

# Status of Chinook Standardization and Developing Technologies

Coded-wire Tag Workshop  
Lynnwood, Washington  
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# Waypoints

- GAPS Consortium progress report
  - Marker selection/standardization
  - Database construction
  - Remaining challenges
- General considerations
  - International harvest management
  - Funding
  - Agency-specific priorities
  - Marker and baseline sample selection

# Project objectives

1. Develop a coast-wide DNA baseline that will resolve lineages and stocks within the region for which the CTC is responsible
2. Facilitate future expansion of the DNA baseline by the addition of novel genetic markers. This will be accomplished via the exchange of DNA samples
3. Develop a data base application to support the dissemination and growth of the baseline

# GAPS Collaborators

## **Agency**

NWFSC

OSU

CDFO

SWFSC

CRITFC

UI

IDFG

ADFG

ABL

WDFW

USFWS Abernathy

USFWS Anchorage

## **P.I.\***

Paul Moran

Michael Banks

Terry Beacham

Carlos Garza

Shawn Narum

Madison Powell

Matt Campbell

Lisa Seeb

Richard Wilmot

Sewall Young

Bill Ardren

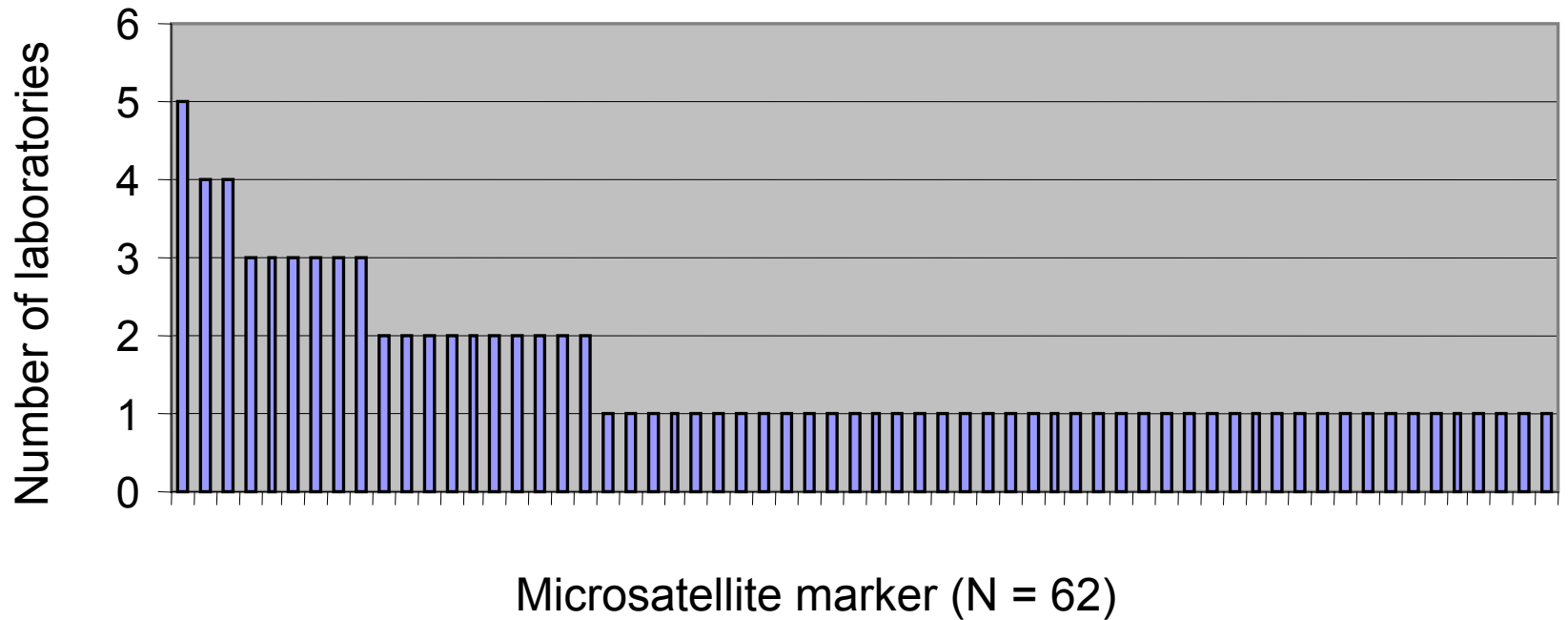
John Wenberg

\*Numerous coPIs not listed

# Two fundamental challenges to standardization of microsatellite data

- Little overlap in marker sets among labs
- Different DNA fragment sizes among platforms and therefore different allele naming conventions

# Only a few markers were widely used among labs

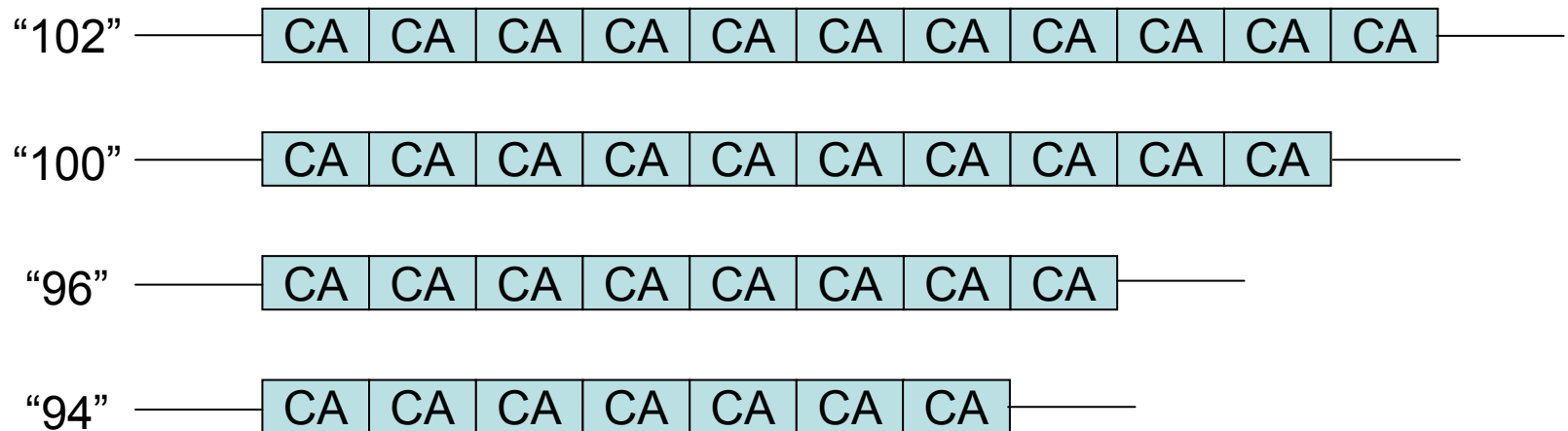


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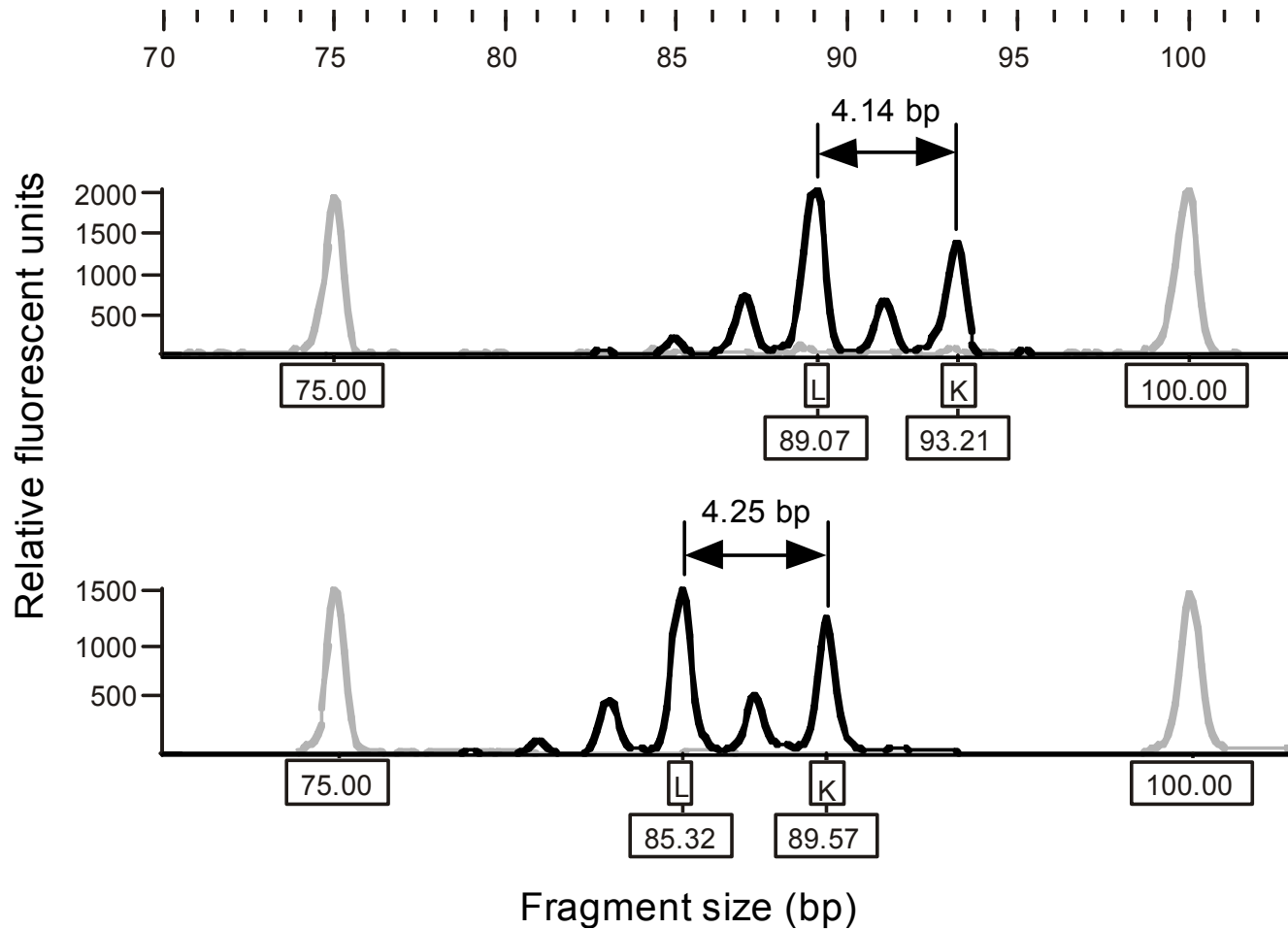
# Microsatellite markers—simple sequence repeats

Allele designations typically related to fragment size





# Substantial differences in size estimates among platforms



# 2-Year GAPS study design

- Year 1: Standardization
  - Selection of a common set of markers
  - Standardization of allele designations
  - Selection of representative populations for year 2
- Year 2: Baseline development
  - Verification via blind samples
  - Sample exchange
  - Data collection and storage
  - Power analysis

# “Marker (=locus) sets” and “Sample sets”

## Markers\*

- 62 sponsored loci
- 25 candidate loci
- 15 finalists for baseline construction

## Samples

- 500-sample survey set  
(10 individuals from each of 47 populations, range-wide)
- 96-sample reference set  
(8 individuals from each of 12 regions)
- 15,000-sample baseline set  
(144 individuals from each of 105 populations )

\*Current focus on microsatellites, future interest in SNPs

# Year 1: Standardization

- Marker selection
  - 500-sample survey set run for 62 loci
  - 25 loci selected for optimization in all labs
  - 96-sample reference set run for all 25 loci
  - 15 loci selected for allele standardization
- Standardization of allele designations
  - Reconciliation among labs
  - “Binning” issues—“lumping” and “splitting”

# Two organizational meetings to coordinate standardization

- Workshop associated with the annual meeting of the North Pacific Anadromous Fish Commission, 4-5 Nov 2003
- *Ad hoc* meeting in Seattle, 10-11 May 2004

# Accomplishments at NPAFC

- Established marker selection criteria
- 25 candidate markers (out of 62 examined)
- Range-wide reference sample set to standardize scoring (N = 96, a subset of the 500)
- Putative baseline populations for next year's data collection phase
- Distribution of genotyping effort among labs-- regional focus
- Database construction and data sharing

# Accomplishments in Seattle

- 25 candidate loci reduced to 15 finalists
- Error-trapping and data reconciliation
- Allele designations, “holotypes,” and vouchers
- Locus “curators” volunteered
- Resolution of the data base, lumping, splitting, and imperfect repeats

# Ahead....

- **28 May** Submit any genotype corrections
- **21 June** New alleles to locus curator
- **June** Data repository—Docushare or FTP server
- **15 July** Final standardized allele designations
- **July 2004** Final report for year 1
- **1 Aug** Baseline and blind samples sent to all labs
- **15 Sept** Genotypes for blind samples submitted to NWFSC
- **1 Oct** Early evaluation of loci—power analysis, Mendelian segregation, etc.
- **13 Oct** Meeting?
- **December** Distribute samples collected in 2004 field season
- **March 2005** Aliquots of DNA from baseline replicate sent to all labs (“Megaswap”)
- **May 2005** “Beta” version of baseline brought online for collaborators and CTC members
- **July 2005** Final report presentation and development of peer-reviewed publication



# Remaining challenges

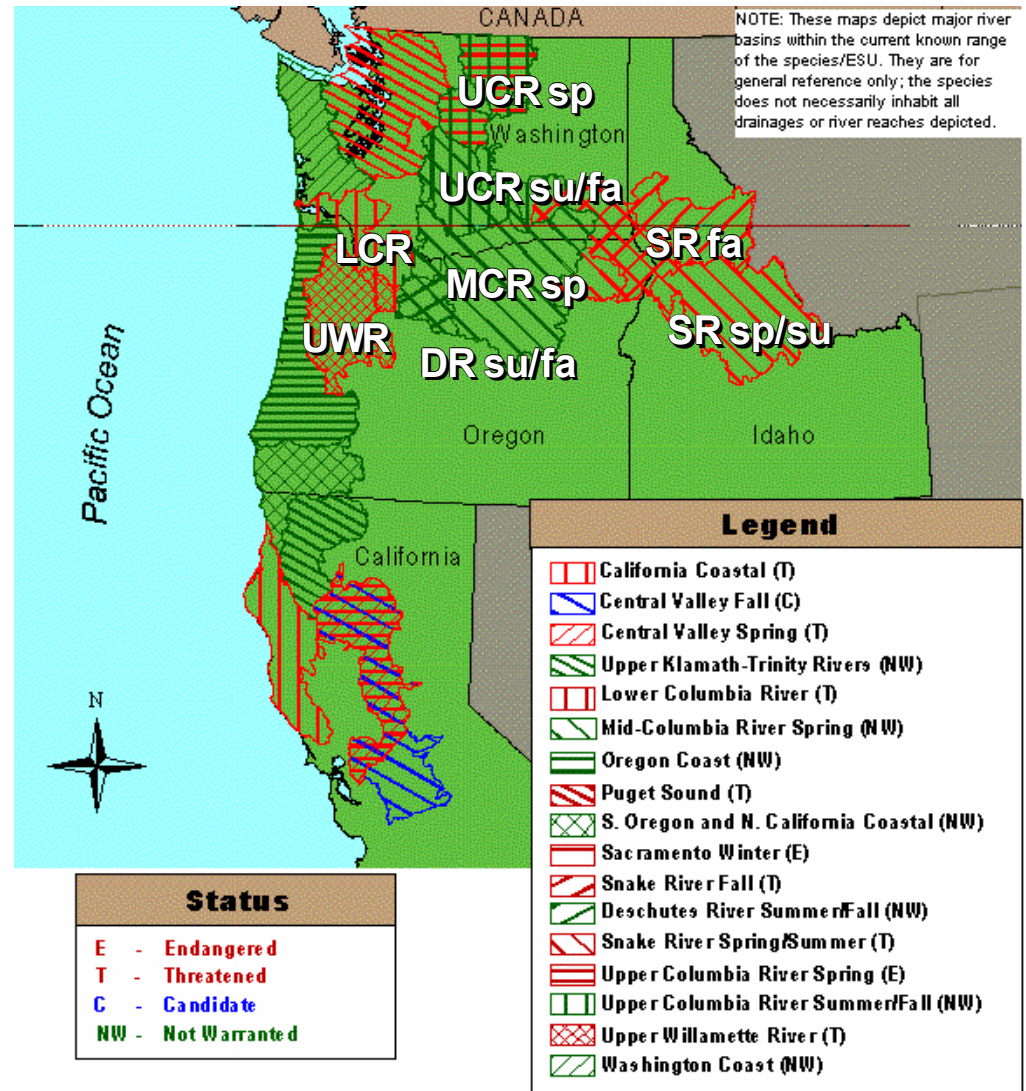
- Get ~15 markers to work in all labs
- Complete standardization of scoring
- Convince ourselves that 15 markers are enough (and not too much)
- Obtain all of the desired samples for the baseline
- Develop safe and secure repository for data

# General observations about standardizing genetic data

- Essential to international fishery management
- Doesn't happen without specific funding
- Requires substantial sacrifice by participating labs
- Agency goals diverge from those of the community

# NWFSC/WDFW Columbia R. Chinook baseline

- 3,000+ individuals
- 63 populations
- All ESUs
- 8 microsatellites
- 176 alleles
- High assignment accuracy



# NWFSC microsatellite baseline for southern coho salmon

## 12 Loci

|        |         |
|--------|---------|
| Ots103 | OtsB3   |
| Ots3   | Oki1    |
| P53    | One13   |
| Ocl8   | Ots213  |
| Oki10  | OtsG83b |
| Oki23  | OtsG422 |

## Applications

Mixed Stock Analysis  
of Ocean-caught juveniles  
off Oregon and Washington

Recovery Planning for  
Oregon Coast and  
Lower Columbia River

D. Van Doornik, unpublished data



# Selection of baseline populations

- Emphasis on major contributors to CTC fisheries, balanced against need to fully characterize Chinook population genetic variation range-wide
- Ultimately to provide a robust, state-of-the-art baseline with ample power to identify stock-of-origin of individuals in CTC fisheries
- Provide a standard reference set of Chinook populations that serve as a focal point for a whole range of conservation and recovery research

# Marker performance summaries

- Quality of amplification and reliability of scoring
- Number of alleles and other measures of variability



# Graphical examples

