Application of Genetic Methods to Salvaged ESA-listed Chinook Salmon

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Acknowledgements

- California Department Fish and Wildlife
- CDFW Tissue Archive
- Genomic Variation Laboratory
- NOAA Southwest Fisheries
 Science Center









Our charge

 Primary objective: Use genetic characteristics to determine the lineage (race) of Chinook Salmon encountered at salvage.

Key evaluation pertains to individuals classified as "older" based on length-at-date criteria.



Why genotype?



- A primary contributor to uncertainty in LOSS estimation is identification of winter run
- The population level context of salvage rates is unknown
- Our activities intended to directly target and reduce one source of uncertainty in the estimation of loss

How do we assign fish?

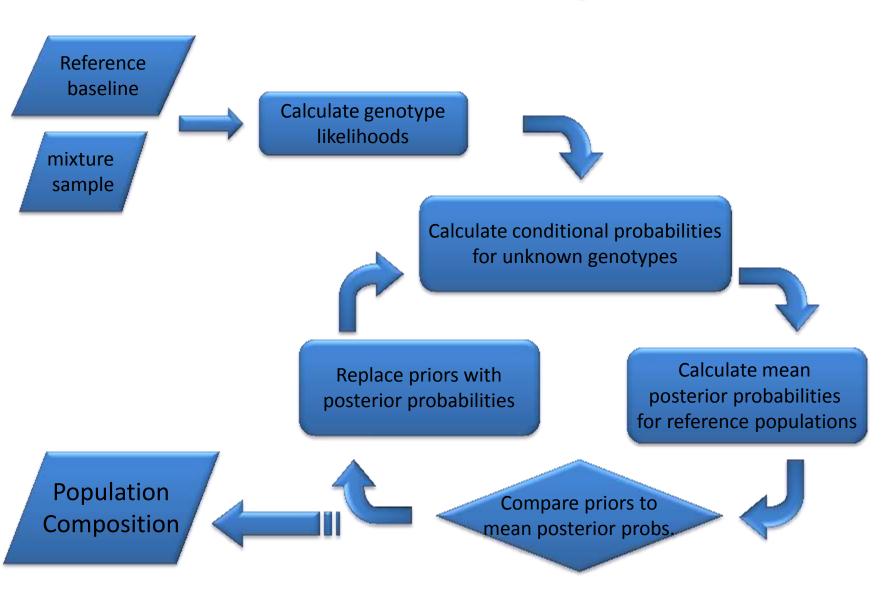
fins





Baselines

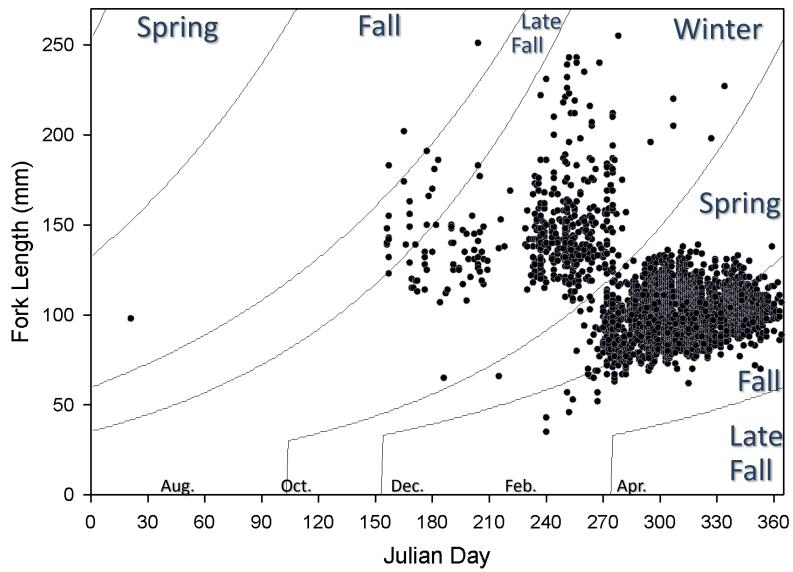
Mixed Stock Analysis



ASSIGNMENT RESULTS

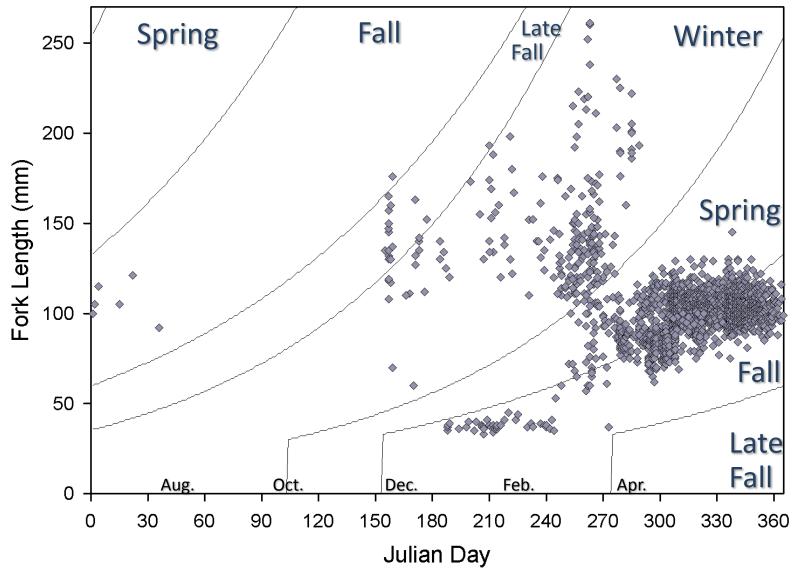
State Water Project and Central Valley Project 2010-2014

Delta Model pronounced winter-run SWP 2010-2014



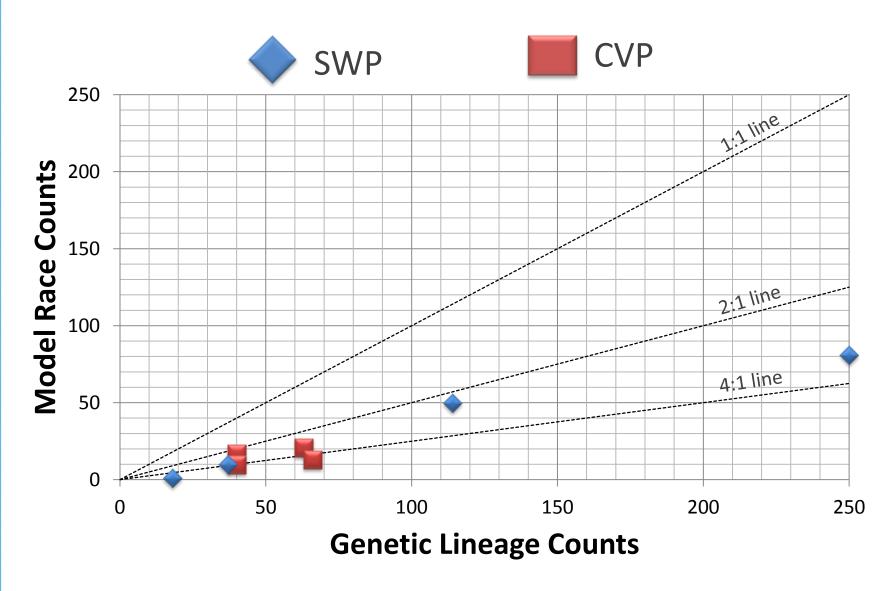
Delta Model pronounced winter-run SWP 2010-2014 Winter lineage Fall Spring 'Late∕ Winter 250 Fall 200 Fork Length (mm) Spring 150 100 Fall 50 Late Fall Feb. Dec. Aug Oct. Apr. 0 60 120 180 210 240 300 330 360 0 30 90 150 270 Julian Day

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Implications

- How does Delta Model inaccuracy affect ESA impacts?
- What does it mean for fish loss density triggers that "older fish" are not winter run?
- How do we implement a system to improve information for real-time operations?

Implications

Most winter run occur within winter run size category Most individuals within winter run category are not winter run

Transitioning away from Delta Model

- Continue refinement of new LOSS calculation tool
 - Fish count parameters include misclassification error
- Unify legal processes (e.g. BiOp remand) with operational enhancements (survival)
- Dynamic tool for predicting and assessing "take"

Dynamic Tool Concept

"take" target

- ► Error Model
- Forecast updates
- ► Genetic refinements
- Dynamic trajectory





