Genome-wide association study (GWAS) of (1) survival of acoustically tagged and (2) *Nanophyetus salmincola* infected steelhead smolts from south/central Puget Sound, Washington

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Definitions

- Genome-wide association study (GWAS)
 - Correlation between genotype genetic "fingerprint" (e.g., SNPs) and phenotype (e.g., survival)
- Steelhead
- Smolt

Statistical association between smolt survival while outmigrating through Puget Sound, WA and smolt's genome (reduced-representation of genome)

Phenotype – Smolt Survival

• Acoustically tagged steelhead smolt



7mm and 9 mm transmitters



Green River: 2014 Nisqually River: 2014, 2015

2014: Reciprocal Translocation

Source: Release

- Green: Green
- Green: Nisqually
- Nisqually: Nisqually:
- Nisqually: Green

GWAS Model (Tassel)

Variables/Parameters		Acoustic – Survival
Dependent variable	Survival Index	Distance traveled (data from Moore and Berejikian)
Fixed Effects		
Factor	Release location	(1) Green River, (2) Nisqually River
Covariate	Lineage	(1) Green River, (2) Nisqually River, Omy05 genotype
Genomic data	~8909 SNPs	
Random Effects	Kinship	Centered IBS - assumed additive genetic variance
Error	Residuals	

MLM: Data = Fixed Effects + Random Effects + Error



















Omy05

- Associated with migratory behavior in *O. mykiss* (residence versus migratory)
 - Nichols et al. 2008 (CA & ID)
 - Hecht et al 2014 (Sashin Lk, AK)
 - Pearse et al 2014 (California)

Pearse et al 2014

- loci in strong linkage disequilibrium associated with resident versus anadromous life-history strategies
- chromosomal inversion
- differences between resident and anadromous populations was maintained by this inversion

PCA - Green and Nisqually Rivers – Omy05 only





2014: Reciprocal Translocation

Source: Release

- Green: Green
- Green: Nisqually
- Nisqually: Nisqually:
- Nisqually: Green

Omy05 genotype

- RR
- AR
- AA



Welch two-sample t-test Min N per group – Power = 0.80 Mann-Whitney U-test

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MODELS or DATA SUBSETS	Ν
All data (all Fixed Effects)	250
2014 data only (all Fixed Effects)	158
Green R. lineages-only (all Fixed Effects, including Factor)	86
Nisqually R. lineages-only (all Fixed Effects, including Factor)	72
Green R. release-only (no Factor; all lineages)	
Nisqually R. release-only (no Factor; all lineages)	70

Fixed Effects		
Factor	Release location	(1) Green River, (2) Nisqually River
Covariate	Lineage	(1) Green River, (2) Nisqually River, Omy05 genotype







PCA using only the Eight significant loci from Nisqually Release data subset



F = 85.56; df = 1,68; p = 1.2e-13; r² = 0.56

Conclusions 1 (Omy05)

- Association between Omy05 genotype (RR v AR) and smolt survival, although influenced by source and release location and the association is statistically weak
- In other studies association between Omy05 and migratory behavior
 - R allele = <u>a</u>nadromy
 - A allele = <u>r</u>esidency
- Arm-waving: In Washington, A allele is maintained in the anadromous population by resident rainbow trout, and the presence of the A allele in a smolt may reduce the individual's probability of survival

Conclusions 2 (MLM - Nisqually Release)

- In Green and Nisqually river fish released from Nisqually River, survival is associated with:
 - Circadian clock (2 genes)
 - Immune system
 - Membrane transport protein
 - Genes of unknown function
- More arm-waving: Since these loci appear important only in fish released from the Nisqually River, they may be important only for the migration segment not in common with the Green River, or for fish that have a longer migration distance.

Conclusions 3 (Fine-print disclaimer)

- How far a naïve steelhead smolt can migrate through Puget Sound is not independent of the smolt's genome.
- This study did not clarify the relative importance of the genome, compared with environmental factors, or how the genome interacts with these environmental factors to affect survival.

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