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
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
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
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
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

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

- 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)
Phylogeographic structure

- High-level topology concordant with geography and management units

Full siblings omitted
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

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
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?
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

Funding Sources

National Marine Fisheries Service
Fisheries Restoration Grant from the California Department of Fish & Wildlife
Thank you!