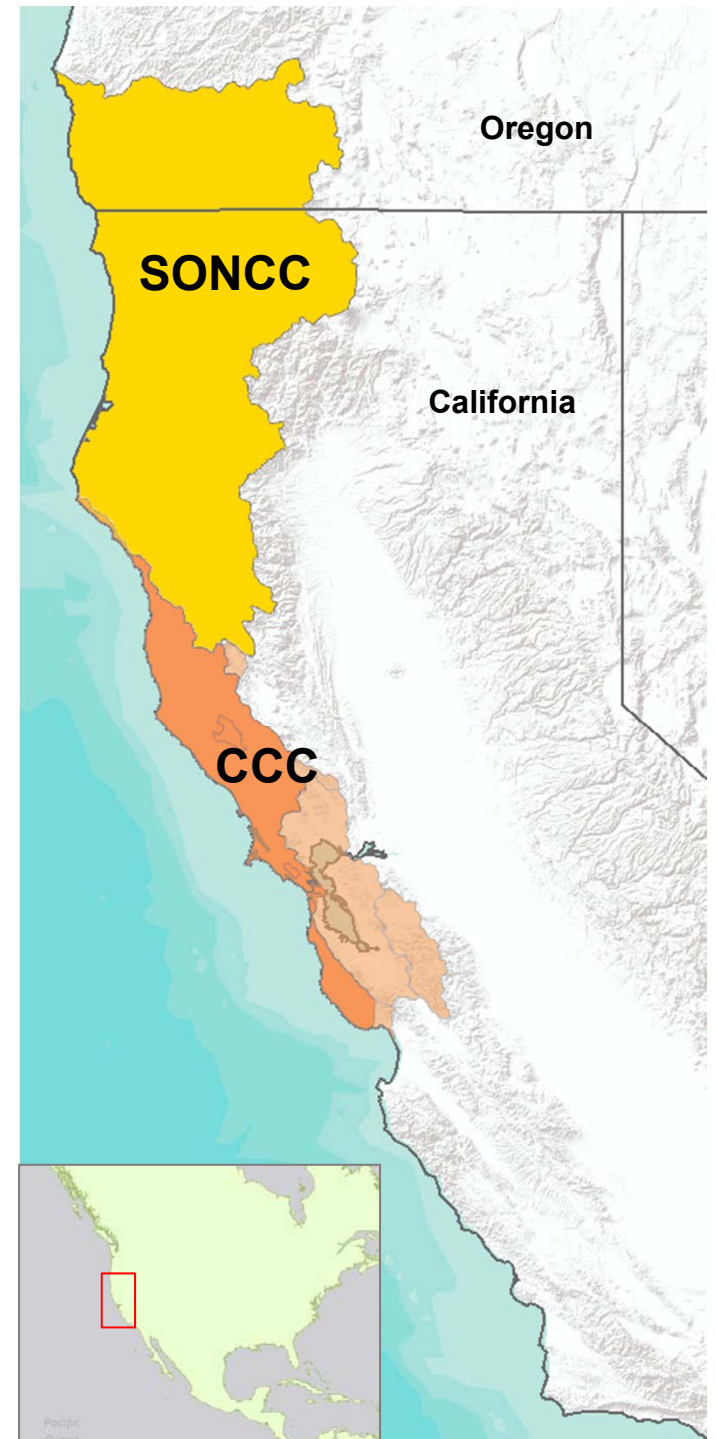# Spatial and temporal variation in structure and abundance of coho salmon in California

John Carlos Garza

Eric C. Anderson

Tommy Williams

Brian Spence
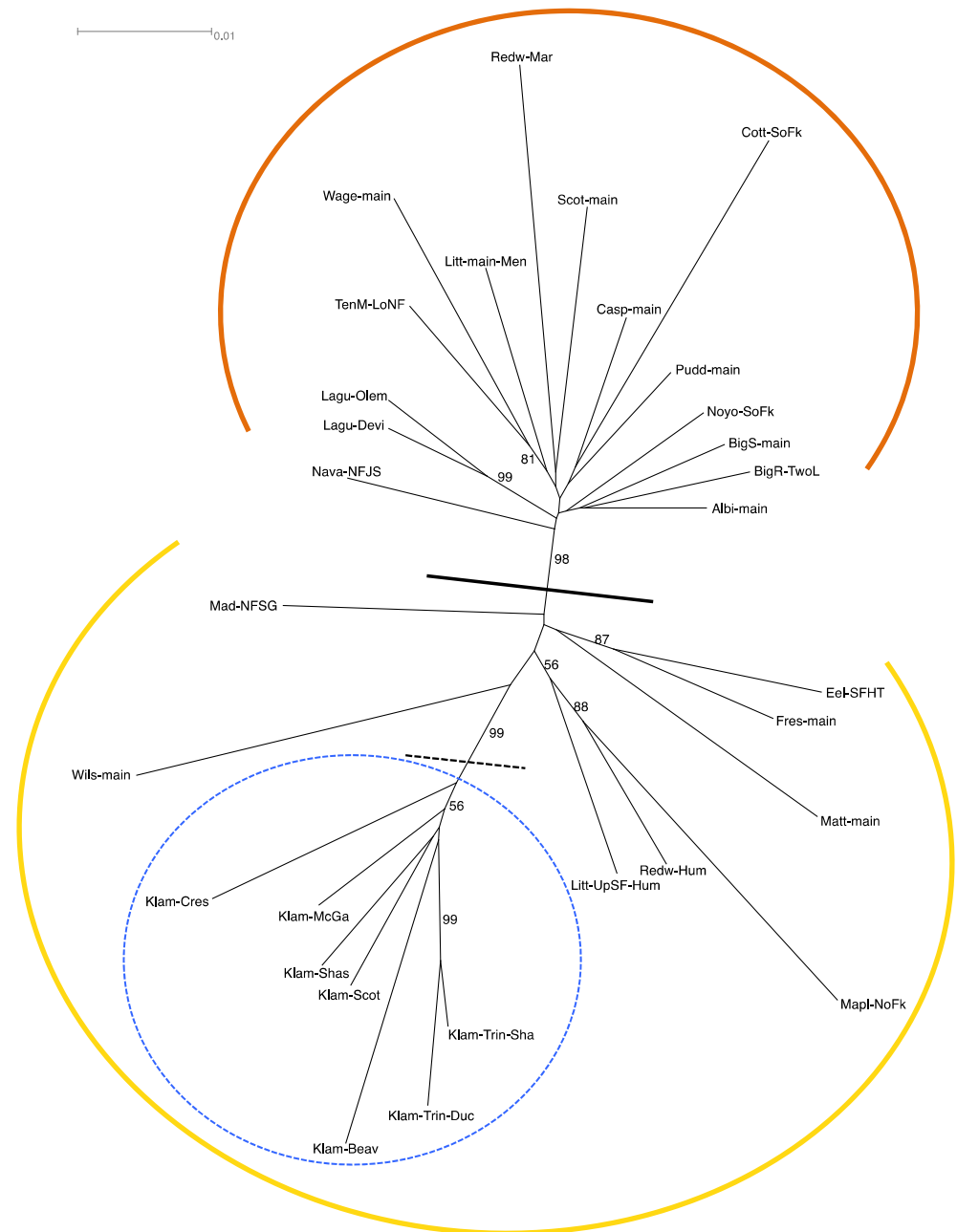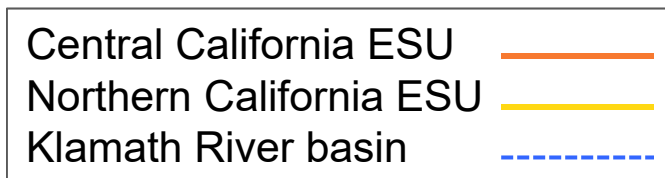
Kerrie Pipal

Libby Gilbert-Horvath

NOAA Fisheries
National Marine Fisheries Service

Status of coho salmon in California, USA

- Population declines, local extinctions

- Management units: Evolutionarily Significant Units (ESUs)

  – Southern Oregon/Northern California Coast Coho Salmon ESU (SONCC) – *Threatened*

  – Central California Coast Coho Salmon ESU (CCC) – *Endangered*

- All populations have protected status

- Life history

  – Anadromous, reproduce in natal streams, semelparous

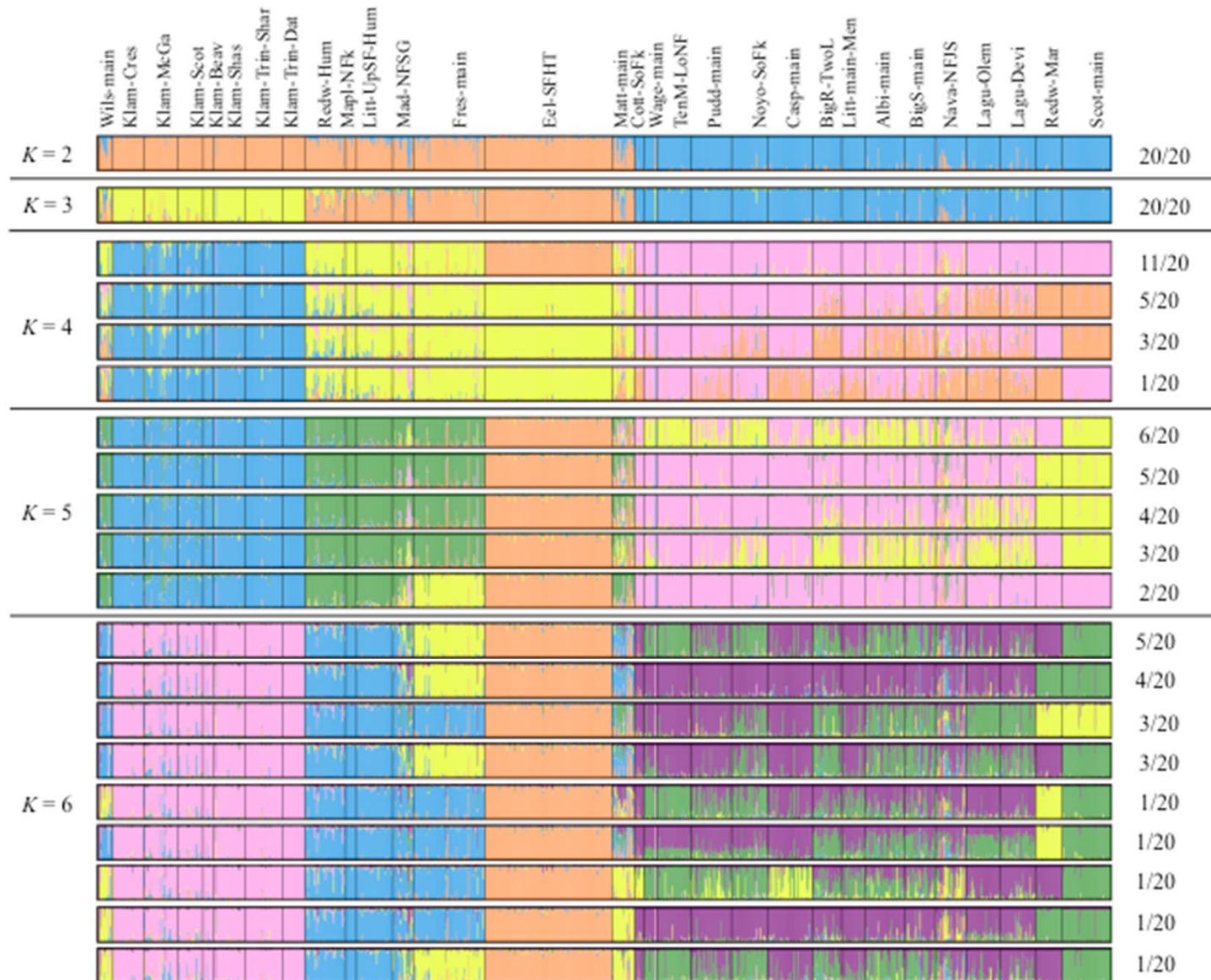 – 3-year life cycle; 3 brood years, little temporal gene flow

Background: phylogeography of coho salmon in California

- 30 sites surveyed for young-of-year in 2003
- Significant hierarchical genetic structure
  - Greatest divergence at broadest geographic scale
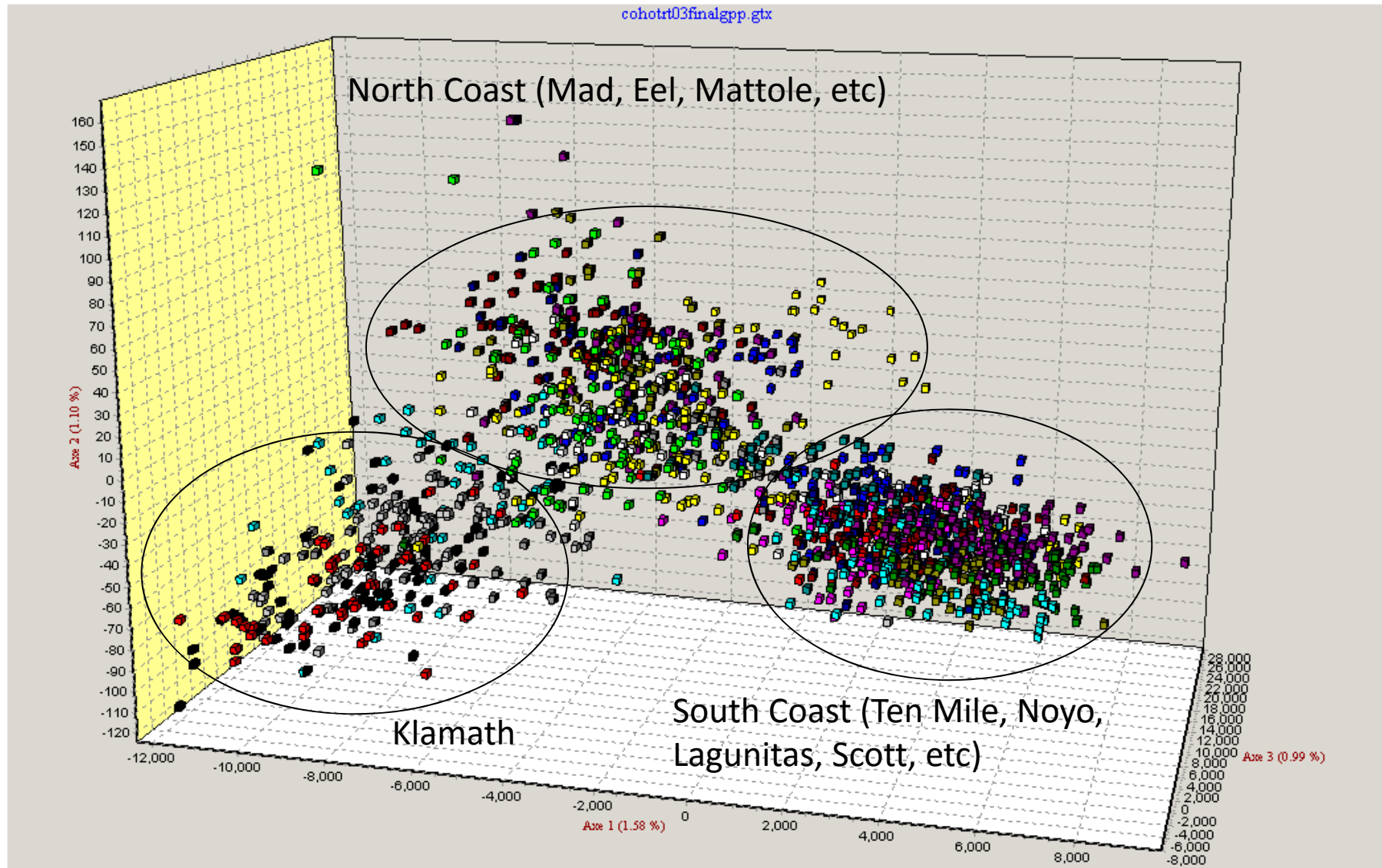- Klamath River basin distinct from other northern populations

Central California ESU ————
Northern California ESU ————
Klamath River basin - - - - - - - -

Gilbert-Horvath et al. (in press), 18 microsatellite loci

Background: phylogeography of coho salmon in California

Bayesian Clustering Analysis-Individual Genotypes

Gilbert-Horvath et al. (in press), 18 microsatellite loci

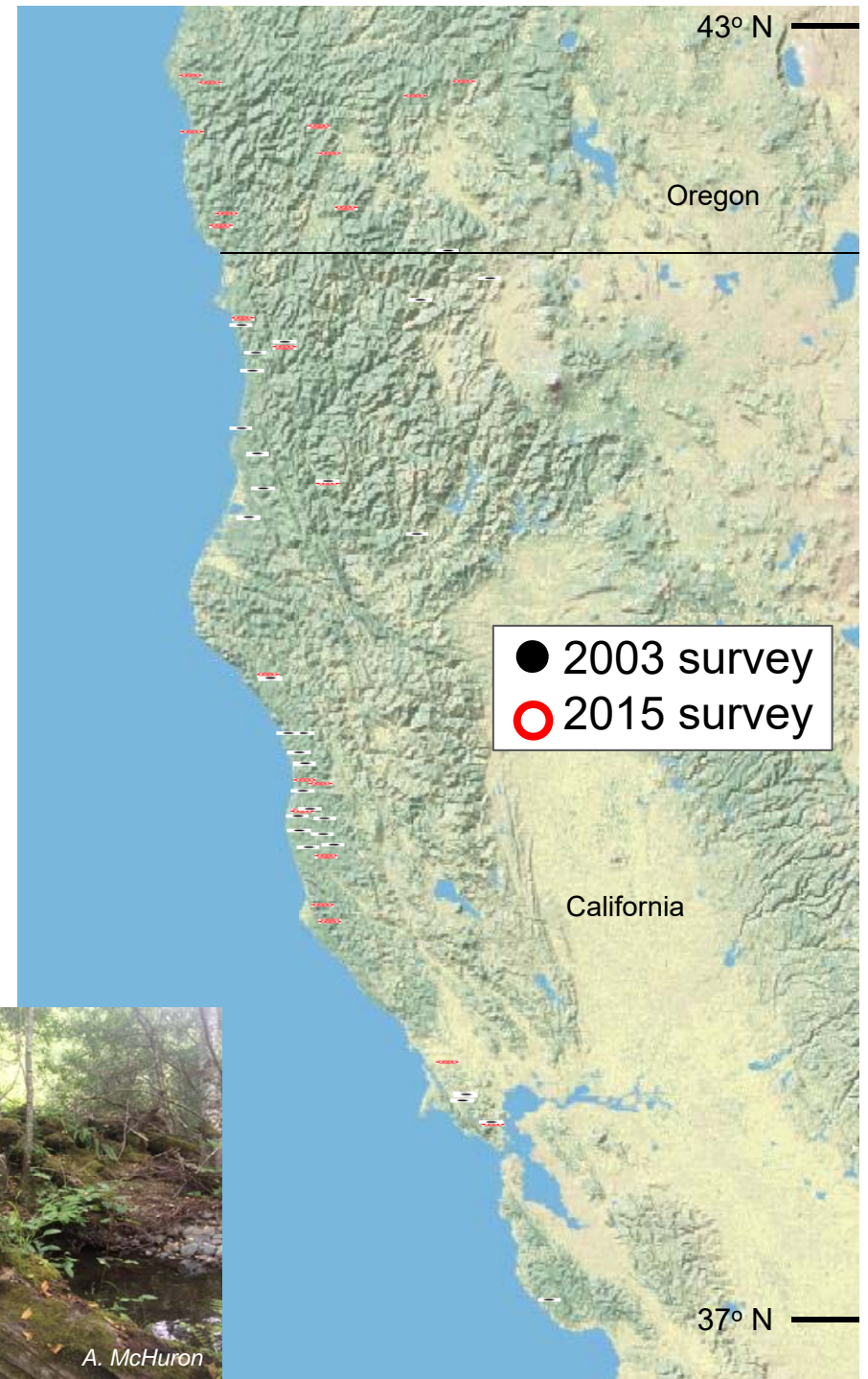# Background: phylogeography of coho salmon in California

Factorial Correspondence Analysis-Individual Genotypes

Gilbert-Horvath et al. (in press), 18 microsatellite loci

Study design: temporal monitoring

- Survey populations at two time points
  - Time series data at a regional scale
  - Examine allele frequency change over time
- Timepoint 1: baseline sampling in rivers throughout California in 2003 (n=1,976)
- Timepoint 2: revisited same sites in 2015 (n=2,223)
  - Expanded to include Oregon sites
- Four generations between surveys
  - Sampled two cohorts of the same brood cycle

Sampling locations

- Sampled juveniles in natal streams

- Spatially stratified electrofishing protocol

- 46 sites yielded coho salmon in 2015

- n=75 maximum per site

● 2003 survey
○ 2015 survey

43° N

Oregon

California

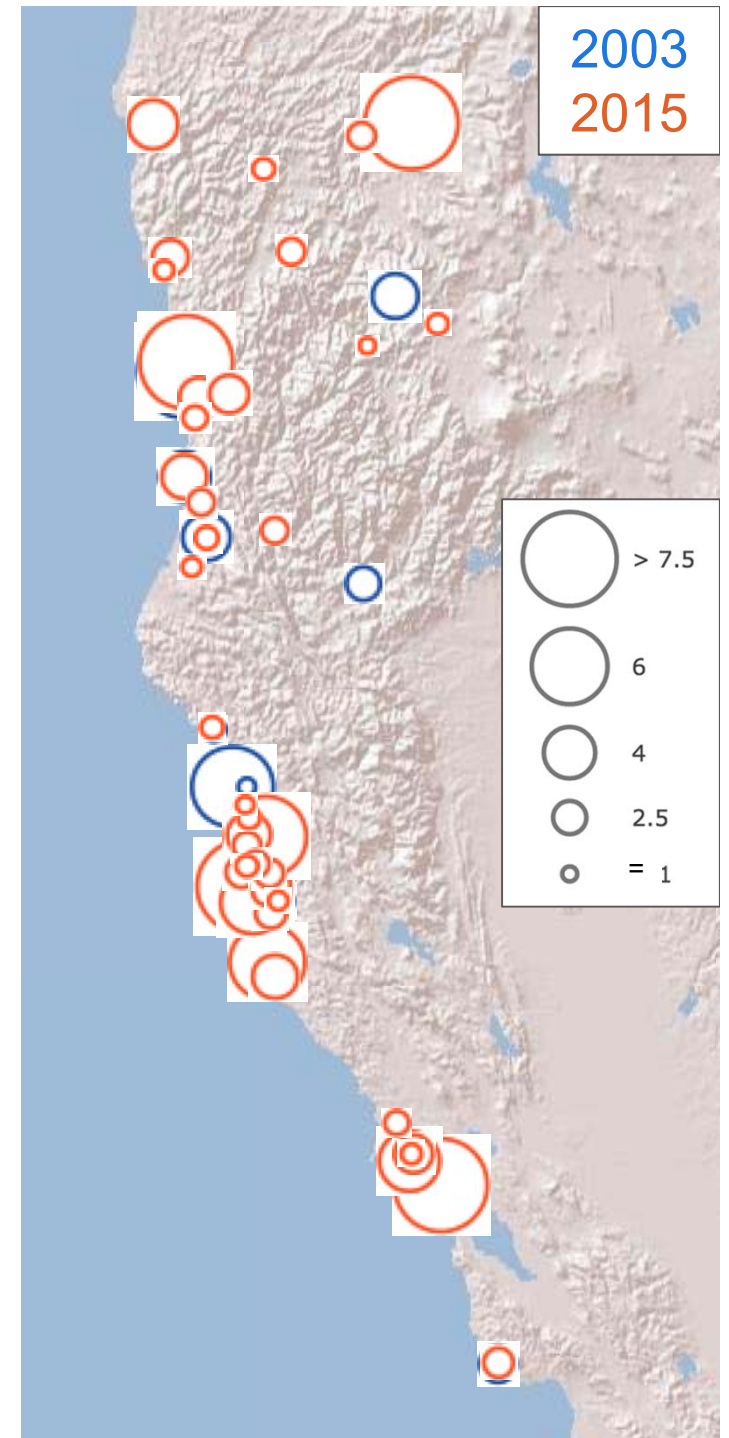37° N

A. McHuron

Analytical objectives

- Analysis of family structure
- Examine patterns of population structure at multiple spatial scales
- Assess temporal stability of genetic composition of populations
- Estimate effective population size (N_e)

Genotype data: 95 SNP loci
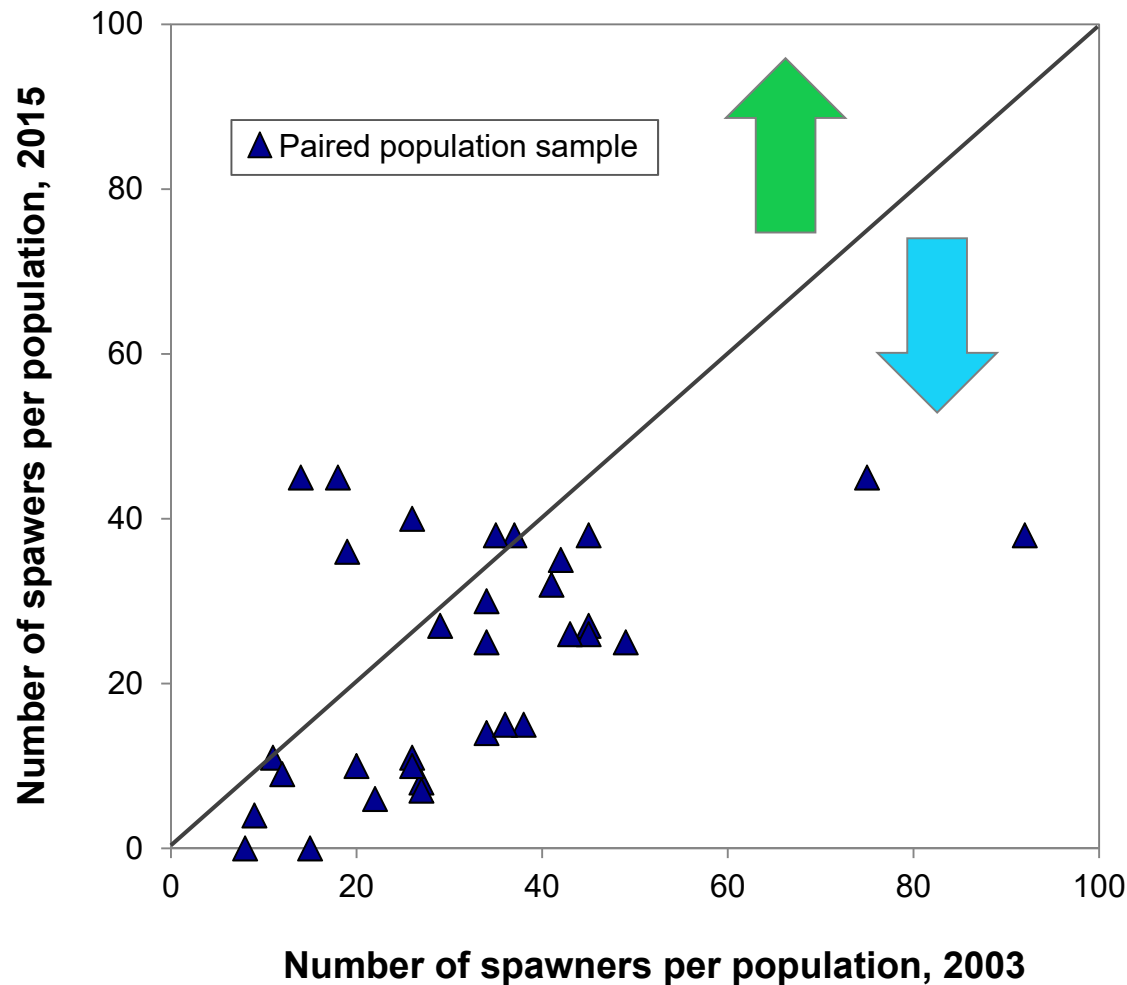n=4,199 individuals

A. McHuron

Results

- Sibship reconstruction: full siblings detected in almost all populations

- Mean sibship size by site ->

- Mean sibship size by year
  - **2003 = 2.2**
  - **2015 = 3.3**

- Family structure may obscure or distort population structure
  - Omit full sibs from population analyses (revised n=2,460)

Results from Colony v2.0.6.1 (Wang 2008, Jones and Wang 2010)
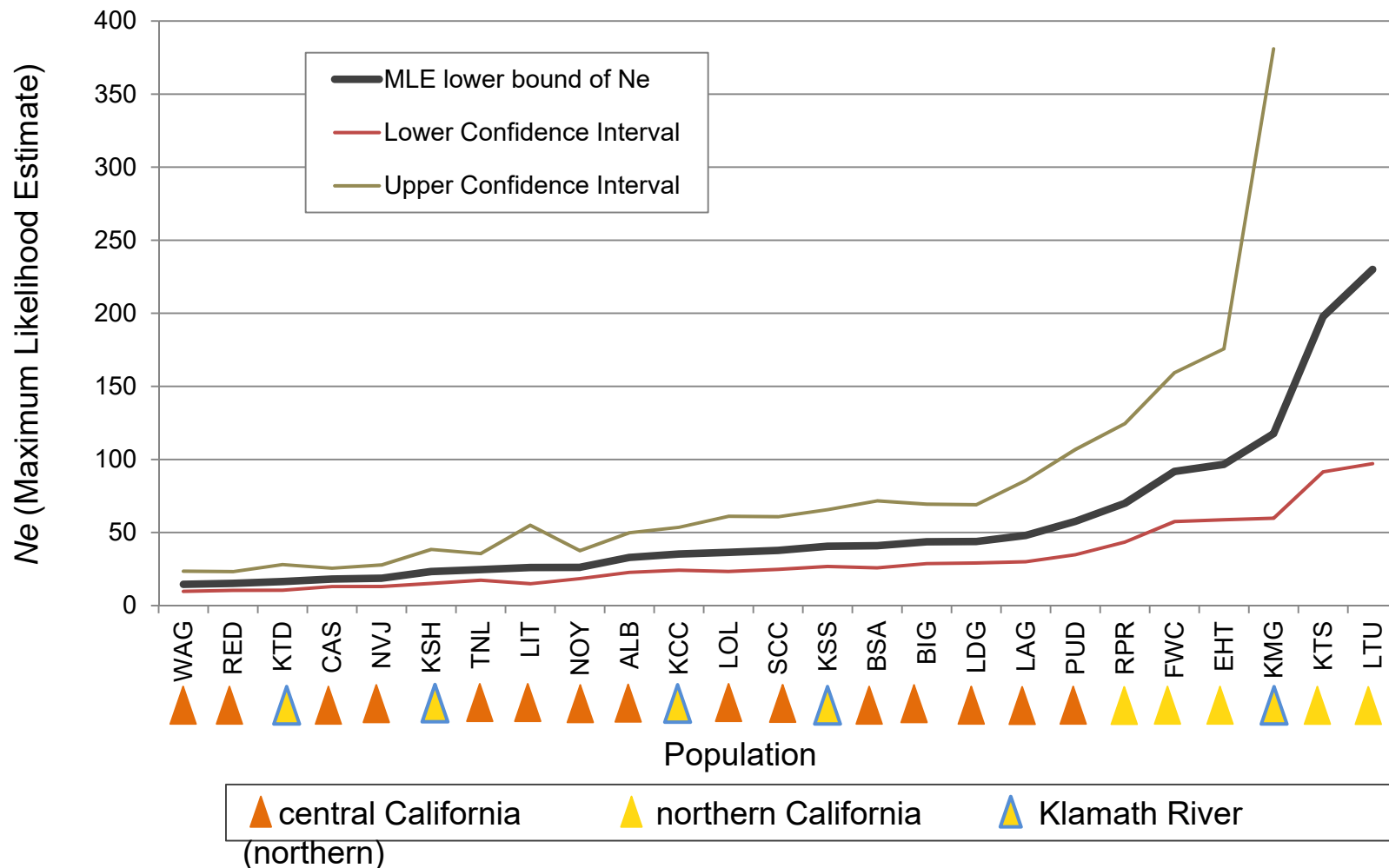
Temporal trends in reproduction

- 32 paired temporal population samples

- Estimated number of spawning adults that produced each sample of juveniles

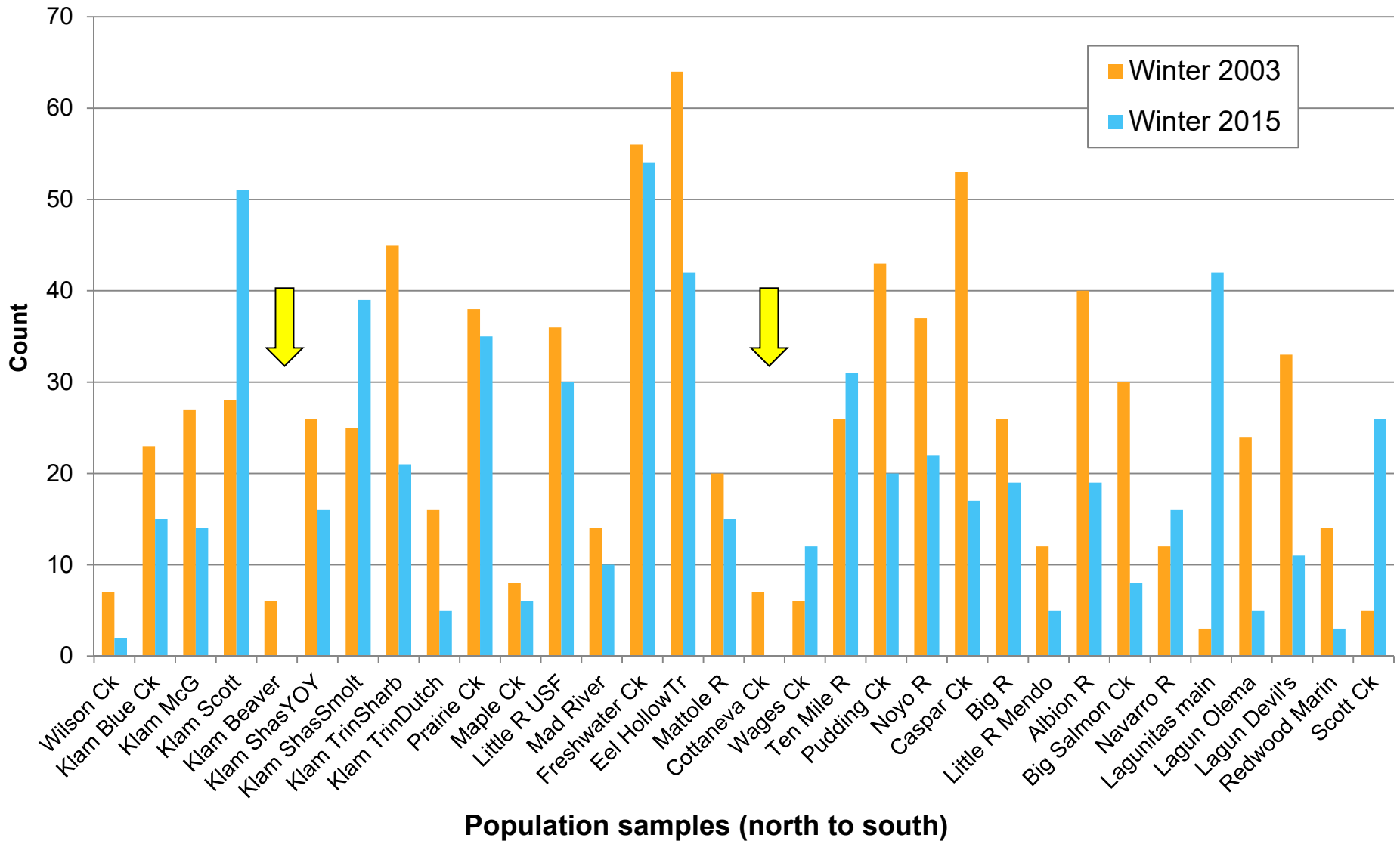- Net decrease in number of spawners between 2003 and 2015

C. Nicol

Results from Colony v2.0.6.1
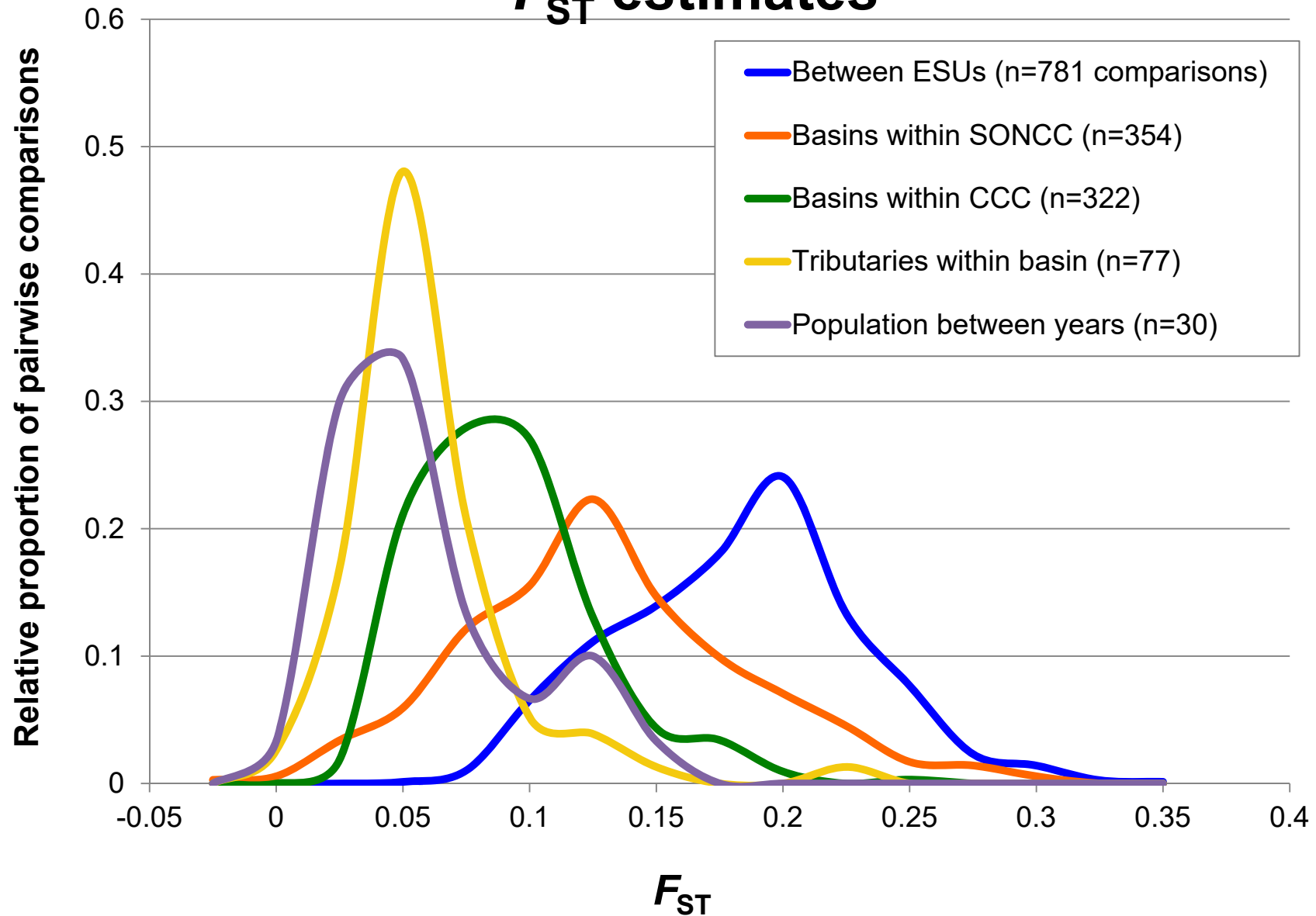
Effective population size

- Method in development: estimating N_e using the temporal method, accounting for family structure using Colony output
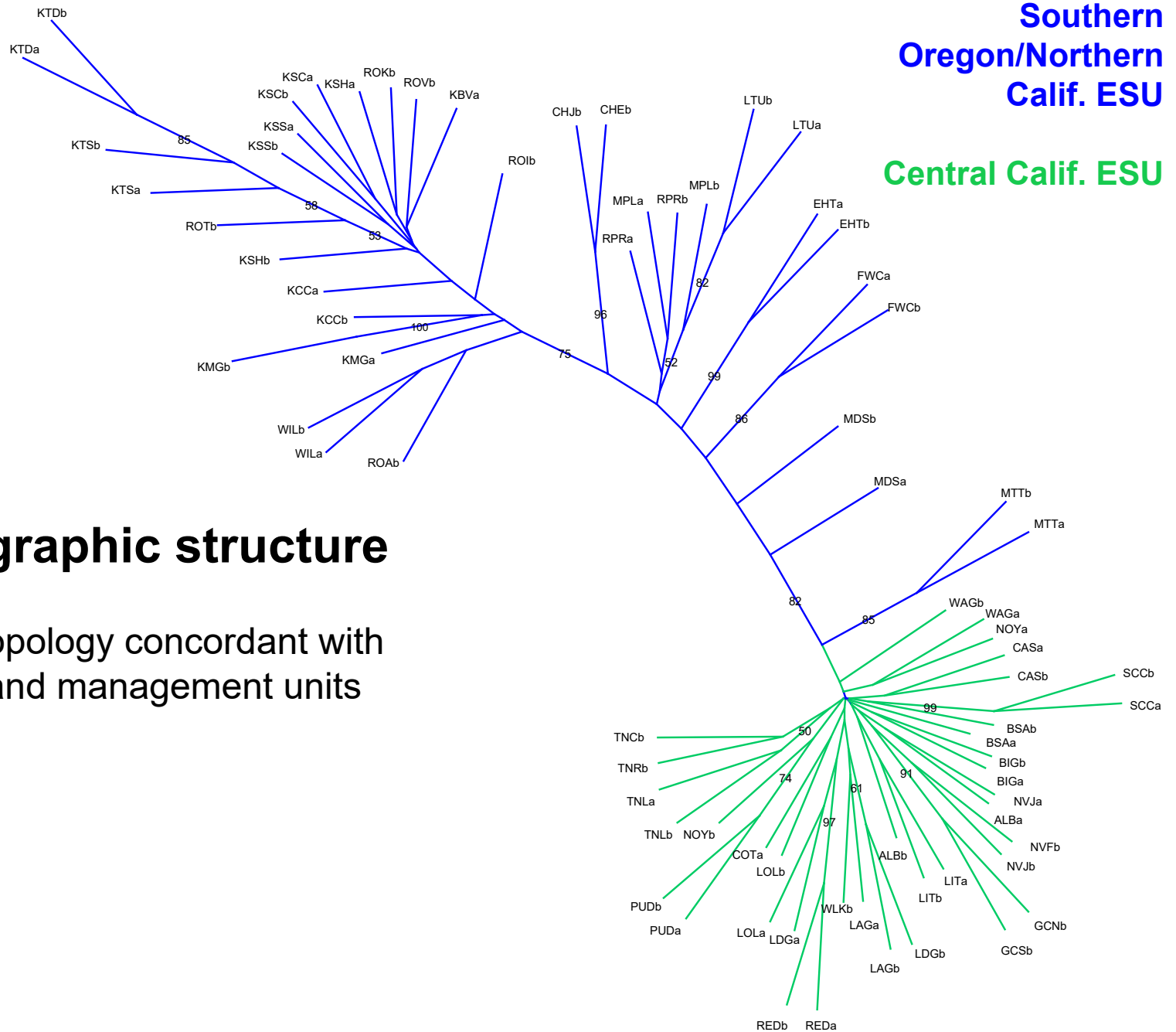- Upper bound of N_e difficult to estimate due to small sample sizes

Temporal trends in reproduction, by population: estimated number of spawning adults in 2003 and 2015

Relative divergence between populations: distributions of pairwise F_{ST} estimates
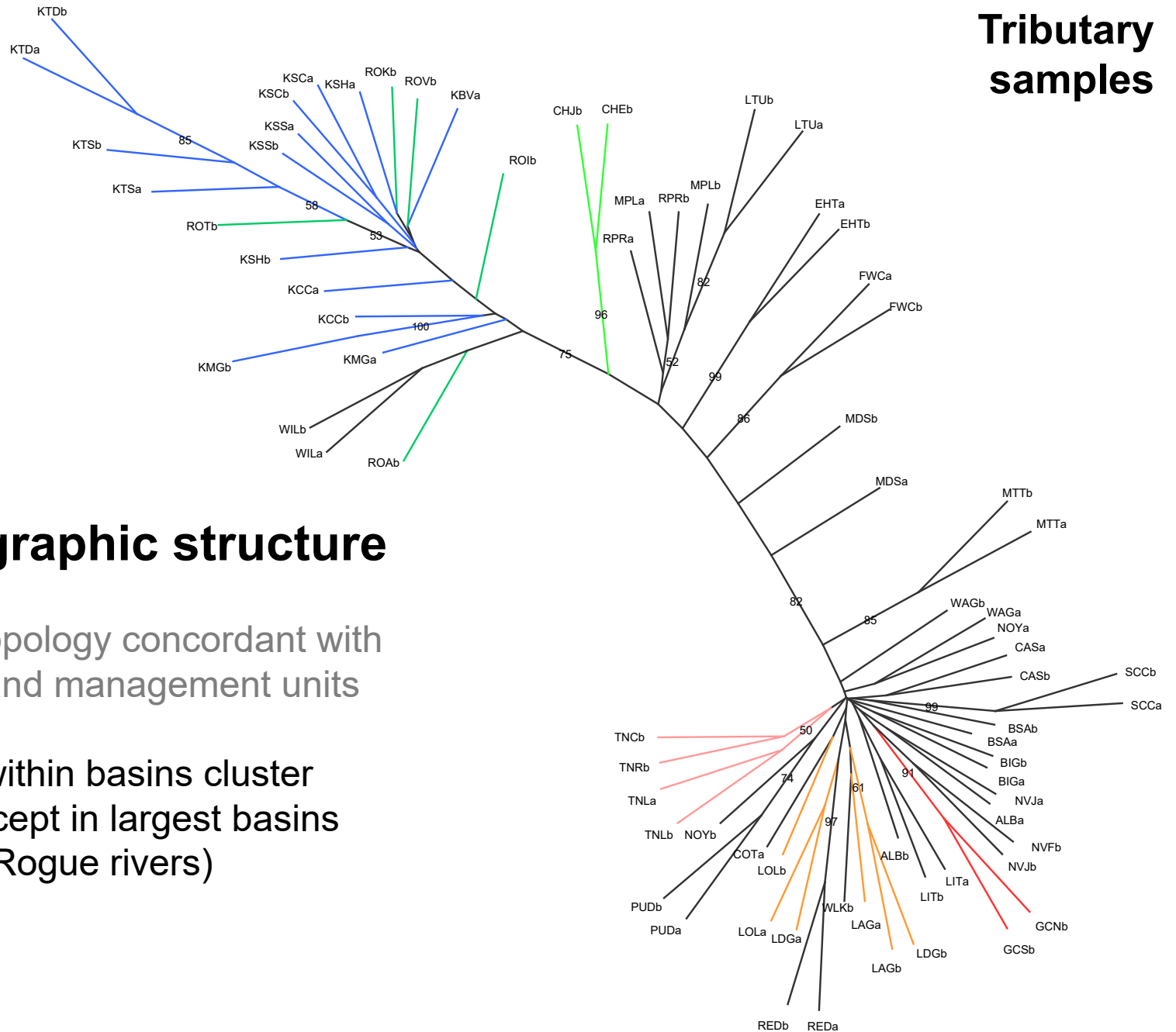
Legend:
- Between ESUs (n=781 comparisons)
- Basins within SONCC (n=354)
- Basins within CCC (n=322)
- Tributaries within basin (n=77)
- Population between years (n=30)

Y-axis: Relative proportion of pairwise comparisons

X-axis: F_{ST}

Phylogeographic structure

- High-level topology concordant with geography and management units

Full siblings omitted

Tributary samples

N

Phylogeographic structure

- High-level topology concordant with geography and management units

- Tributaries within basins cluster together, except in largest basins (Klamath & Rogue rivers)

Phylogeographic structure

- High-level topology concordant with geography and management units

- Tributaries within basins cluster together, except in largest basins (Klamath & Rogue rivers)
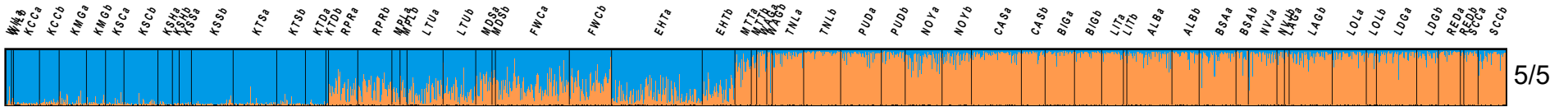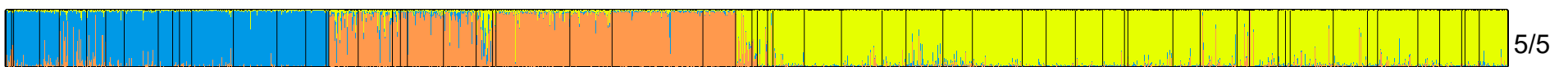
- Temporally coherent genetic composition in majority of paired temporal samples
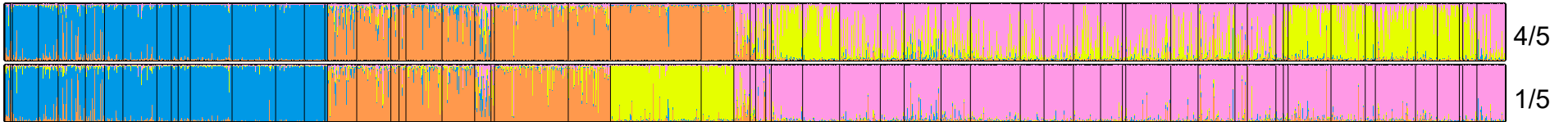
Fractional ancestry

K = 2

K = 3

K = 4

K = 5

K = 6

Structure v2.3.4 on paired temporal populations, full siblings omitted
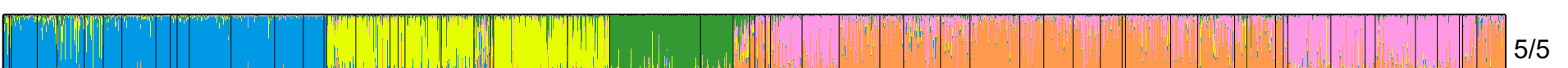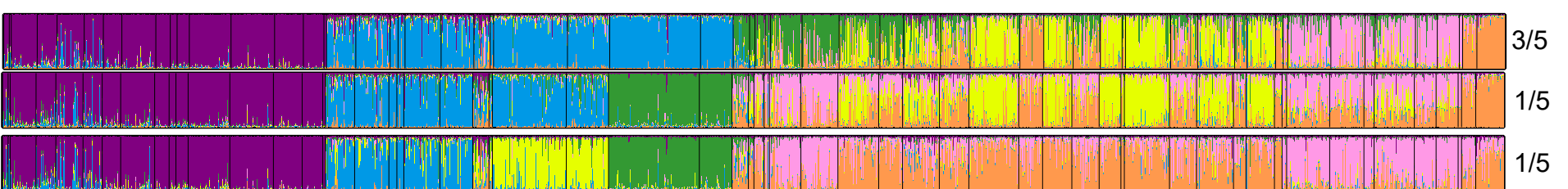
Genetic analysis of Mattole River coho salmon young-of-year

- Baker Creek tributary, Mattole River, California

- YOY (young-of-year) were sampled
  - August 2013 (Brood year 12/13)
  - August 2014 (Brood year 13/14)

- Genetic analyses – 90 SNP loci
  - Colony v2 to resolve familial relationships
  - Population assignment test using nearby reference populations
  - Ancestry analysis

Ancestry analysis (Structure v2.3.4)

MTTBa: BY12
MTTBb: BY13

Cottaneva — COTa

Eel River — EHTa, EHTb

Freshwater Ck — FWCa, FWCb

Mad R — MDSa, MDSb

Mattole R — MTR, MTTa, MTTb, MTTBa, MTTBb, MTTC

Pudding Ck — PUDa, PUDb

Ten Mile R — TNLa, TNLb

$K = 2$ (5/5)

$K = 3$ (3/5)
$K = 3$ (2/5)

$K = 4$ (3/5)
$K = 4$ (2/5)

$K = 5$ (4/5)
$K = 5$ (1/5)

$K = 6$ (2/5)
$K = 6$ (1/5)
$K = 6$ (1/5)
$K = 6$ (1/5)

Conclusions

- Statewide decrease in number of spawning adults that produced the sampled juveniles
  - Impact of 5-year drought on habitat
- Regional-scale geographic structure remains concordant with management unit boundary
- Significant spatial population structure
  - Particularly between ESUs, and among populations of northern ESU
- Little divergence between tributaries of the same basin
- Minimal temporal structure: within-population genetic composition relatively consistent over time
- Ancestry and affiliation of small populations influenced by migrants from nearby basins

Implications for conservation

- Connectivity of populations
- Extinction risk in susceptible small populations
  - Benefit of straying from productive populations
- Periodic re-evaluation of strategies
  - Identify populations or areas of concern
  - Where are recovery efforts having a positive impact?

A. McHuron

Acknowledgements

- NOAA Fisheries Service, Southwest Fisheries Science Center, Fisheries Ecology Division
  - Molecular Ecology Team: Ellen Campbell, Anthony Clemento, Cassie Columbus, Laney Correa
  - Landscape Ecology Team: Heidi Fish, Alex McHuron, Casey Sheridan, Emily Tucker

- California Department of Fish & Wildlife

M. Bond

Thank you!