What is the role of **population genetics** in conservation?
Delineate ESU/DPS boundaries, stock identification (GSI),
parentage based tagging, and hatchery broodstock management
(e.g. inbreeding avoidance).

> How is the emerging field of ‘**adaptation genomics**’ different?
Emerging due to change in our ability to find and quantify the effects of specific genetic elements using genome-wide DNA data:

<table>
<thead>
<tr>
<th>Year</th>
<th>1996</th>
<th>2006</th>
<th>2016</th>
</tr>
</thead>
<tbody>
<tr>
<td>Locus</td>
<td>1</td>
<td>Microsatellites/SNPs</td>
<td>1,000s→1,000,000 of SNPs</td>
</tr>
</tbody>
</table>

Fraction of genome

Sanger sequencing

Whole genome re-sequencing

ddRAD

RADtag (Baird 2008)

- Phylogeny
- Population Structure
- QTL Mapping
- Pedigree Mapping
- Association Mapping
- Population Genomic Scans

Divergence limited

Recombination limited

Linkage Diseq. limited

Peterson et al. 2012, *PLOS One*
Higher Level Taxonomy, phylogeny
Species & Sub-species Relationships, phylogeography
Population Structure, Migration, Stock ID)
Relatedness Parentage Pedigrees, Inbreeding
Individual identification, Fitness, Behavior

Level of biological question

Scale of genetic data
Single-locus DNA sequences "Next-generation Sequencing" (NGS) Allozymes, Microsatellites, SNPs

Type of genetic data
"Neutral" Population Genetic Data "Adaptive" or "Functional" Genomic Variation

MOLECULAR ECOLOGY

NOAA Fisheries National Marine Fisheries Service
Adaptive Genomic Variation (AGV); Specific SNPs or genomic regions that have been shown to have an adaptive evolutionary effect in wild populations. Almost always uncertain, and likely to have intraspecific variation.
Early vs. Late Age-of-Return in Atlantic Salmon:

EE, EL, LL
2yo, het, 3yo

VGLL3 is associated with lipid storage and age of puberty in humans.

> Sex-dependent dominance reversal.
> Explains 39% of variance.

Barson et al. 2015
Genomic ‘islands of divergence’ in coastal and migratory Cod:

- >10,000 SNP loci
- LG1 = 29,521,491 bp
- 1,262 genes

Smoltification in steelhead/Rainbow Trout:

>Numerous genomic studies of life-history in *O. mykiss*:


>Results highly variable, but many have associated one region of chromosome Omy5 with correlated life-history traits.
Smoltification in steelhead/Rainbow Trout: Omy5.

- **Rapid** adaptation of Rainbow Trout above barriers associated with evolution on one genomic region.

- **Repeated parallel evolution** from standing variation.

- Significant effect of above-barrier population age. (natural populations fixed)

- **Individual** smoltification effects.

- **Genomic** characterization in progress.

Parallel evolution of residency in *O. mykiss*

**Single evolutionary event**

**Parallel evolution**

Waples et al. 2004

Pearse et al. 2014
Parallel evolution of residency in *O. mykiss*

**Single evolutionary event**

![Tree diagram showing single evolutionary event](image)

Waples et al. 2004

**Parallel evolution**

![Tree diagram showing parallel evolution](image)

Pearse et al. 2014

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**Figure 1:** Map of geographic distribution of Chinook salmon populations from California, Oregon, Washington, Idaho, and British Columbia. The map illustrates the distribution of genetic markers across different populations and the relationships between them. The labels indicate the presence of specific genetic markers in each population, with populations grouped into geographic regions for analysis.

**Figure 2:** Tree diagram showing the evolutionary relationships among Chinook salmon populations. The tree branches represent evolutionary changes, with the markers indicating the genetic changes that occurred. The tree is divided into clades, each representing a group of populations that share a common ancestry.

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**Methods**

In this study, we jointly consider the genetic and life-history diversity of Chinook salmon populations. Populations were selected to represent the geographic range of the species, and genetic data were collected from hatchery samples to reflect indigenous gene pools. The genetic data were used to test the hypothesis of parallel evolution of life-history traits in Chinook salmon. Genotype data were analyzed using a suite of 32 polymorphic loci, and the results were compared to previous studies on parallel evolution.

**Results**

We found evidence for parallel evolution of life-history traits in Chinook salmon, with specific traits confined to a single genetic lineage. This suggests that evolutionary processes have led to current patterns of genetic diversity. The results support the hypothesis of parallel evolution, indicating that evolutionary changes that occurred in different glacial refugia have been important in shaping the present day diversity in Pacific salmon.
Parallel evolution of Summer/Winter run-timing in steelhead

Genome-wide microsatellite and SNP loci

Arciniega et al. 2016, Conservation Genetics
Parallel evolution of Summer/Winter run-timing in steelhead

Waples et al. 2004

Prince et al. In Prep

Arciniega et al. In Prep

NOAA Fisheries
National Marine Fisheries Service
Applied Conservation & Management:

How should we incorporate Adaptive Genomic Variation into steelhead management?

How is ‘Conservation Genomics’ different?

“all naturally spawned anadromous *O. mykiss* (steelhead) populations below natural and manmade impassable barriers”

NMFS 2006
Approaches to Adaptive Genomic Variation:

A) Passive Monitoring
B) Active Management
C) Marker Assisted Conservation
Passive Monitoring & Process Management:

AGV is subject to same genome-wide forces as neutral loci

Figure 1 | Schematic diagram of interacting factors in conservation of natural populations. Traditional conservation genetics, using neutral markers, provides direct

Allendorf et al. 2010, Nature Reviews Genetics
Active Management:

> Follows existing ESA listing process.

> Additional potential level for Management Unit designation (Adaptive Group).

> Likely only useful for major phenotypes.  
  >> Will not capture all AGV.

> Identify source populations for re-introductions.  
  (He et al. 2016 Con Bio)

Funk et al. 2012, TREE
Marker Assisted Conservation:

> Use of genotype at specific loci to select individuals for breeding.

> Widely used for livestock and crops.

> Hatchery broodstock selection.

> Released animals must be fit in their environment.

> Habitat is critical.
Adaptive variation reflects ecological conditions:

> Relative reproductive success of alternative individuals.

> Balance of selection.

> Non-equilibrium populations.

> River connectivity, geologic time and intermittent fish passage...

> Dynamic equilibrium!

*since 1920*

*Carmel River*

*today 2016*
**Summary:** What should we do with this information?

- Adaptive genomic variation can be targeted for conservation.

- Even genes of major effect are probabilistic indicators of individual phenotype. (Major exception; immune system genes)

- Focus on evolutionary *processes* that promote diversity rather than an idealized genetic composition. Evaluate that diversity using neutral and adaptive loci.
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Bureau of Reclamation
... then he yelled "evolution!"
and simply jumped out ...