Questions about hatchery genetics

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Overview

• Population structure of salmonids
  • Metapopulation structure
  • Natural gene flow

• Genetics of complex traits
  • Heritability
  • Gene expression/phenotypic plasticity

• Hatchery Reform Review

• Example
Population structure of salmonids

- Metapopulation is a web of populations that act as sources and sinks of migrants

- Salmon have a colonizing life history to find and occupy available habitat

- In addition to finding and testing new habitat, migrants prevent occupied habitat from being vacated if the local population is fading

- Gene flow among subpopulations of a metapopulation is expected
Hierarchical gene diversity

• Gene diversity of a unit is divided among hierarchical levels
  • Diversity of individuals relative to subpopulation
  • Diversity of individuals relative to total population
  • Diversity of subpopulation relative to total population (the metapopulation)

• Hierarchical gene diversity quantified in Wright’s F-Statistics
  • Fis
  • Fit
  • Fst
Fst – Gene diversity of subpopulations relative to total population

- Puget Sound ESU of Chinook salmon Fst ~ 0.06 (GAPS 2007)
- Puget Sound DPS of steelhead Fst ~0.03 (Warheit 2014)
- Skagit River bull trout Fst ~0.15 (Smith 2010)
- Maryland Brook trout stream 20km^2 Fst ~0.17 (Kazyak et al 2015)
Gene flow/exchange of migrants

- $F_{st} = \frac{1}{4N_m+1}$ for a metapopulation at equilibrium
- $N_m = \frac{1}{4\left(\frac{1}{F_{st}}-1\right)}$
  - Puget Sound Chinook $F_{st} = 0.06$; $N_m = 3.9$ per generation
  - Puget Sound steelhead $F_{st} = 0.03$; $N_m = 8.1$ per generation
  - Skagit River bull trout $F_{st} = 0.15$; $N_m = 1.4$ per generation
  - Brook trout stream $F_{st} = 0.17$; $N_m = 1.2$ per generation

- Population genetics: 1 migrant per generation prevents loss of alleles through genetic drift
Genetics of complex traits

• Multilocus traits
  • Many genes interacting

• Genotype x Environment interaction
  • The same genetic background is expressed differently in one environment vs another – phenotypic plasticity

• Heritability
  • Observed phenotypic traits can be inherited anywhere from 0% to 100%
Domestication

• Cultured fish are subjected to directional selection for traits of economic interest from fertilization to harvest; this is not how PNW hatcheries operate

• PNW hatchery selection is inadvertent
  • Relaxation of selection on natural incubation and rearing fitness traits
  • Relaxation of selection on mate choice
  • Potential for inadvertent selection for return-time and size-at-spawning

• Genetic change requires a heritable basis to selected (or no-longer-selected) traits
Wenatchee River Spring Chinook

- Hatchery fish have lower reproductive success than natural fish

- Hatchery fish stray and naturally-spawned progeny of hatchery fish also stray

- Natural progeny of hatchery fish have the same reproductive success as natural progeny of natural fish
  - Reproductive success is a result of spawning habitat not genetics of parents

Hatchery Reform

• Fish hatchery practices used to focus on measurable deliverables
  • Fish spawned, juveniles reared and released

• Spawning practices were revised through the 1990s to ensure hatchery brood is representative of entire natural run

• Genetics began to be taken into account also in the 1990s

• HSRG report in 2004 codified recommendations for Western WA that had already been in progress
Hatchery Reform Glossary

• pHOS – proportion of hatchery-origin spawners in nature
• pNOB – proportion of natural-origin spawners in hatchery broodstock
• PNI – proportion of natural influence = pNOB/(pNOB + pHOS)
  • PNI = the proportion of parents per generation that are natural-origin
• Effective population size – Ne – measure of genetic diversity
• Spawning plan
  • 1:1 - spawn each female with a different male
  • Matrix - combine x females’ eggs, divide into x units, fertilize each unit with a different male
Spawning plan

• 1:1 spawning preserves genotypic diversity, maintains the highest level of genetic diversity

• Matrix spawning prevents loss of alleles by ensuring greatest number of possible crosses per generation
Recovery program example – SF Nooksack
Genetic diversity goals for captive rearing program

• Goal: Maintain population structure in system
  • Captive brood recruitment: Avoid merging two spring populations

• Goal: Minimize loss of genetic diversity (maintain Ne)
  • Spawning protocol
    • Reduce variance in reproductive success
    • Avoid crossing closely-related individuals

  • Pairwise relatedness (Rxy) was estimated for all individuals maturing each year.
Ryman-Laikre effect

• Reduction in Ne from amplifying a few individuals

• Manage by not amplifying individuals disproportionately
SF Nooksack spring Chinook program summary

<table>
<thead>
<tr>
<th>Year</th>
<th>Juveniles into Captive Brood</th>
<th>Captive Females spawned</th>
<th>Captive males spawned</th>
<th>Returning program females spawned</th>
<th>Returning program males spawned</th>
<th>Smolts Released</th>
<th>Redds in SF before 1 Oct</th>
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<tr>
<td>2007</td>
<td>20</td>
<td>0</td>
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<td>0</td>
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<td>0</td>
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<td>0</td>
<td>0</td>
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<td>0</td>
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<td>2010</td>
<td>760</td>
<td>2</td>
<td>10</td>
<td>0</td>
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<td>2012</td>
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<td>342</td>
<td>707,683</td>
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<td>2018</td>
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<td>434</td>
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<td>610</td>
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<td>2019</td>
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<td>~320</td>
<td>~320</td>
<td>1,680,450</td>
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Smolts released are CWT’d but not fin-clipped so program adults are identifiable
Goal: Maintain genetic diversity

Ne from temporal variance in allele frequencies

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<thead>
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<th>From</th>
<th>To</th>
<th>Ne</th>
<th>CI lower</th>
<th>CI upper</th>
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<tr>
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<td>90s baseline</td>
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<td>2008 juveniles</td>
<td>2016 anadromous</td>
<td>363.5</td>
<td>284.5</td>
<td>463.4</td>
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Goal: Maintain population structure in Nooksack

Pairwise Fst between 2016 anadromous returns and juveniles screened for captive brood

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<tr>
<th></th>
<th>08SF</th>
<th>09SF</th>
<th>10SF</th>
<th>11SF</th>
<th>08NF</th>
<th>09NF</th>
<th>10NF</th>
<th>11NF</th>
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<td>2016 anadromous</td>
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<td>0.0065</td>
<td>0.0062</td>
<td>0.0119</td>
<td>0.0196</td>
<td>0.0136</td>
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Conclusion

• Colonization and gene flow are part of salmonid life history

• Hatchery programs can be used to maintain genetic resources

• Hatchery practices have evolved substantially over the past 150 years