

# 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

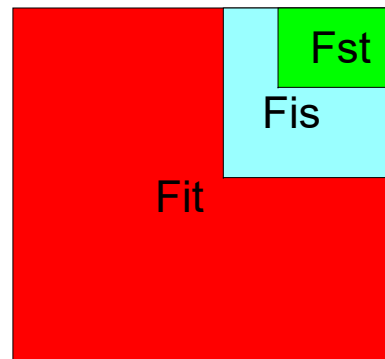
# Population structure of salmonids

- 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
  - $F_{is}$
  - $F_{it}$
  - $F_{st}$



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<sup>2</sup> Fst ~0.17 (Kazyak et al 2015)



# Gene flow/exchange of migrants

- $F_{st} = 1/(4Nm+1)$  for a metapopulation **at equilibrium**
- $Nm = [(1/F_{st})-1]/4$ 
  - Puget Sound Chinook  $F_{st} = 0.06$ ;  $Nm = 3.9$  per generation
  - Puget Sound steelhead  $F_{st} = 0.03$ ;  $Nm = 8.1$  per generation
  - Skagit River bull trout  $F_{st} = 0.15$ ;  $Nm = 1.4$  per generation
  - Brook trout stream  $F_{st} = 0.17$ ;  $Nm = 1.2$  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

Ford et al 2012, Ford et al 2015a, Ford et al 2015b



# 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 –  $N_e$  – 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

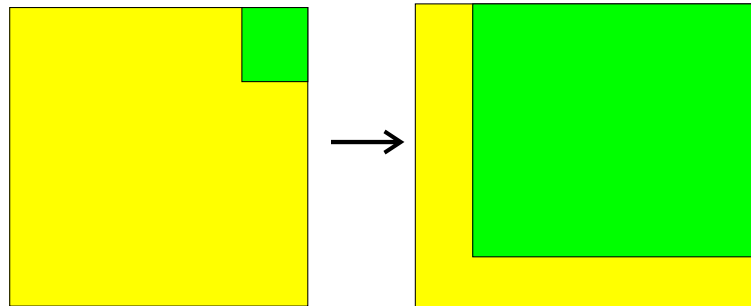


# Genetic diversity goals for captive rearing program

- Goal: Maintain population structure in system
  - Captive brood recruitment: Avoid merging two spring populations
- Goal: Minimize loss of genetic diversity (maintain  $N_e$ )
  - Spawning protocol
    - Reduce variance in reproductive success
    - Avoid crossing closely-related individuals
  - Pairwise relatedness ( $R_{xy}$ ) was estimated for all individuals maturing each year.

# Ryman-Laikre effect

- Reduction in  $N_e$  from amplifying a few individuals



- Manage by not amplifying individuals disproportionately

# SF Nooksack spring Chinook program summary

Year	Juveniles into Captive Brood	Captive Females spawned	Captive males spawned	Returning program females spawned	Returning program males spawned	Smolts Released	Redds in SF before 1 Oct
2007	20	0				0	129
2008	414	0				0	177
2009	1,069	0				0	181
2010	760	2	10			0	197
2011	1,093	15	15			1,989	188
2012	1,045	91	91			32,677	201
2013	0	285	171			155,740	97
2014	0	189	160		5	677,410	58
2015	0	144	135	8	8	343,240	33
2016	0	175	108	95	162	361,882	252
2017		50	0	342	392	707,683	430
2018				434	434	1,400,000	610
2019				~320	~320	1,680,450	ytd

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

From	To	Ne	CI lower	CI upper
80s baseline	90s baseline	<b>106.4</b>	76.6	151.5
80s baseline	2008 juveniles	<b>94.3</b>	78.6	112.1
80s baseline	2016 anadromous	<b>170.5</b>	139.7	205.9
2008 juveniles	2016 anadromous	<b>363.5</b>	284.5	463.4

# Goal: Maintain population structure in Nooksack

Pairwise  $F_{st}$  between 2016 anadromous returns and juveniles screened for captive brood

	08SF	09SF	10SF	11SF	08NF	09NF	10NF	11NF
2016 anadromous returns	0.0088	0.0065	0.0062	0.0119	0.0196	0.0136	0.0153	0.0233

# 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