNPs?

Use information from 12 INFORMATIVE SNP Loci

Create “new” SNP loci and run MSA as we did for the Cross Validation
Chapter 3 – Kuskokwim Populations
Chapter 4 – Phylogeography of Chum Salmon in Western Alaska
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Chapter 1

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