Genetic and Phenotypic Risks of Inbreeding in Chinook Salmon Across Two Hatchery Management Regimes

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Effectiveness of managed gene flow to reduce genetic and phenotypic risks associated with captive breeding of Chinook salmon



1: Effectiveness of managed gene flow in reducing genetic divergence associated with captive breeding



2: Evaluate effects of managed gene flow on trait-linked loci



3: Genetic and phenotypic risks of inbreeding in hatchery and wild populations of Chinook salmon



4: Characterize genetic and phenotypic differences in disease resistance between integrated and segregated populations of Chinook salmon

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Inbreeding



- The mating of related individuals
- F "the probability that both alleles at a locus are identical by descent"
- More likely to occur in small populations



Inbreeding depression (IBD)

• A reduction in fitness due to inbreeding



Inbred steelhead and rainbow trout had 71% and 89% reduced marine survival compared to controls (Thrower and Hard 2009)





Aim: To quantify genetic, phenotypic, and demographic effects of inbreeding in hatchery and supplemented wild populations of Chinook salmon

Objectives:

- 1. Estimate inbreeding coefficients in the wild founders and four generations of the segregated and integrated hatchery lines
- 2. Quantify the effect of inbreeding on fitness traits
- 3. Build an Integral Projection Model (IPM) to determine how inbreeding depression affects productivity in supplemented wild populations

Inbreeding coefficients using 5,328 loci



Effective number of breeders, N_b





Generational Lag of Inbreeding Coefficients









Generational Lag of Inbreeding Coefficients





Effects of Inbreeding on Fitness



Effects of Inbreeding on Fitness

No correlation of inbreeding with:

- Return time to Roza
- Spawn time
- Forklength
- Weight
- Condition factor
- Fecundity
- Reproductive effort

Quantifying Risks to Productivity

Aim: To understand how inbreeding affects the fitness and productivity of supplemented wild populations

Objectives:

- 1. Build an Integral Projection Model (IPM) using four functions to link genetics and phenotypic variability to demographic processes:
 - Survival S(t,z,f) = probability that an individual with trait value *z* and inbreeding coefficient *f* at time *t* survives to *t*+1
 - Growth G(t,z'|z,f) = probability that individual with z and f at time t will shift to any z' at time t+1
 - Recruitment R(t,z,f) = number of offspring that an individual with z and f produces from time t to time t+1
 - Inheritance I(t,z',f'|z,f) = probability that an individual with z and f at time t produces an offspring of trait value z' and inbreeding coefficient f' at time t+1
- 2. Conduct sensitivity analyses to quantify the importance of each parameter and function to population growth rate.

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