Can rapid genetic assessment (RGA) improve passage decisions at Willamette basin dams?

Implications for reintroduction of spring-run Chinook salmon in the South Santiam River

Dan Bingham, Hans Berge, Scott Blankenship, and Gregg Schumer Cramer Fish Sciences, Genidaqs





What is needed to recover spring-run Chinook salmon in the Willamette?

• Create self-sustaining populations upstream stream of dams





What is needed to recover spring-run Chinook salmon in the Willamette?

- Create self-sustaining populations upstream stream of dams
- Cohort Replacement Rate (CRR) > 1.00





What is needed to recover spring-run Chinook salmon in the Willamette?

- Create self-sustaining populations upstream stream of dams
- Cohort Replacement Rate (CRR) > 1.00
- We need to know the origin of returning adults to achieve CRR>1.00





The power of genetic baselines

• Genetic baselines allow us to query existing data to identify population of origin





The power of genetic baselines

- Genetic baselines allow us to query existing data to identify population of origin
 - Allele frequencies from local populations
 - Archived tissues from transported adults
 - Archived tissues from hatchery brood (PBT)





The power of genetic baselines

- Genetic baselines allow us to query existing data to identify population of origin
 - Allele frequencies from local populations
 - Archived tissues from transported adults
 - Archived tissues from hatchery brood (PBT)
- Rapid genetic assessment (RGA) harnesses the power of genetic baselines in real-time





Real-time





Real-time

• Genetic data is available to inform a specific management action during a specific management event.





Real-time

- Genetic data is available to inform a specific management action during a specific management event.
- Example:
 - RGA is used to inform selective transport of natural-origin fish in a reintroduction program





What is needed to complete RGA?

• Genetic baseline





What is needed to complete RGA?

- Genetic baseline
 - i.e., Archived tissues





What is needed to complete RGA?

- Genetic baseline
 - i.e., Archived tissues
- Logistics: management event and action need to be feasible in real-time
 - 1. Capture
 - 2. Tag
 - 3. Sample
 - 4. Mail
 - 5. Hold
 - 6. Genetic Analysis (24 to 48 hrs)
 - 7. Sort
 - 8. Release





What are examples of RGA?

Table 1. Examples of RGA programs.

RGA		Timeframe	
Program	Species	(hrs)	Purpose
USBOR	Chinook	24 to 48	ID of run of Chinook salmon salvaged at Central Valley Project
USFWS	Chinook	24 to 48	ID of Endangered Winter Run Chinook in Sacramento River
Avista Power	Bull trout	24 to 48	ID of population of origin in Pend Oreille (trap and haul)
USFWS	Bull trout	24 to 48	ID of population of origin in NF Tieton River
WGF	Sauger	24 to 48	ID of hybridization with nonnative walleye for hatchery breeding





What are examples of RGA?

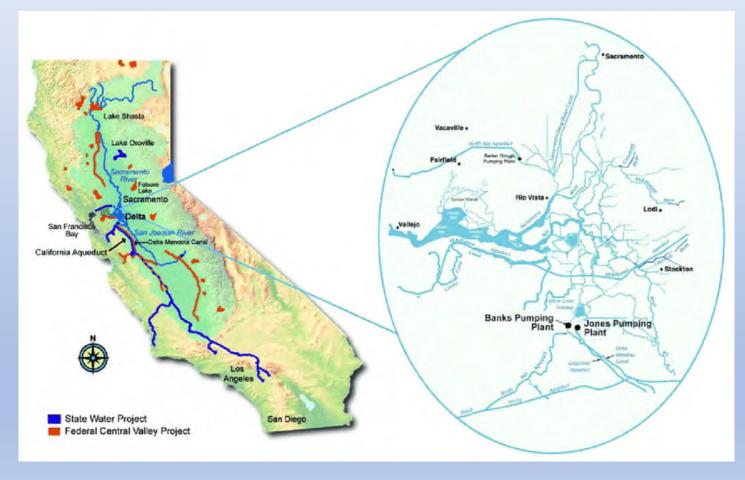
Table 1. Examples of RGA programs.

RGA		Timeframe	
Program	Species	(hrs)	Purpose
USBOR	Chinook	24 to 48	ID of run of Chinook salmon salvaged at Central Valley Project
USFWS	Chinook	24 to 48	ID of Endangered Winter Run Chinook in Sacramento River
Avista Power	Bull trout	24 to 48	ID of population of origin in Pend Oreille (trap and haul)
USFWS	Bull trout	24 to 48	ID of population of origin in NF Tieton River
WGF	Sauger	24 to 48	ID of hybridization with nonnative walleye for hatchery breeding

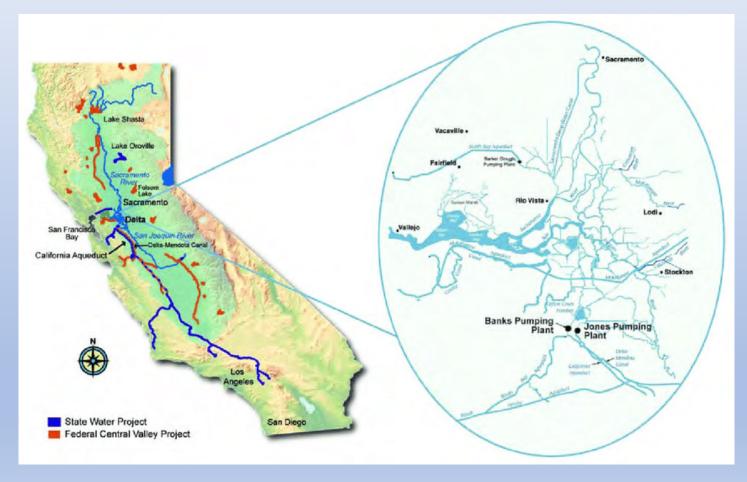




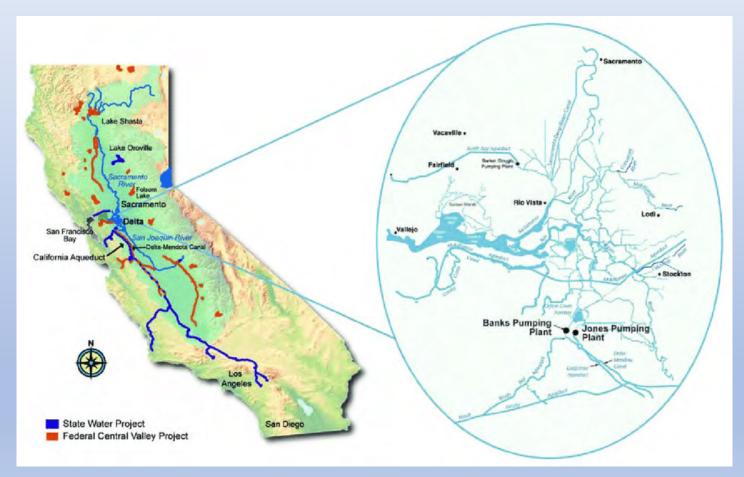
• Real-time GSI is used to confirm entrainment of Endangered Chinook in the CVP



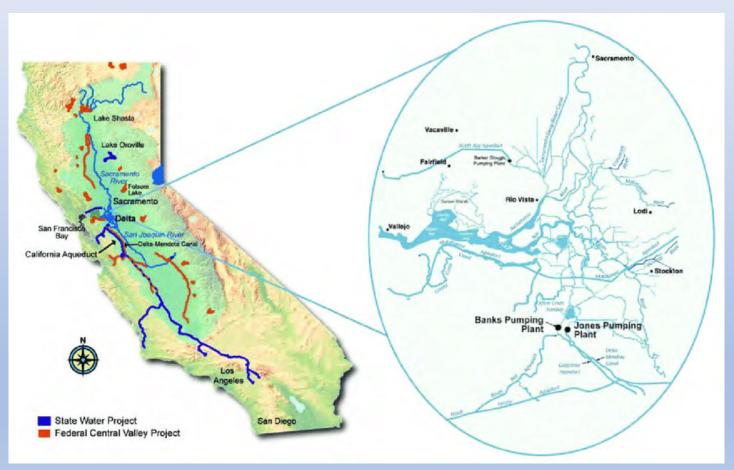
- Real-time GSI is used to confirm entrainment of Endangered Chinook in the CVP
- The genetic baseline is allele frequencies from local populations



- Real-time GSI is used to confirm entrainment of Endangered Chinook in the CVP
- The genetic baseline is allele frequencies from local populations
- The management event is fish salvage
- The management action is reallocation of water if WRCS are present



- Real-time GSI is used to confirm entrainment of Endangered Chinook in the CVP
- The genetic baseline is allele frequencies from local populations
- The management event is fish salvage
- The management action is reallocation of water if WRCS are present
- No water curtailment since inception of RGA



How is RGA used?

 Table 1. Examples of RGA programs.

RGA		Timeframe	•
Program	Species	(hrs)	Purpose
USBOR	Chinook	24 to 48	ID of run of Chinook salmon salvaged at Central Valley Project
USFWS	Chinook	24 to 48	ID of Endangered Winter Run Chinook in Sacramento River
Avista Power	Bull trout	24 to 48	ID of population of origin in Pend Oreille (trap and haul)
USFWS	Bull trout	24 to 48	ID of population of origin in NF Tieton River
WGF	Sauger	24 to 48	ID of hybridization with nonnative walleye for hatchery breeding





• Real-time GSI ensures propagation of winter-run Chinook and avoidance of inbreeding in the hatchery



- Real-time GSI ensures propagation of winter-run Chinook and avoidance of inbreeding in the hatchery
- Genetic baseline is allele frequencies from local populations and genotypes from parents



- Real-time GSI ensures propagation of winter-run Chinook and avoidance of inbreeding in the hatchery
- Genetic baseline is allele frequencies from local populations and genotypes from parents
- The management event is hatchery supplementation of the local WR population
- The management action is selective use of winter-run Chinook for broodstock, avoidance of inbreeding, and liverelease of Non-WR



- Real-time GSI ensures propagation of winter-run Chinook and avoidance of inbreeding in the hatchery
- Genetic baseline is allele frequencies from local populations and genotypes from parents
- The management event is hatchery supplementation of the local WR population
- The management action is selective use of winter-run Chinook for broodstock, avoidance of inbreeding, and liverelease of Non-WR
- The ecological benefit is supplementation of the natural WR population and live release of non-WR



What are examples of RGA?

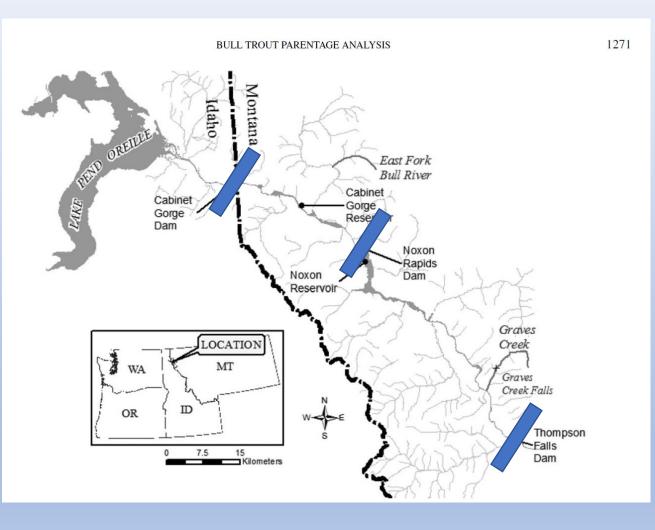
Table 1. Examples of RGA programs.

RGA		Timeframe	•
Program	Species	(hrs)	Purpose
USBOR	Chinook	24 to 48	ID of run of Chinook salmon salvaged at Central Valley Project
USFWS	Chinook	24 to 48	ID of Endangered Winter Run Chinook in Sacramento River
Avista Power	Bull trout	24 to 48	ID of population of origin in Pend Oreille (trap and haul)
USFWS	Bull trout	24 to 48	ID of population of origin in NF Tieton River
WGF	Sauger	24 to 48	ID of hybridization with nonnative walleye for hatchery breeding

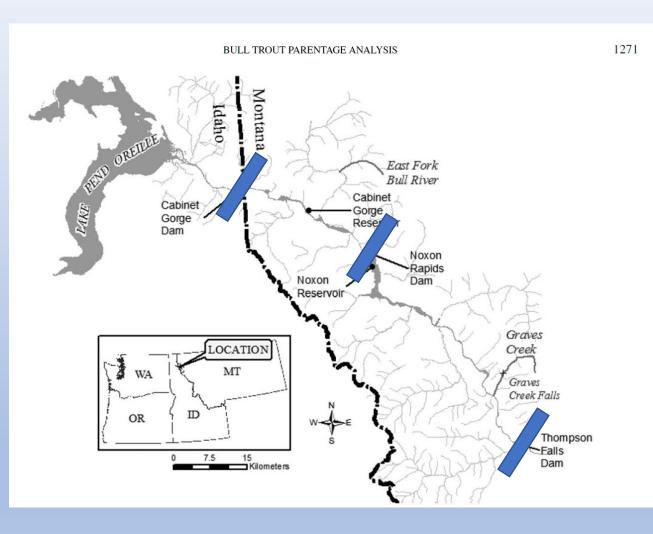




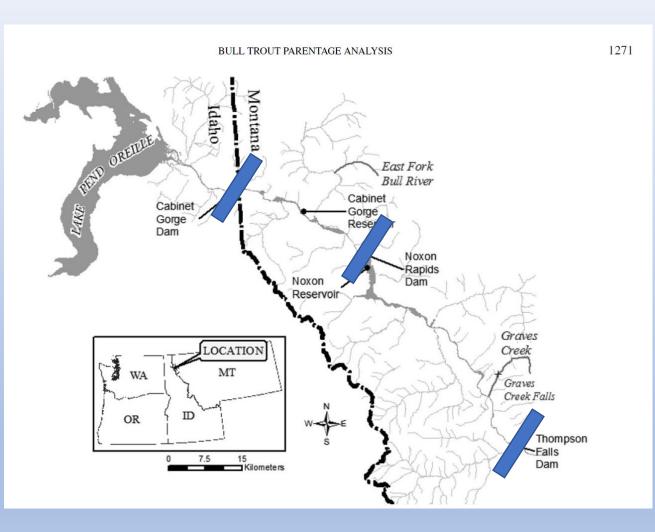
• Real-time GSI is used to confirm the number of dams that adfluvial bull trout must be passed above for spawning



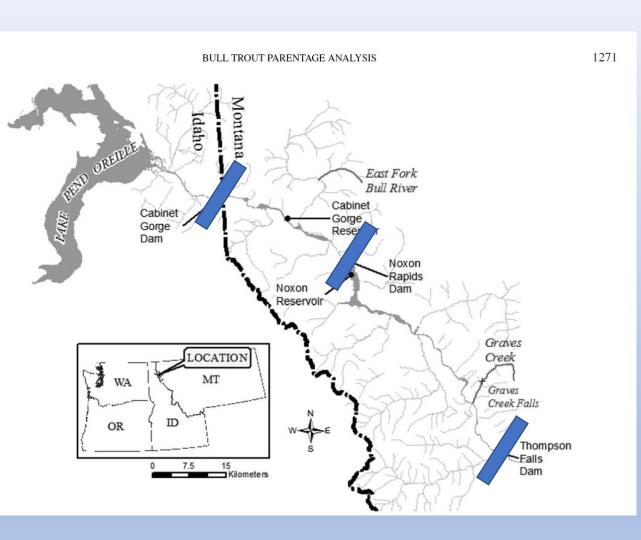
- Real-time GSI is used to confirm the number of dams that adfluvial bull trout must be passed above for spawning
- The genetic baseline is allele frequencies from ~40 local populations



- Real-time GSI is used to confirm the number of dams that adfluvial bull trout must be passed above for spawning
- The genetic baseline is allele frequencies from ~40 local populations
- The specific management event is upstream transport of bull trout



- Real-time GSI is used to confirm the number of dams that adfluvial bull trout must be passed above for spawning
- The genetic baseline is allele frequencies from ~40 local populations
- The specific management event is upstream transport of bull trout
- The specific management action is transport to tributary of origin



- Real-time GSI is used to confirm the number of dams that adfluvial bull trout must be passed above for spawning
- The genetic baseline is allele frequencies from ~40 local populations
- The specific management event is upstream transport of bull trout
- The specific management action is transport to tributary of origin
- The ecological benefit is confirmed reproductive success by transported adult bull trout

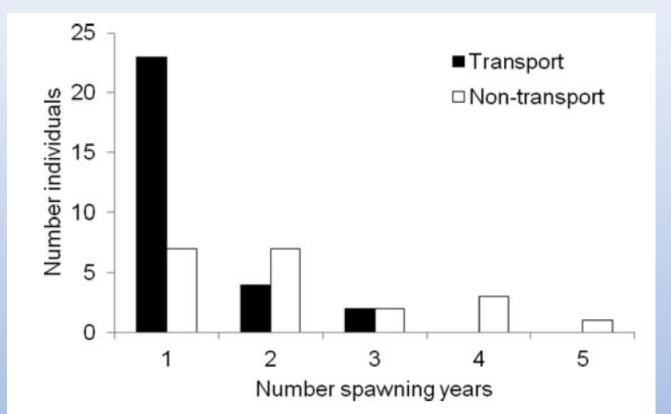
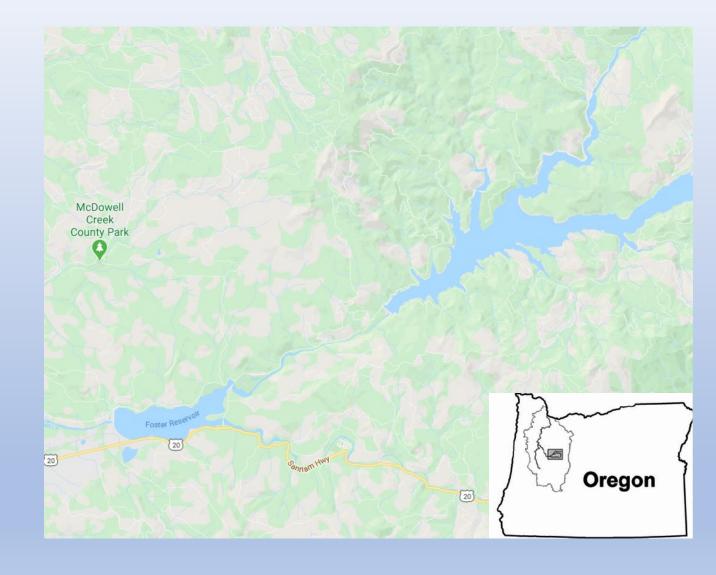
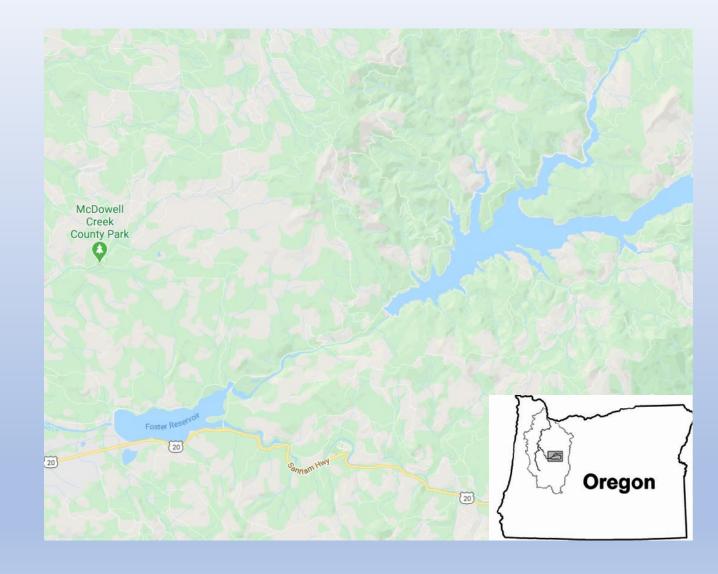


FIGURE 3. Spawning frequency based on parentage assignments for adult Bull Trout in East Fork Bull River and Graves Creek. Black bars represent upstream transport fish and white bars represent nontransport fish.



• 85% of production occurred upstream of Foster (2016 HGMP)



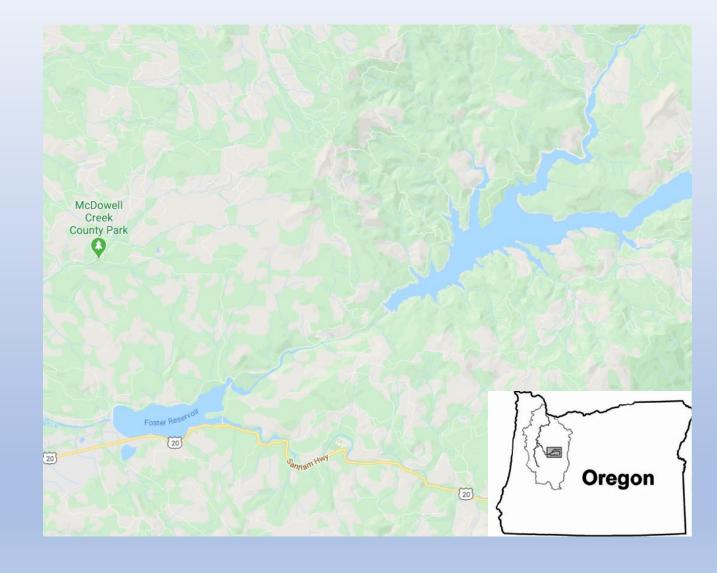
- 85% of production occurred upstream of Foster (2016 HGMP)
- 2008 BiOp identified access to historical spawning habitat as a key factor limiting natural production and recovery



- 85% of production occurred upstream of Foster (2016 HGMP)
- 2008 BiOp identified access to historical spawning habitat as a key factor limiting natural production and recovery
- Trap-and-haul reintroduction program for spring-run Chinook (RPA 4.6 2008 BiOp)

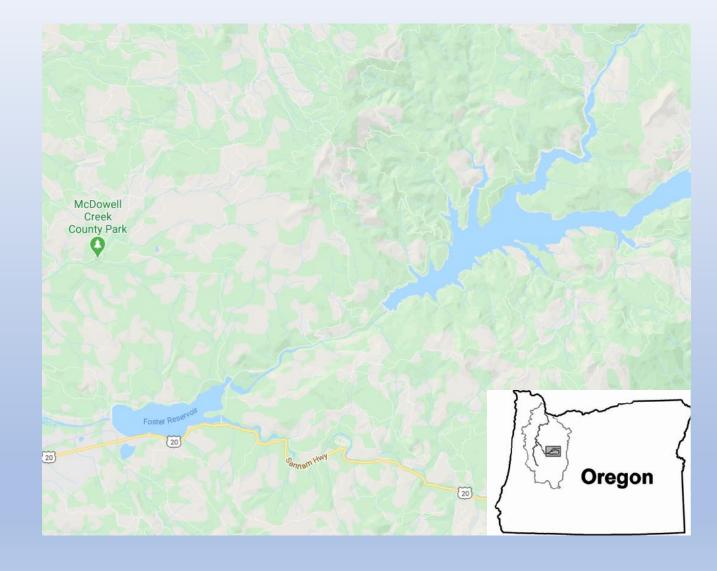


Goals and Challenges of the Reintroduction Program



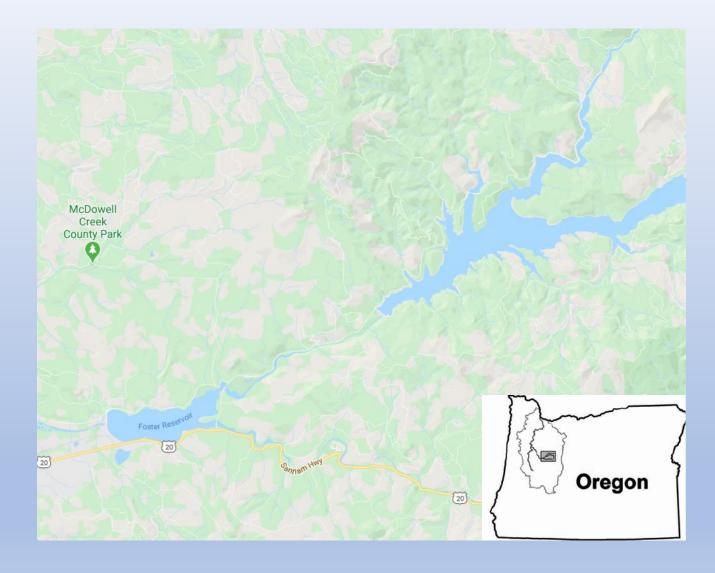
Goals and Challenges of the Reintroduction Program

• Goal of reintroduction is to exclude hatchery-origin spring Chinook (pHOS=0.00) (2016 HGMP)



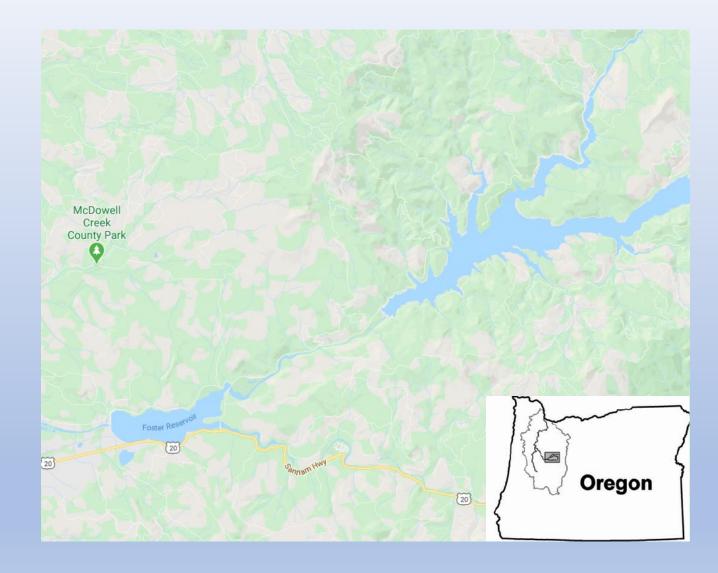
Goals and Challenges of the Reintroduction Program

- Goal of reintroduction is to exclude hatchery-origin spring Chinook (pHOS=0.00) (2016 HGMP)
- However, as many as 30% of passed unmarked spring Chinook have been of hatcheryorigin (2016 HGMP)



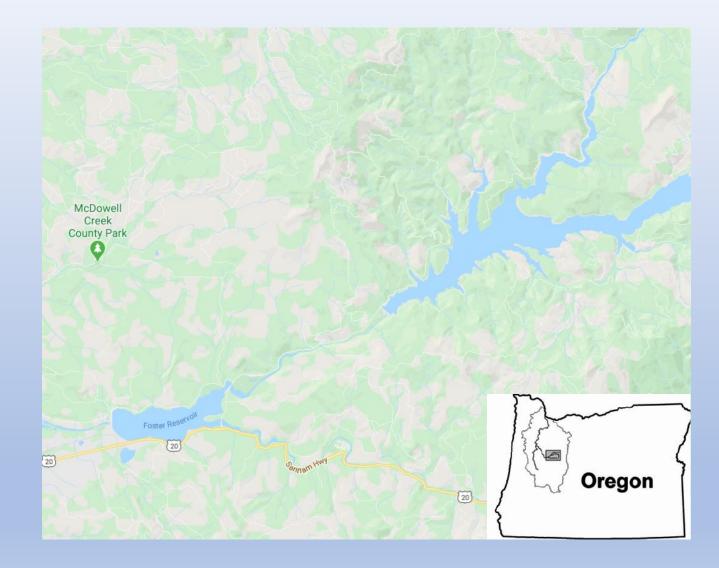
Goals and Challenges of the Reintroduction Program

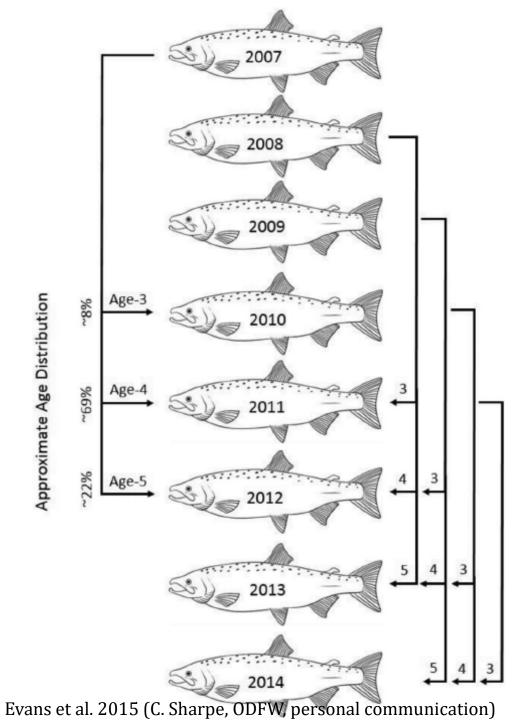
- Goal of reintroduction is to exclude hatchery-origin spring Chinook (pHOS=0.00) (2016 HGMP)
- However, as many as 30% of passed unmarked spring Chinook have been of hatcheryorigin (2016 HGMP)
- A future goal is to create a selfsustaining population upstream of Green Peter (CRR>1.00) (2016 HGMP)



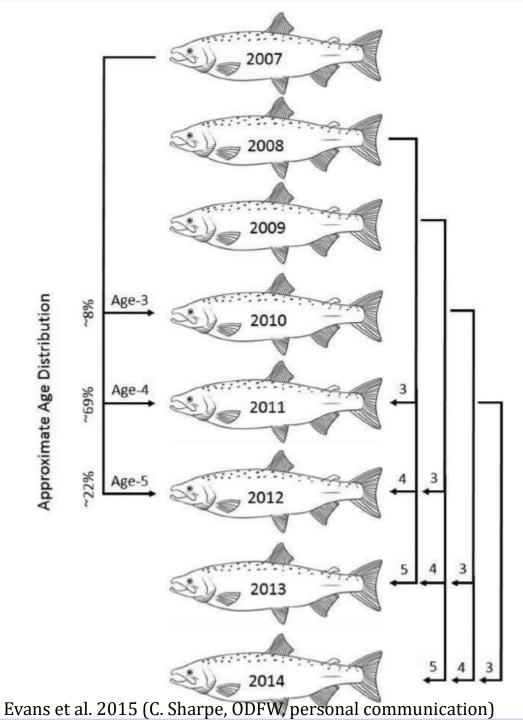
Goals and Challenges of the Reintroduction Program

- Goal of reintroduction is to exclude hatchery-origin spring Chinook (pHOS=0.00) (2016 HGMP)
- However, as many as 30% of passed unmarked spring Chinook have been of hatchery-origin (2016 HGMP)
- A future goal is to create a selfsustaining population upstream of Green Peter (CRR>1.00) (2016 HGMP)
- However, identification of natal natural-origin spring Chinook is a challenge

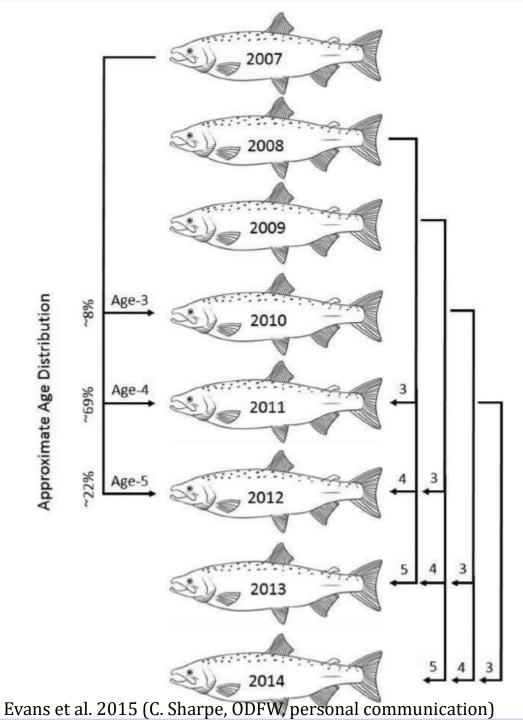




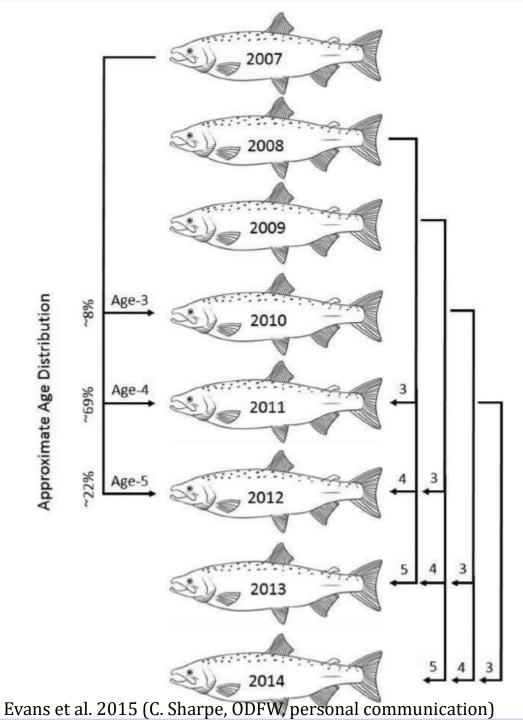
- A genetic baseline
 - Archived tissues are available from hatchery brood stock for last three years
 - Archived tissues are available from passed unmarked fish for >10 years

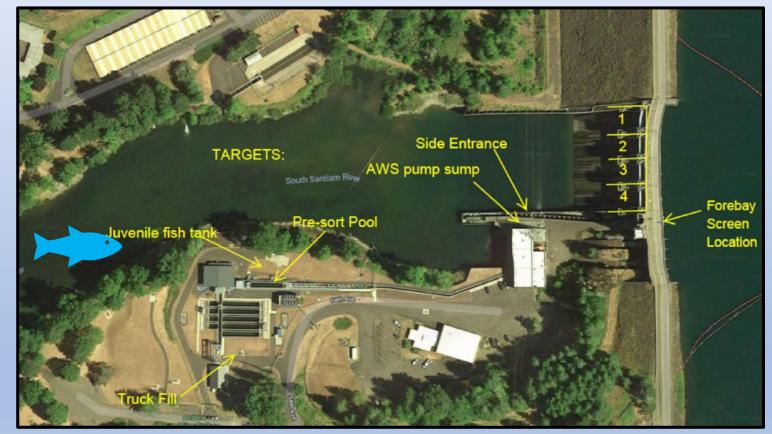


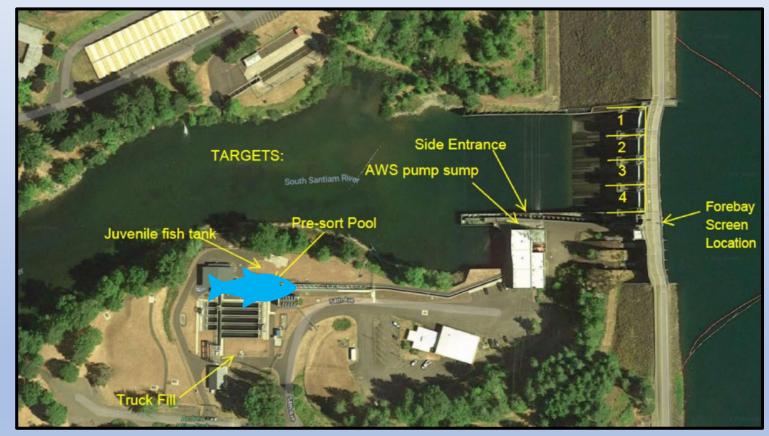
- A genetic baseline
 - Archived tissues are available from hatchery brood stock for last three years
 - Archived tissues are available from passed unmarked fish for >10 years

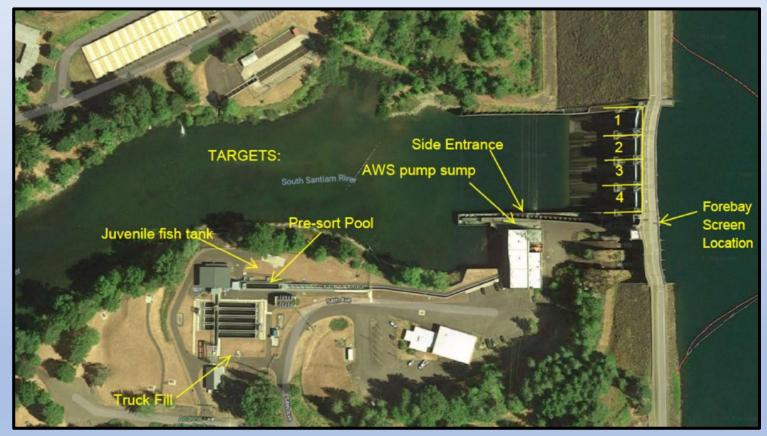


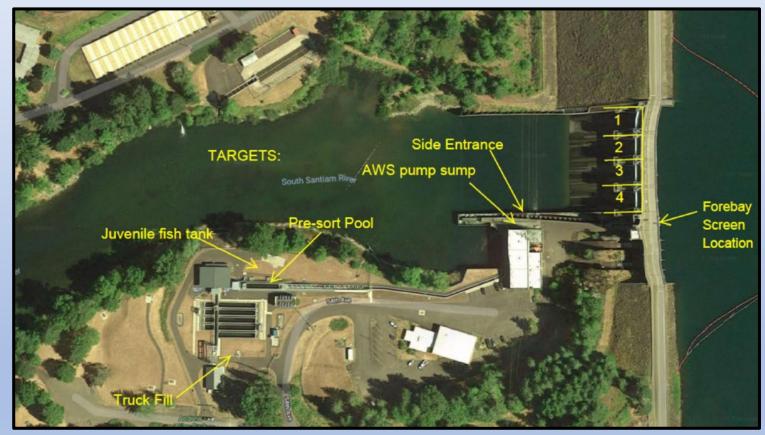
- A genetic baseline
 - Archived tissues are available from hatchery brood stock for last three years
 - Archived tissues are available from passed unmarked fish for >10 years
- The management event and action need to be possible in real-time
 - 1. Capture
 - 2. Tag
 - 3. Sample
 - 4. Mail
 - 5. Hold
 - 6. Genetic Analysis (24 to 48 hrs)
 - 7. Sort
 - 8. Release

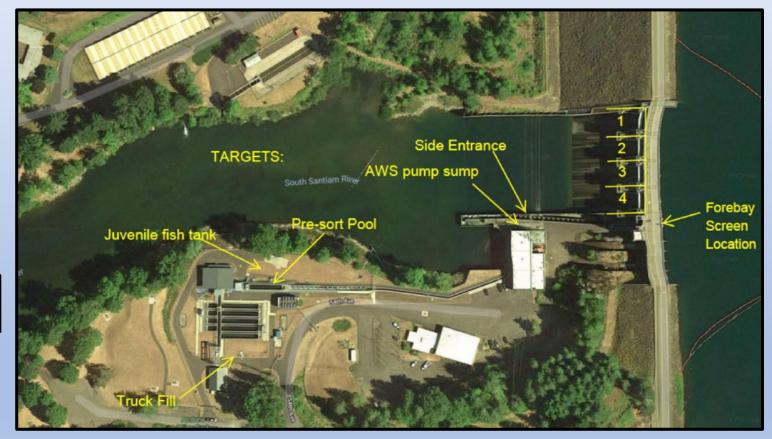


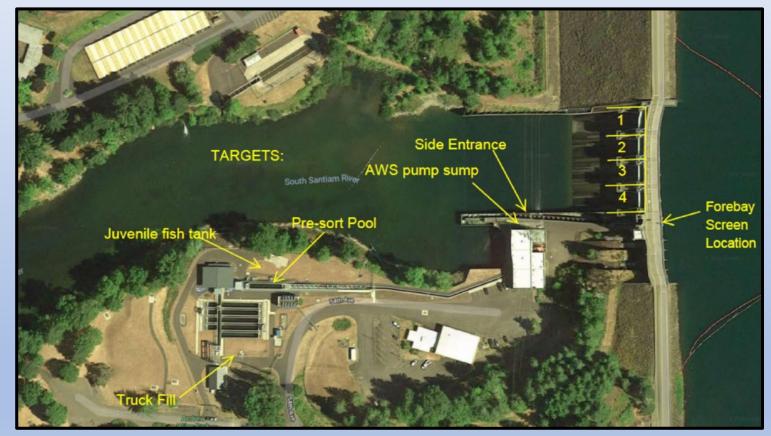


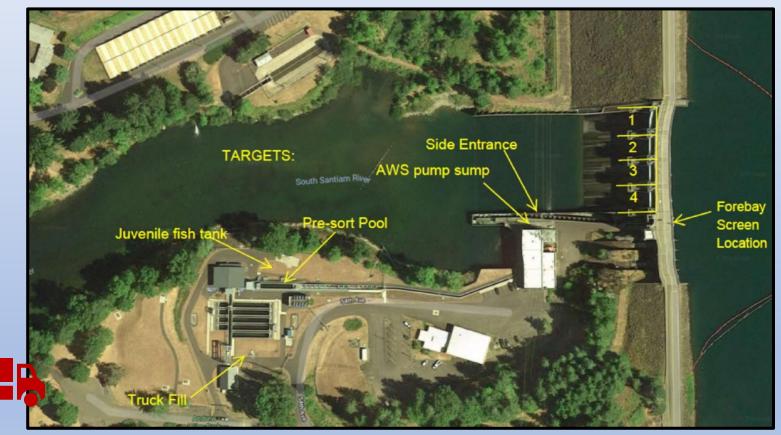












What happens if RGA is successful?





What happens if RGA is successful?

• Achieve BiOp compliance





What happens if RGA is successful?

- Achieve BiOp compliance
- Predict and model CRR





Conclusions

- RGA appears feasible at Foster
 - Genetic baselines
 - Logistics





Conclusions

- RGA appears feasible at Foster
 - Genetic baselines
 - Logistics
- RGA provides data for modeling CRR





Conclusions

- RGA appears feasible at Foster
 - Genetic baselines
 - Logistics
- RGA provides data for modeling CRR
- Next steps
 - Feasibility analysis
 - Development of an SOP





Acknowledgements

- USACE Portland District
- ODFW
- Rich Piaskoski
- Brett Boyd
- Ida Royer
- Chad Helms
- Lindsey Belcher
- Ryan Flaherty



dan.bingham@fishsciences.net