What Have We Learned from Genetic Tagging of Salmon and Steelhead Hatchery Programs

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Hatcheries in salmonid management

- Hatcheries are powerful tools for modifying salmonid populations. Modifications can be of negative, positive or neutral with respect to population/ESU viability and evolution.

- Considerations very different for large- and small-scale hatchery programs, and for different species.

- The Devil is in the Details! We must use science-based approach, informed by monitoring, to direct operations, evaluate where in the spectrum effects are occurring and mitigate appropriately

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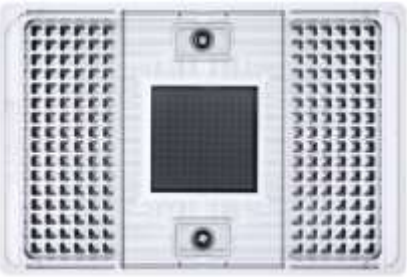
- Tagging data are core of monitoring and evaluation. Coded wire tags are the most commonly issued tag- over 1B in salmonids- but recovery rates are ~0.2%.

Intergenerational (Parentage-based) Genetic Tagging

- Highly efficient, intergenerational (pedigree-based) genetic tagging method
  - Genotype parents with polymorphic molecular markers (e.g. SNPs)
  - Sampling and genotyping in offspring generation with same markers
  - Large-scale parentage analysis to identify parents
- Information obtained for each tag recovery is nearly the same as for CWTs
- By genotyping two parents, you tag “all” of their of offspring and it requires no juvenile handling, but MUCH higher tagging rates feasible.

Validation of parentage-based tagging

- Anderson and Garza (2006; Genetics) found that a 100 (SNP) marker genotype can identify parental pairs with false positive rate < 1 fish per 300,000 offspring. Feasible with current methodology



96.96 array

- Anderson (2012) described software for the large scale parent pair/offspring analysis with SNP markers.

- Economic and operational feasibility study led by SWFSC staff recently completed (Satterthwaite et al. 2015)

- Widely implemented, primarily in Idaho, British Columbia and California.

Parentage-based tagging –the other stuff

In addition to stock-of-origin and cohort, PBT gives you large pedigrees

- Near parametric estimates of variance in family size
- Conduct large quantitative genetic studies of phenotype: run timing, age at maturity, disease resistance
- Map genes for phenotypic traits to locations in the genome
- Evaluate different hatchery/release practices and consequences for fecundity, marine survival and straying
- Estimate straying and reproductive success of strays
- Study relative productivity of hatchery and natural fish by sampling at weirs, fish ladders and carcasses (carefully)
- Same data can be used for genetic stock identification of ALL sampled fish.

Parentage-based tagging in California hatcheries

Anadromous fish hatcheries

Hatchery programs with current broodstock sampling

Steelhead: Russian River; Mad River; Central Valley (four programs)

Coho salmon: Klamath River-Iron Gate; Russian River

Chinook salmon: Feather & San Joaquin River- spring run; Sacramento- winter run & late fall run

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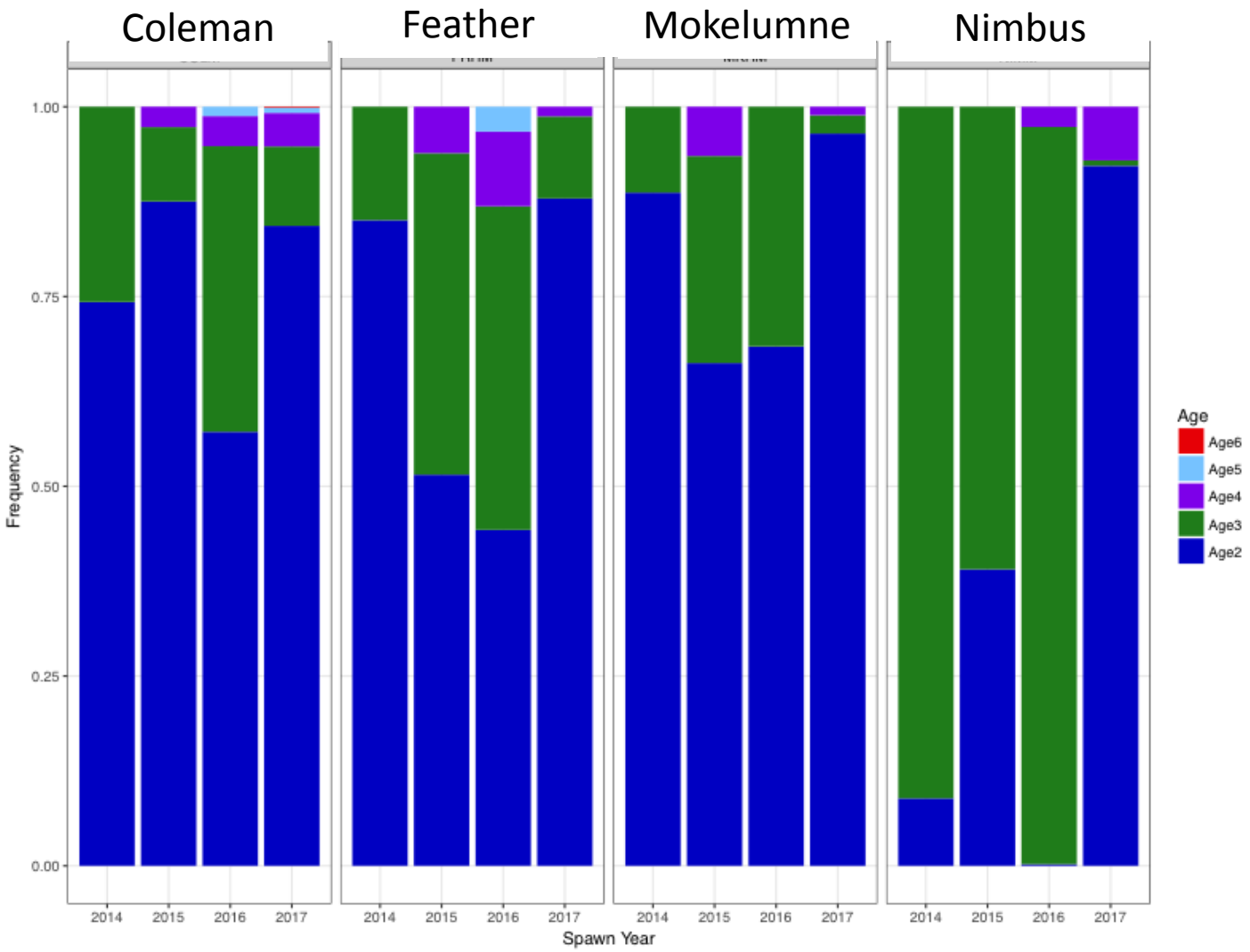
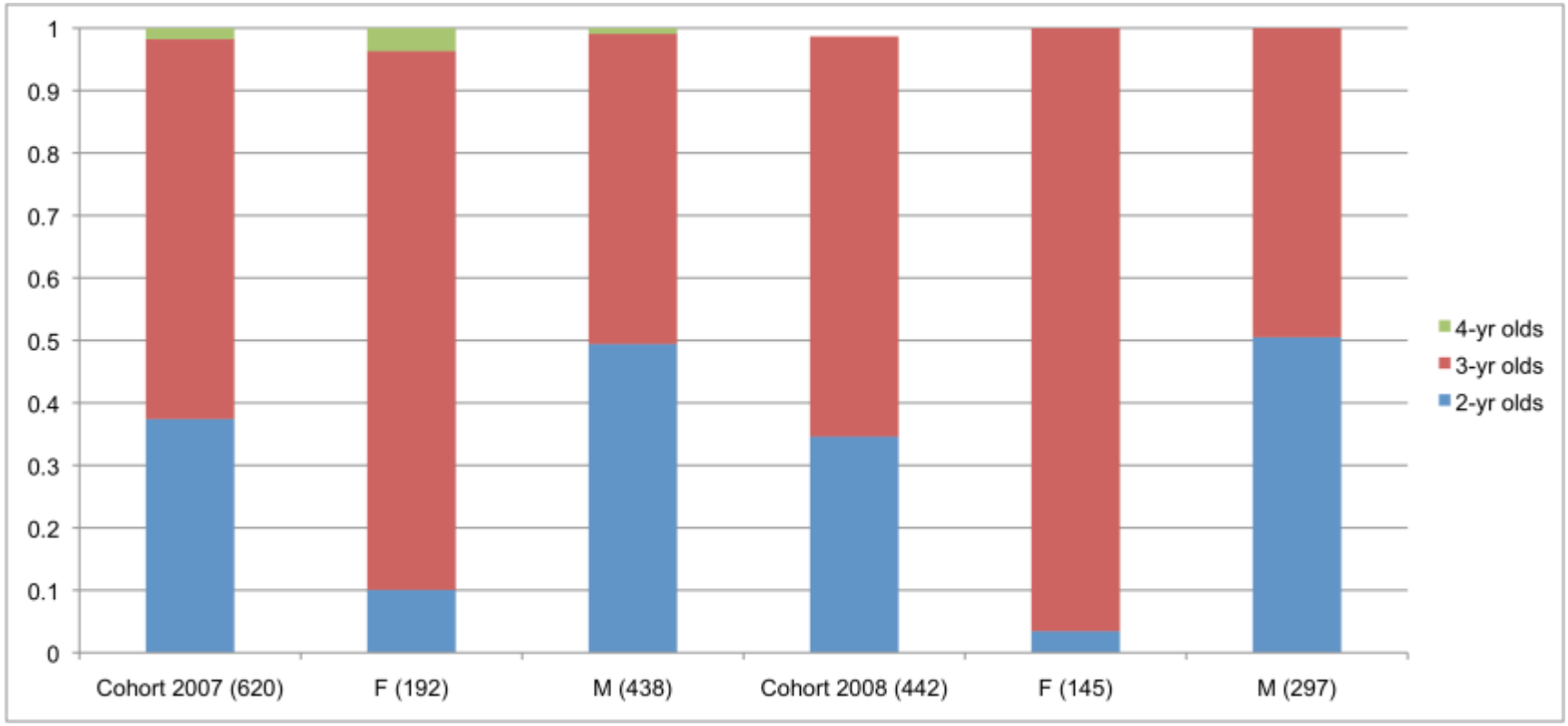
Steelhead and coho salmon mostly untagged.

Age structure of spawners: Central Valley steelhead



Age structure of spawners: Russian River steelhead



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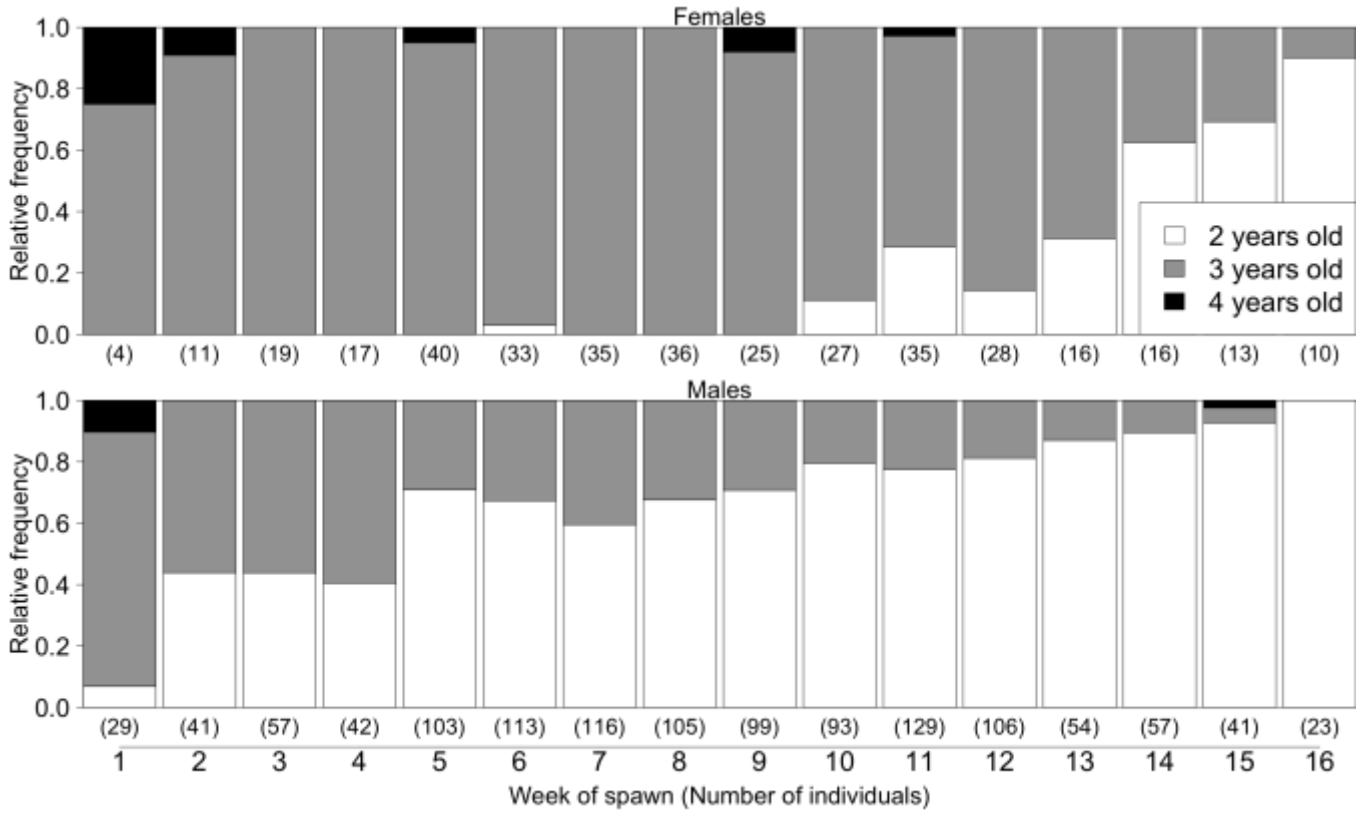
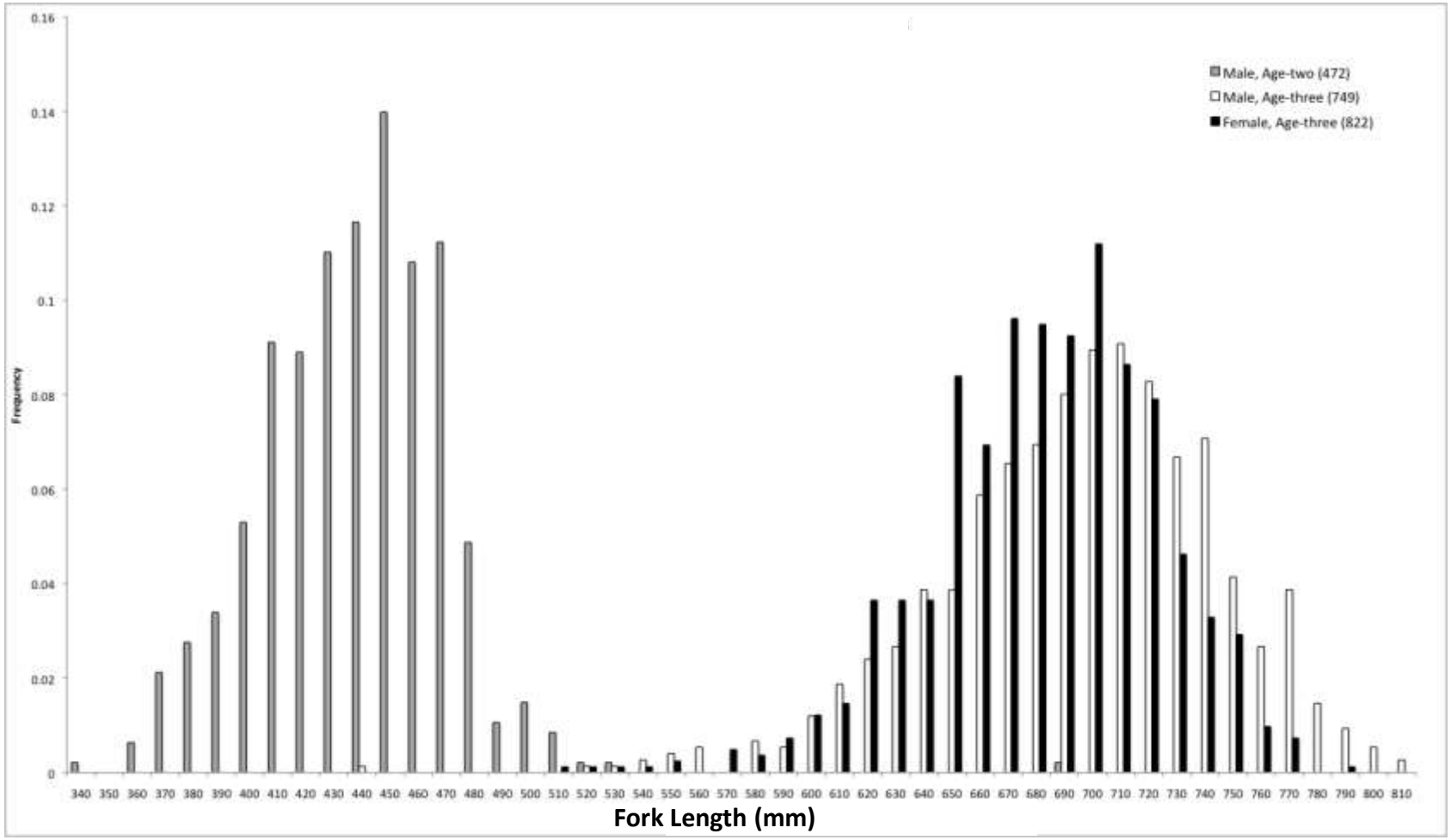
Age structure of return timing: Russian River steelhead

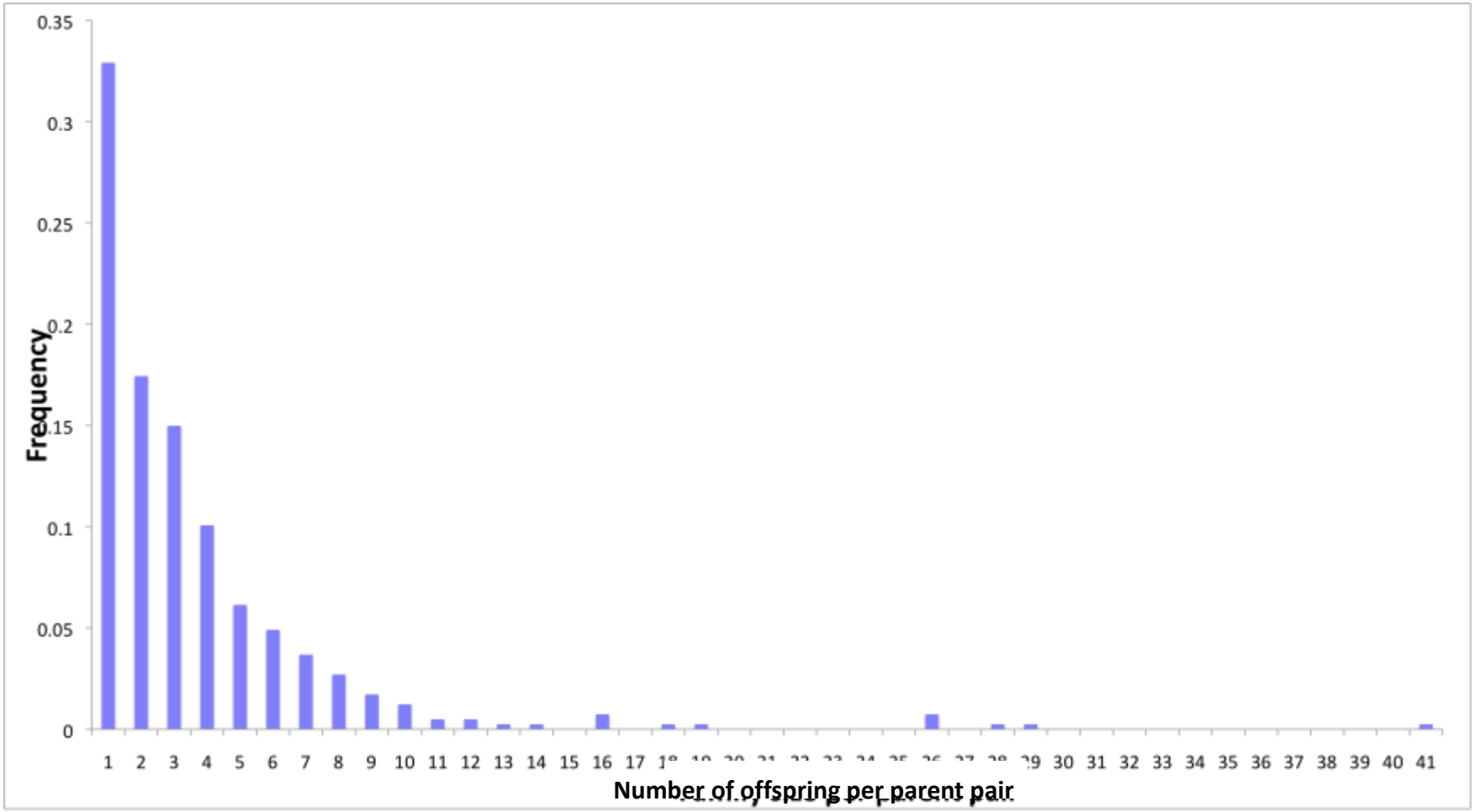


Two year olds return later than three year olds

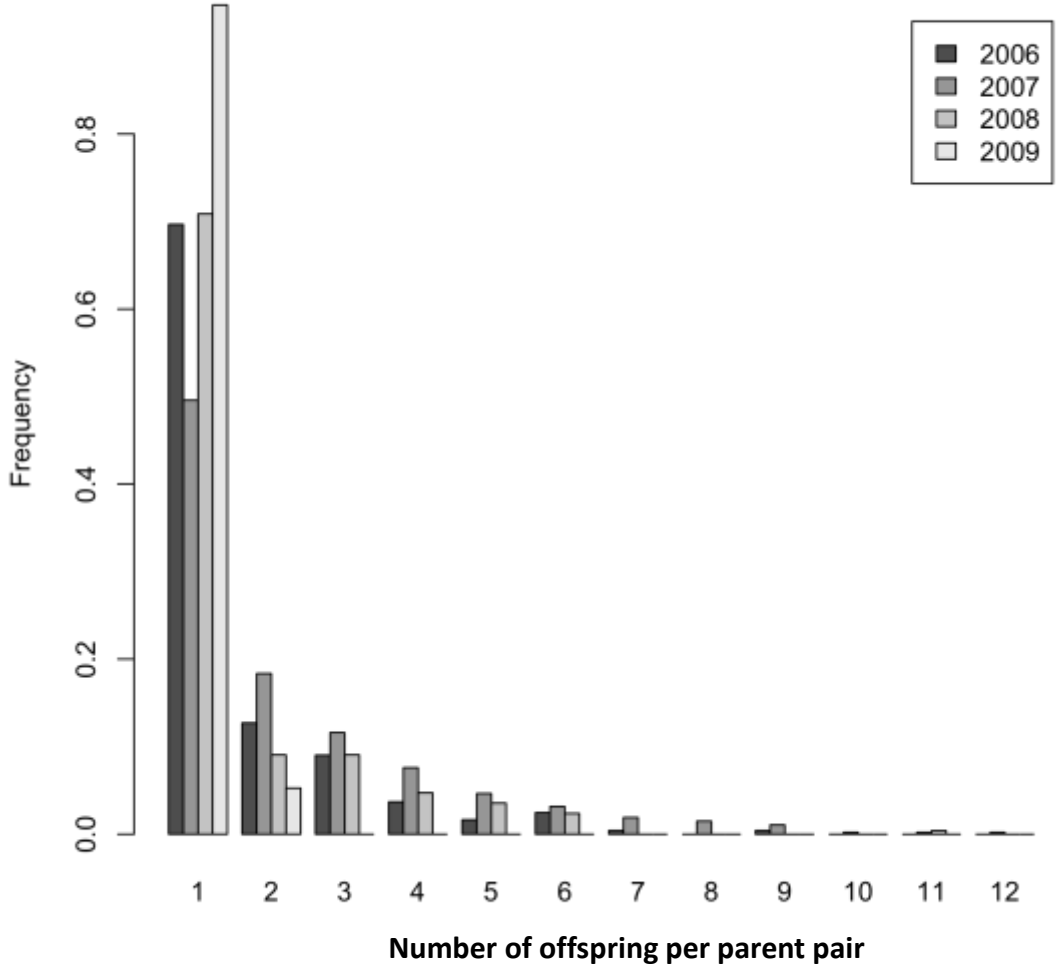
Age structure, size at age: Klamath River (Iron Gate) coho salmon



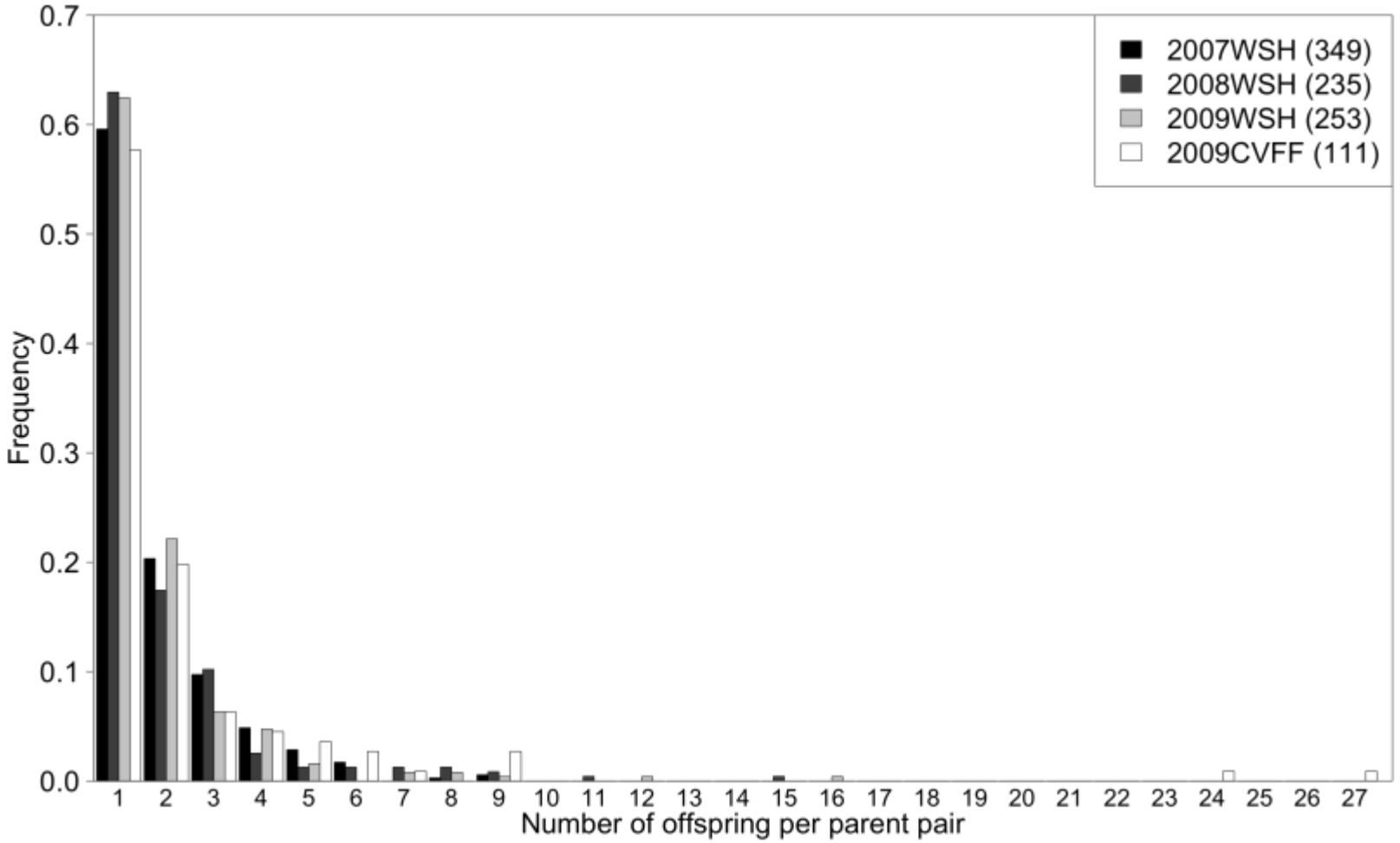
No. of offspring per parent pair: Klamath River coho salmon



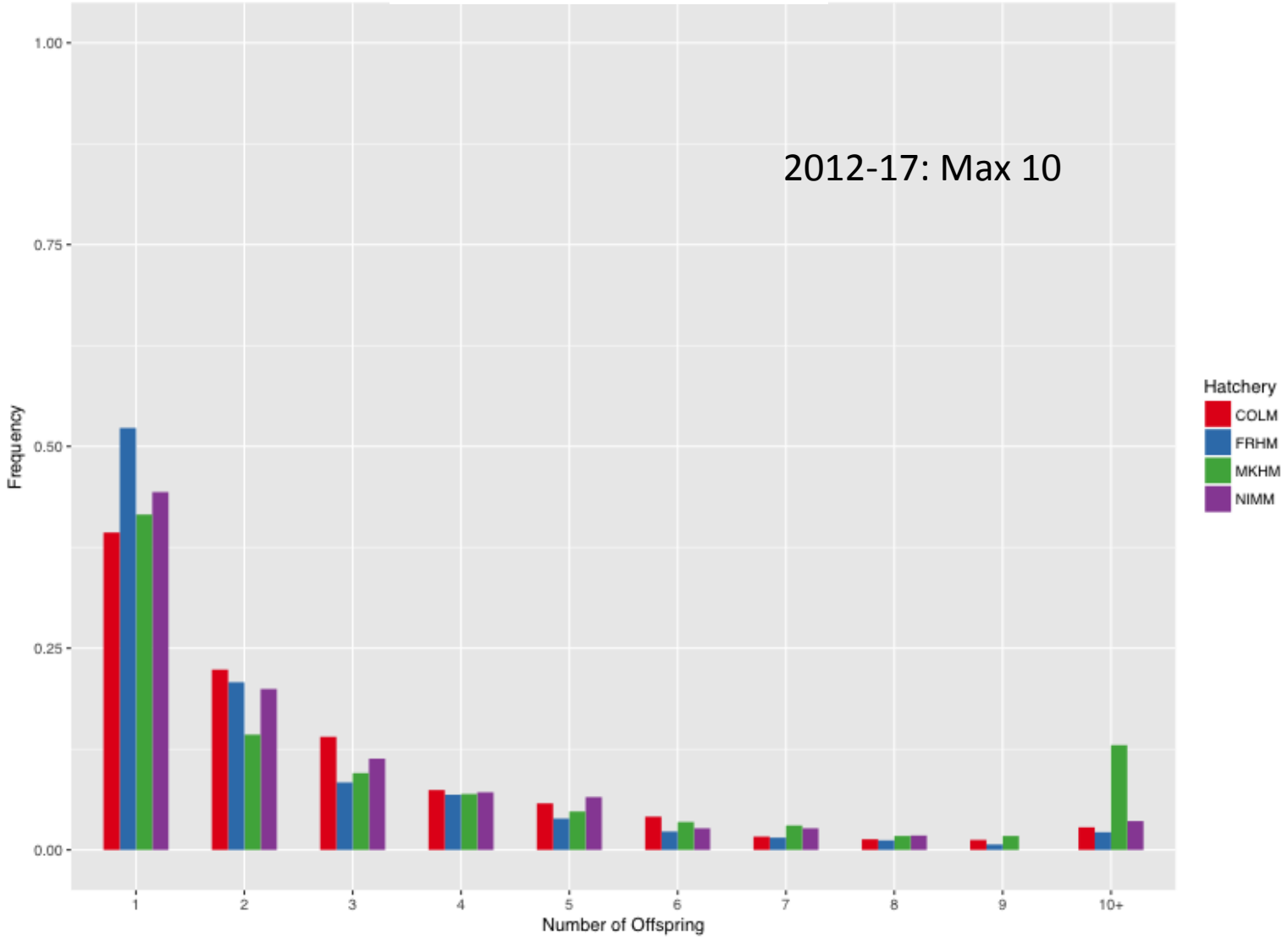
No. of offspring per parent pair: Feather River Chinook salmon



No. of offspring per parent pair: Russian River steelhead



No. of offspring per parent pair: Central Valley steelhead



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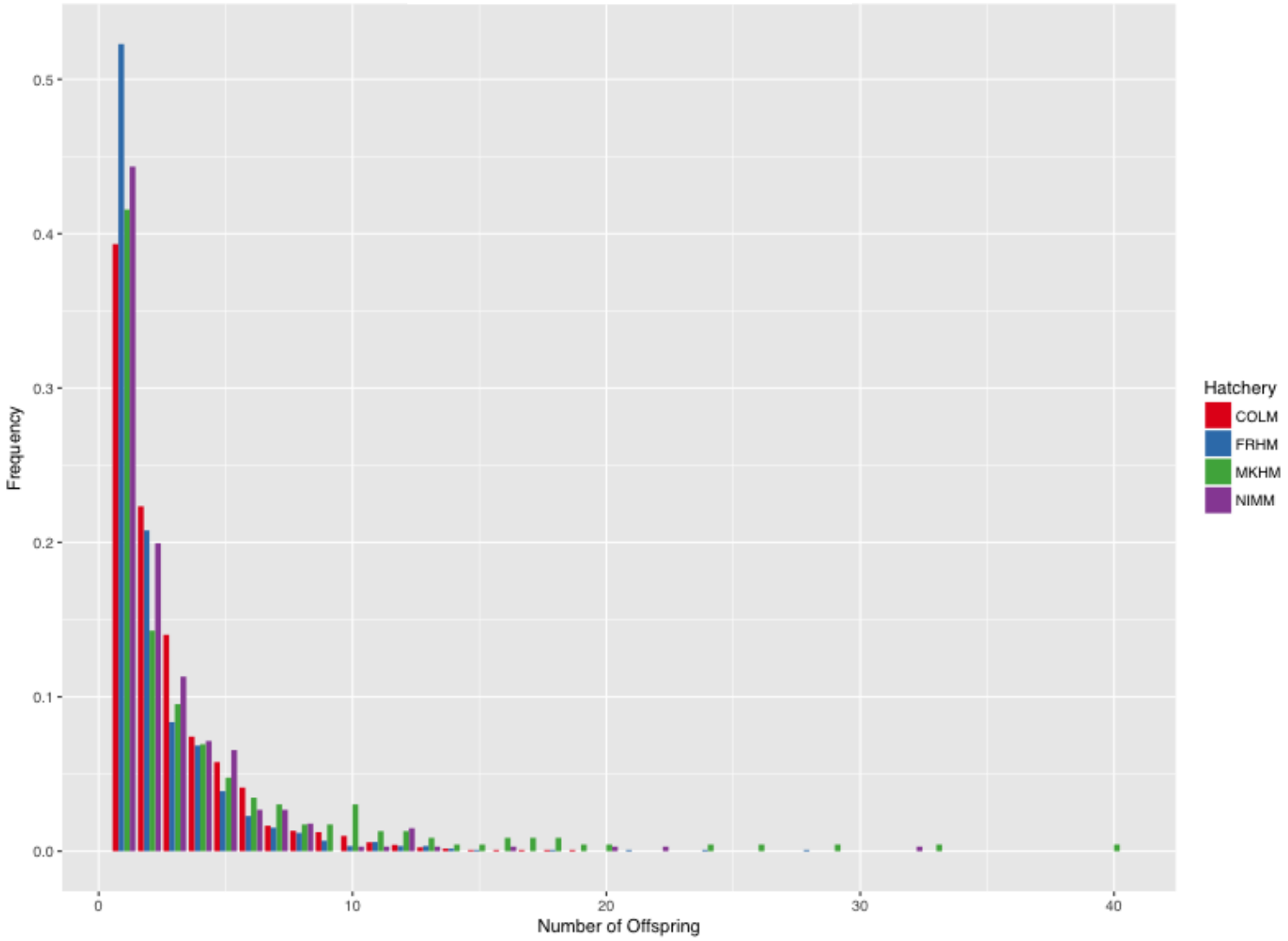
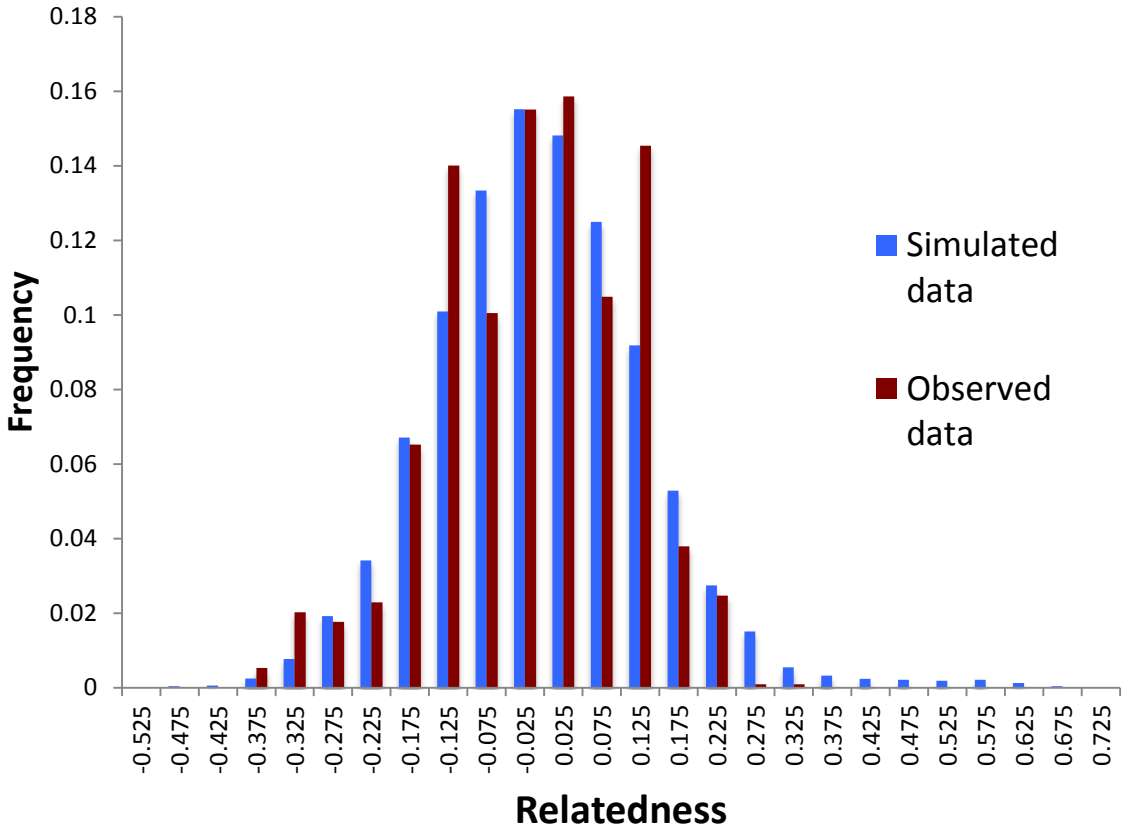


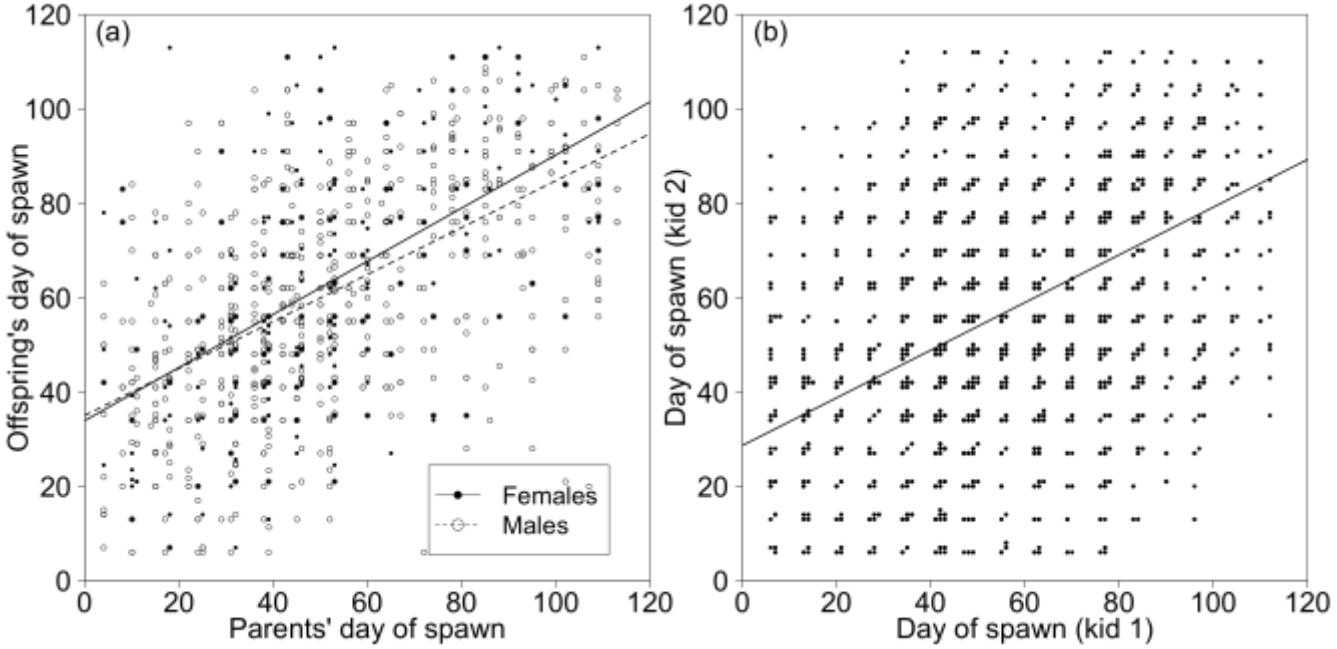
Inbreeding in hatchery mating

Feather River Hatchery Steelhead

Clear signal of inbred matings producing fewer anadromous adult returns



Heritability of Run Timing: Russian River steelhead



Statistics-Males	
R^2	0.321
Heritability H^2	0.497

Statistics-Females	
R^2	0.320
Heritability H^2	0.563

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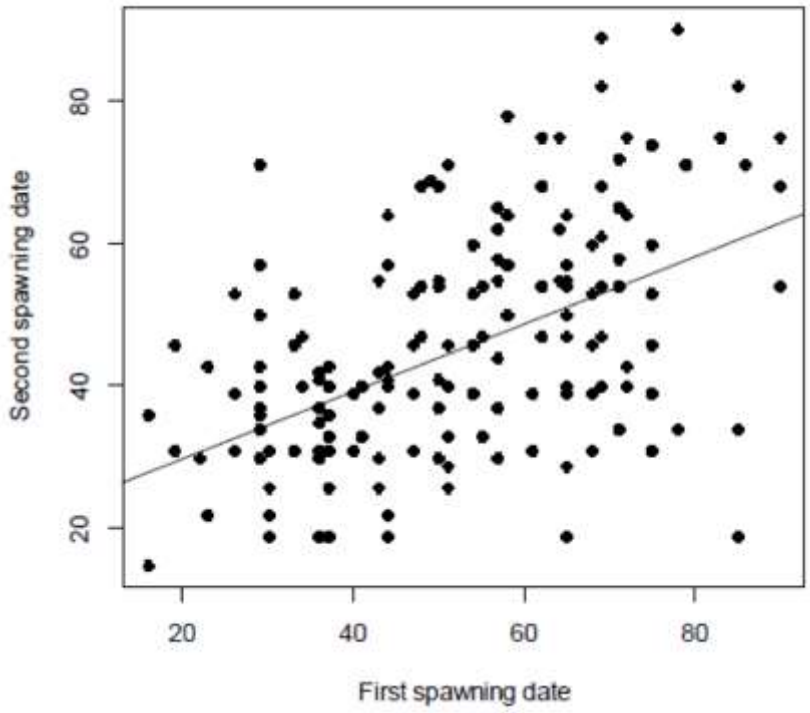
Heritability of Run Timing: Russian River steelhead

Iteroparity and repeat spawning

Matching samples analysis

Correlation between 1st and 2nd spawn dates for iteroparous fish
R^2=0.31



Iteroparity in Central Valley Hatchery Steelhead

Matching samples analysis

Hatchery program	Spawn year 2012	2013	2014	2015	2016	2017
Coleman	3.9% (33)	1.7% (15)	4.3% (38)	4.0% (55)	11.9% (54)	7.8% (70)
Feather River	4.1% (27)	2.5% (30)	5.4% (72)	17.4% (76)	9.8% (12)	2.7% (23)
Nimbus	0.4% (1)	0% (0)	0% (0)	0% (0)	0% (0)	0% (0)
Mokelumne River	6.4% (13)	7.2% (7)	3.7% (6)	4.2% (5)	0% (0)	0.3% (2)

Iteroparous fish strongly biased towards females.

Parentage-based tagging – Conclusions

-Pedigrees that come with genetic tag recoveries are valuable

-Inference about salmonid life history has already led to management changes

-Large number of age-2 spawners in steelhead programs

-Return/spawn timing highly heritable in steelhead

-About 60% of returning adult Chinook are singletons, but only ~30% of coho salmon and ~40% of steelhead have no full siblings amongst returning adults

-Inbreeding causing some mortality in steelhead programs, and could be reduced by use of genetic broodstock management as with coho programs

-Iteroparity rates are similar to those in other hatchery stocks, except Nimbus. Mostly females.

Parentage-based tagging – Challenges & Opportunities

-Education and communication with managers and agency staff

-Evaluate operational constraints

-Evaluate remaining technical issues and refine protocols

-Immediately expand use in steelhead and other untagged stocks

-Reduce genotyping costs and turn-around time

-Establish shared databases.

Thank you!

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