Development of standardized DNA baselines for high-seas and bycatch applications

> Division of Commercial Fisheries Alaska Department of Fish and Game



#### **Standardized Databases**

- Species-wide databases are a prerequisite for many applications
- Transparency and repeatability are necessary for PSC and NPAFC Treaty projects
- Coordination and shared effort maximizes use of limited research funds



Chum Salmon Applications, Standardized Allozyme Baseline



Chinook Salmon Applications, Standardized Allozyme Baseline

#### Three Types of Genetic Markers

#### -Protein

- Allozymes
- -DNA repeat variation
  - microsatellites
- -DNA sequence polymorphism
  - SNPs (single nucleotide polymorphisms)

#### All Can Be Standardized

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- DNA repeat variation
  - Microsatellites
    - difficult to standardize

#### Microsatellite

• Variation scored by estimating repeats



Two-Year study design funded by Chinook Technical Committee (CTC) (\$1.1 million)

- Year 1 (FY04): Standardization
  - Select a common set of markers
  - Standardize allele designations
  - Select baseline populations for year 2
- Year 2 (FY05): Baseline development, 16,000 individuals
  - Verification via blind samples
  - Sample exchange
  - Data collection and storage
  - Power analysis

#### Genetic Analysis of Pacific Salmon (GAPS) Collaborators

Alaska Department of Fish and Game

Columbia River Intertribal Fish Commission

Canadian Department of Fisheries and Oceans

NOAA (Alaska Fisheries Science Center, Southwest Fisheries Science Center, Northwest Fisheries Science Center)

Oregon State University

Washington Department of Fish and Wildlife

#### Current Development of DNA Baseline Chinook Salmon



#### Three Types of Genetic Markers

#### – Protein

- Allozymes
  - standardization easy and completed
- DNA repeat variation
  - Microsatellites
    - difficult to standardize
- DNA sequence polymorphism
  - SNPs (single nucleotide polymorphisms)
    - -automatic standardization

#### Pacific Salmon Commission Expert Panel

- David G. Hankin, Chair Fisheries Biology, Humboldt State University
- Gary S. Morishima, CEO, MORI-ko, LLC
- John H. Clark, Chief Scientist, Alaska Dept. of Fish and Game
- **Richard B. Deriso**, Chief Scientist, Tuna-Billfish Program, Scripps
- Carlos Garza, Supervisory Geneticist, NOAA Fisheries SW Center
- Brian E. Riddell, Research Scientist, Pacific Biological Station
- **Carl Schwarz**, Prof., Statistics and Actuarial Science, Simon Fraser
- James B. Scott, Chief Scientist, Wash. Dept. of Fish and Wildlife

http://www.psc.org

Peer reviewers for Expert Panel Report were all senior scientists:

- Don Campton, USFWS
- Peter Lawson, NOAA
- Terry Quinn, UAF
- John Skalski, UW
- Carl Walters, UBC

(genetics)

(fishery management)

(population dynamics, sampling theory)

(statistics)

(population dynamics, management theory) **Finding 17.** Over the past 20 years, first allozymes and more recently microsatellite markers have become the dominant tool for use in GSI. However, we believe that microsatellites will be replaced in the next several years by SNPs as the tool of choice for population genetic applications, as has already occurred in human genetics. The first step in the transition in marker type is the identification of appropriate SNP markers, a process that is already underway for Chinook salmon through a multiagency effort. SNP marker development and databases are also well underway for sockeye and chum salmon. Factors driving the replacement currently include the ease of data standardization, cost, and high throughput. Costeffectiveness should rapidly improve as more SNPs are developed and multiplex processes drive the cost of analysis down.

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• Single nucleotide polymorphism



DNA sequence (A, T, C, or G)

# Relative divergence of different classes of DNA markers:



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Markers subject to natural selection can have greatest information content for stock identification study:



## SNPs in structural genes offer enhanced resolution:

Gene	Function
Type II Keratin	filament protein
Growth Hormone 2	growth control
GPDH & GPDH2	energy conversion
Hepatocyte Growth Factor Activator	GF activator
MHC2_091 (4)	immune response
p53	tumor suppressor
Preproinsulin	blood glucose control
Prolactin	hormone activity
Replication Factor C2 (2)	replication protein
Serpin	proteinase inhibitor
TF3 & TF10	iron transport
One_U301(CJFK)	immunoregulation
Zona Pellucida	sperm binding

### **CTC SNP Initiatives**

- CTC has funded the GAPS group to develop an additional 70 SNPs for Chinook salmon
- Anticipated SNPs by 2007
  - Greater than 155 SNPs in Chinook salmon
  - Greater than 100 in chum salmon
- High throughput and cost effective analyses being developed in multiple labs

#### Number of Salmonid Laboratories Surveying SNPs



Cooperative Efforts to Develop Range-wide SNP Baselines

- Chinook salmon
  - ADFG, NOAA-ABL, NOAA-NWFSC, NOAA-SWFSC, USFWS-Abernathy, DFO, WDFW, CRITFC, IDFG, OSU, WSU
- Chum salmon
  - ADFG, NOAA-ABL, NOAA-NWFSC, WDFW, FA (Japan), VNIRO (Russia), NFRDI (Korea)

#### Current Development of Pacific Rim SNP Baseline Chinook Salmon



Chum salmon: Preliminary data on 74 populations to test assignments for 36 existing SNPs:

#### **Excellent resolution of major lineages**



#### **Immature Chum BASIS** Cruise Aug-Sep 2004





#### 2004 Stock Composition

**Honshu** Hokkaido Russia W. Alaska **Vukon F. Z** Kusko F. N. Pen. S. Pen. **Kodiak Susitna S.** Central SE Alaska Washinton/BC

rom Auke Bay Lab





#### Approach Chum and Chinook Salmon

- Neutral and selective "random" SNPs
  - Development of adequate numbers well underway
- Development of targeted or "designer"
  SNPs to differentiate W. Alaska for both chum and Chinook
  - High throughput screening using TGCE (Temperature gradient capillary electrophoresis)

• Western Alaska Salmon Stock Identification Program (WASSIP)

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- Largely unfunded mandate to identify composition of interception fisheries in eastern Bering Sea (chum and sockeye)
- Original concept included BSAI bycatch
  - BSIA bycatch removed from current plan
  - All analyses depend upon same baseline populations



WASSIP sampling 2006-2007:

Identify stock composition in districts from Chignik to Kotzebue

![](_page_39_Figure_0.jpeg)

Chum salmon populations needed for bycatch baseline (by region)

![](_page_40_Figure_1.jpeg)

(need to add up to 200 populations)

- Western Alaska Salmon Stock
  Identification Program (WASSIP)
- AYKSSI project to address Chinook salmon

AYK SSI funded \$500,000 collaboration among:

- Alaska Department of Fish and Game
- University of Washington
- NOAA Fisheries

Objectives:

• Complete standardized DNA baseline

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- Analyze stock composition from 2002-2006 BASIS cruises

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- Develop run reconstruction model to forecast western Alaska Chinook salmon runs

![](_page_48_Figure_0.jpeg)

![](_page_49_Figure_0.jpeg)

Chinook salmon populations needed for bycatch baseline (by region)

![](_page_50_Figure_1.jpeg)