## Large-scale Genetic Tagging Experiment with Chinook salmon from the Feather River Hatchery Allows for Pedigreebased Inference

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#### North America Hatchery Releases (in Millions)





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## Hatcheries make and release millions of fish.



## **Q:** Can we use genetics to identify population, age and cohort?

# A: If we know an individual's parents, then we also know the exact age and source population of that fish.

Parentage-based tagging (PBT) uses genetic information from the parental breeding generation (broodstock) to "tag" the offspring

- Sample parents
- Breed as per usual
- Capture offspring as outmigrants, at sea, or upon return to spawn
- Genotype sample and locate parents in database







Central Valley Chinook salmon generally return to spawn at 2-4 years old.





PBT identifies offspring ages by finding their parents in the database.



## **Feather River Hatchery (FRH)**

- One of the largest tributaries to the Sacramento River
- Construction of Oroville Dam and FRH in 1967
- Sampling
- Analysis









Feather River Hatchery spring-run PBT tag recoveries from fish returning to the hatchery (using *snppit*):





Hooray! Woot! Woot!



## Feather River Hatchery spring-run PBT tag recoveries:







## Feather River Hatchery spring-run PBT tag recoveries:







Feather River Hatchery spring-run PBT tag recoveries by cohort:







### **Tagging Results**

- Recovered genetic tags from 4956 adult spawners
- Recovered 71% of recorded mate pairs (2006-2009)
- When accounting for samples that did not yield genotypes, natural origin broodstock and broodstock from other hatchery programs, proportion of adults with genetic tags recovered near 100% of expected proportions.
- Contrast with CWT ocean recoveries: only 85% of FRH spring yield correct tags.

|           | Offspring recoveries [and number analyzed] in year: |         |                        |                |                |                |                |                |                |       |  |
|-----------|---|---------|------------------------|----------------|----------------|----------------|----------------|----------------|----------------|-------|--|
| SpawnYear | Sampled   | Removed | Parent<br>Pairs in Db. | 2008<br>[3981] | 2009<br>[1458] | 2010<br>[1877] | 2011<br>[1674] | 2012<br>[1286] | 2013<br>[1314] | Total |  |
| 2006      | 1148  | 126     | 0.753                  | 3              | 541            | 17             | 0              | 0              | 0              | 561   |  |
| 2007      | 1423  | 130     | 0.829                  | -              | 56             | 1272           | 213            | 0              | 0              | 1541  |  |
| 2008      | 4717  | 736     | 0.711                  | -              | -              | 26             | 572            | 22             | 0              | 620   |  |
| 2009      | 1494  | 36      | 0.970                  | -              | -              | -              | 36             | 1106           | 68             | 1210  |  |
| 2010      | 2059  | 182     | 0.896                  | -              | -              | -              | -              | 4              | 1020           | 1024  |  |
| 2011      | 1843  | 169     | 0.967                  | -              | -              | -              | -              | -              | 0              | 0     |  |
| 2012      | 1299  | 13      | 0.980                  | -              | -              | -              | -              | -              | -              | 0     |  |
| 2013      | 1394  | 80      | 0.905                  | -              | -              | -              | -              | -              | -              | 0     |  |
| sum       | 15377   | 1472    | sum:                   | 3              | 597            | 1315           | 821            | 1132           | 1088           | 4956  |  |
|           |   |         | scaled:                | 4              | 786            | 1594           | 1099           | 1176           | 1208           | 5866  |  |





## Age Distribution









Pedigrees chart the familial relationships among individuals. We found 829.







Difference between 'by blood' or 'by marriage'.















#### **Reproductive Success**









#### Parental relatedness and number of offspring





Number of returning offspring





#### Heritability of physical traits: Length

Heritability of length-at-age for male and female offspring







#### Heritability of physical traits: Length



Heritability of length-at-age for male and female offspring







Heritability of physical traits: Age-at-maturity.



| All Offspring |        | Kid Age |       |       | Males  | Males Kid Age |       |       |       | Females |        | Kid Age |       |       |
|---------------|--------|---------|-------|-------|--------|---------------|-------|-------|-------|---------|--------|---------|-------|-------|
| Pa Age        | Ma Age | 2       | 3     | 4     | Pa Age | Ma Age        | 2     | 3     | 4     | Pa Age  | Ma Age | 2       | 3     | 4     |
| 2             | 3      | 0.069   | 0.931 | 0.000 | 2      | 3             | 0.121 | 0.879 | 0.000 | 2       | 3      | 0.017   | 0.983 | 0.000 |
| 3             | 3      | 0.012   | 0.971 | 0.017 | 3      | 3             | 0.020 | 0.964 | 0.016 | 3       | 3      | 0.003   | 0.978 | 0.019 |
| 3             | 4      | 0.035   | 0.914 | 0.051 | 3      | 4             | 0.063 | 0.902 | 0.036 | 3       | 4      | 0.000   | 0.930 | 0.070 |
| 4             | 3      | 0.016   | 0.945 | 0.039 | 4      | 3             | 0.017 | 0.966 | 0.017 | 4       | 3      | 0.014   | 0.928 | 0.058 |
| 4             | 4      | 0.035   | 0.860 | 0.105 | 4      | 4             | 0.063 | 0.875 | 0.063 | 4       | 4      | 0.000   | 0.842 | 0.158 |





## Conclusions

- PBT performs extremely well as an efficient and effective tagging strategy
- Pedigrees allow for important biological inference and insight into the potential effects of various hatchery practices
- In the future, how can we use this type of information to adaptively manage hatchery populations?
- Large pedigrees may be useful for mapping the genes associated with observed phenotypes.







#### Acknowledgements:

- Thanks to the molecular ecology team and the SWFSC Santa Cruz Lab
- Anna Kastner, A.J. Dill and the staff at the Feather River River Hatchery
- Lea Koerber, Rob Titus, and the staff at the CDFW Tissue Archive
- Bureau of Reclamation and Deaprtment of Water Resources
- Partial funding from CEQI and CALFED

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