


Status and Trend of Okanogan summer/fall Chinook

Chief Joseph Hatchery
2022 Annual Program Review

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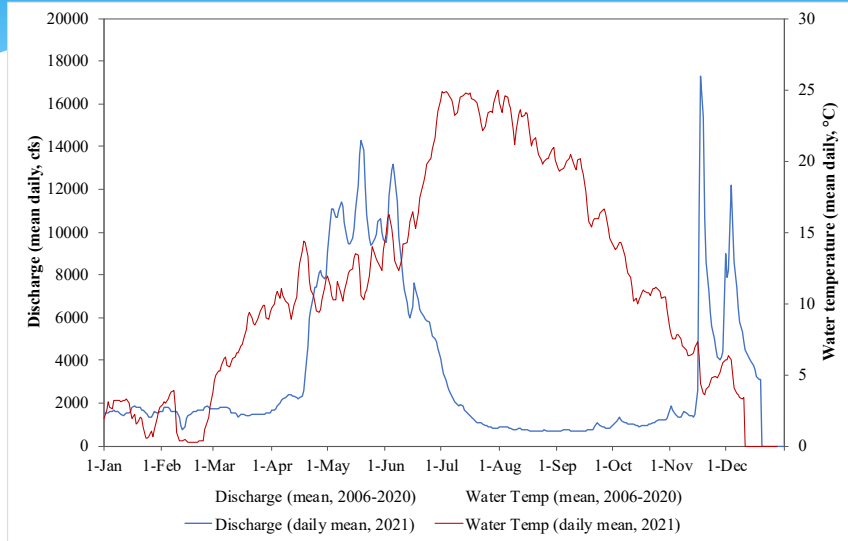


KMQ 1: What is the current status and recent historical trend of the naturally-spawning population in terms of Viable Salmonid Population (VSP) parameters?

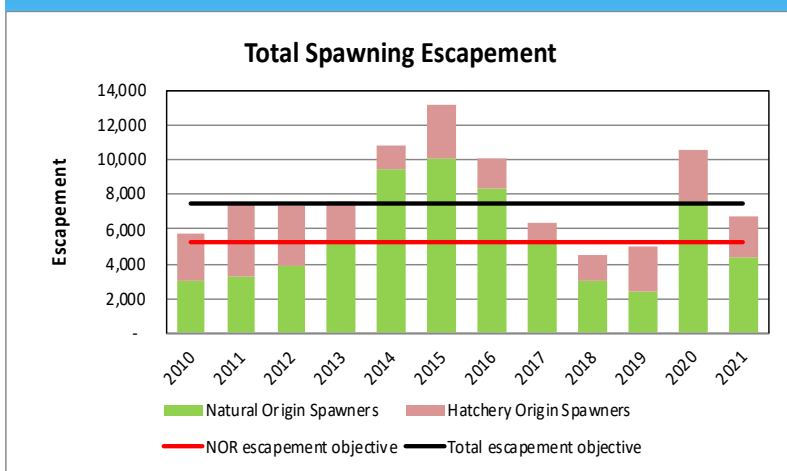
Viable Salmonid Population (VSP)

- Independent of other populations
(distance, genetics, stray rates, size)
- Negligible risk of extinction
(less than 5% over 100 yr timeframe)
- Abundance, Productivity, Spatial Structure, Diversity

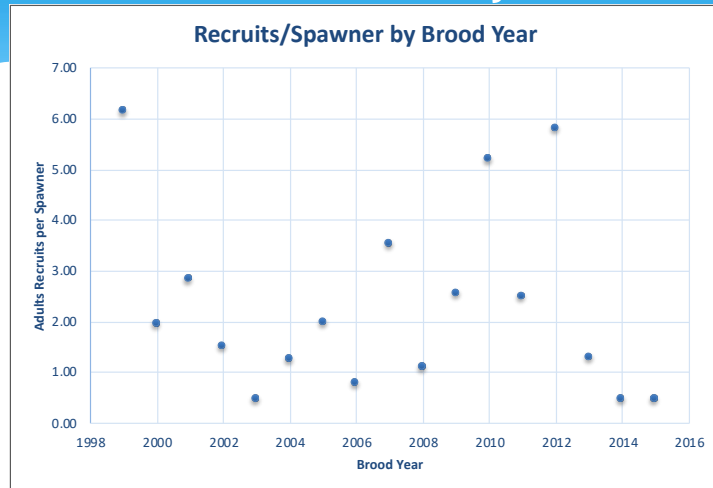
Water discharge and temperature



Abundance



Productivity

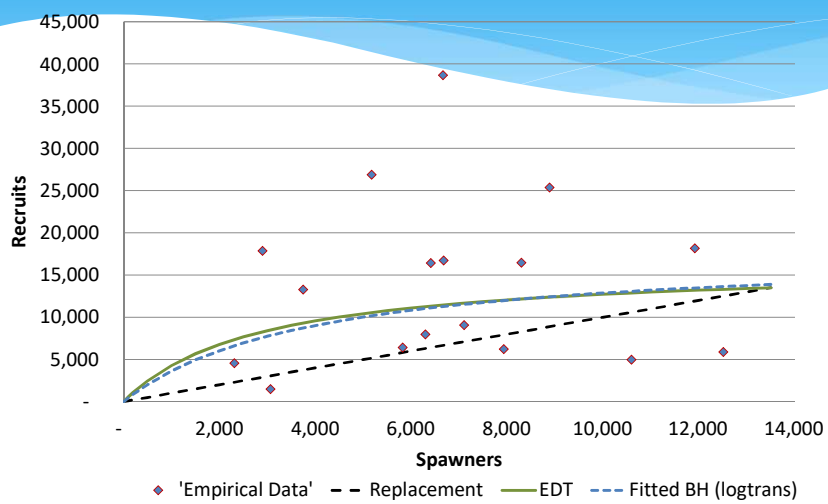


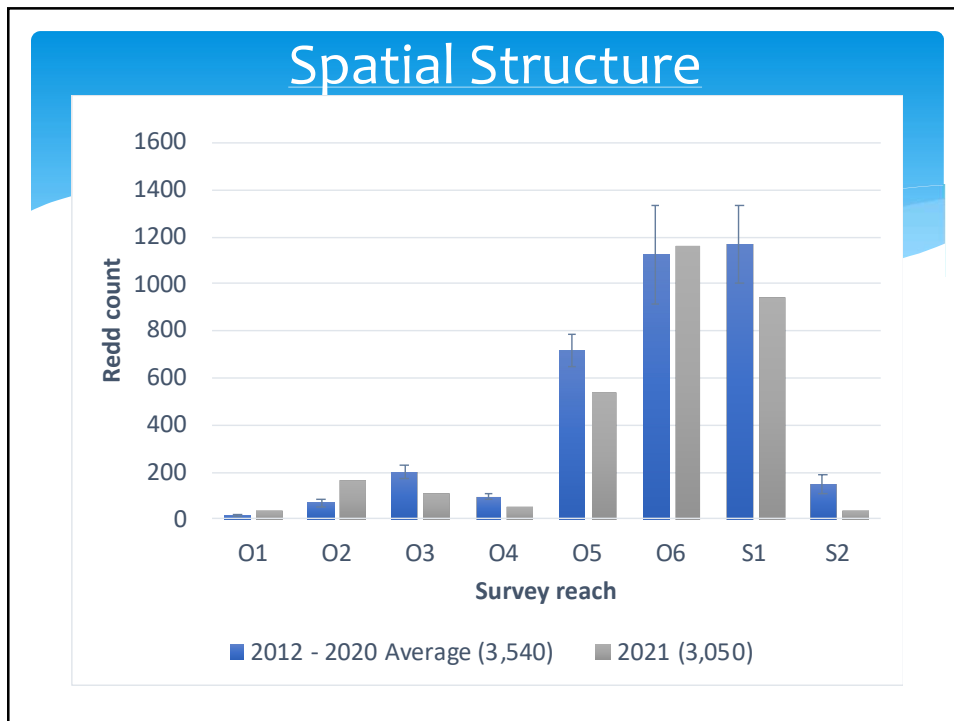
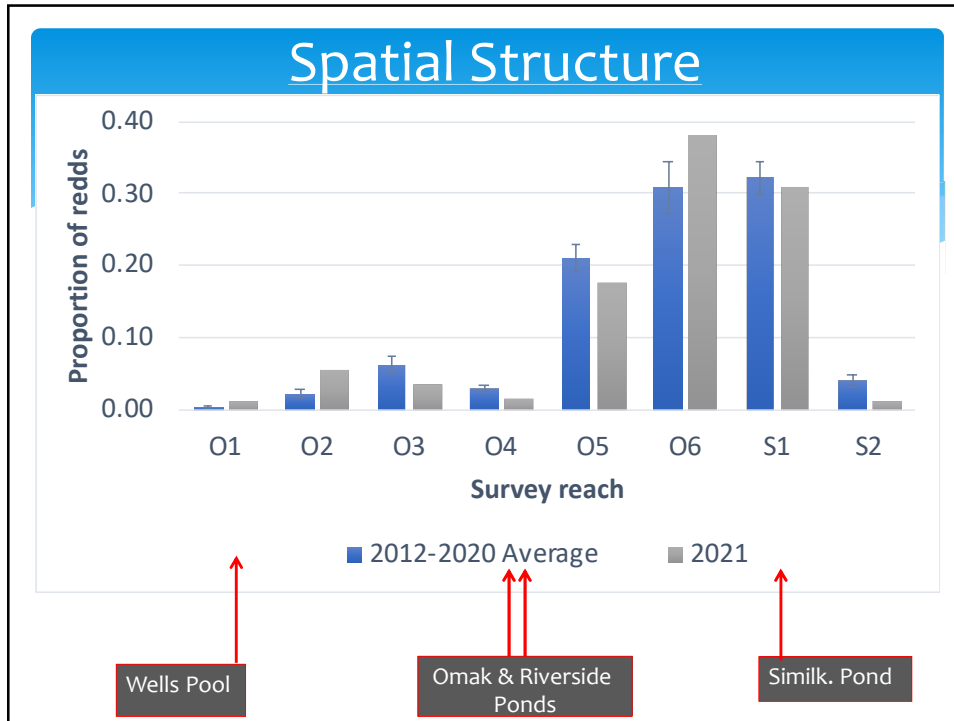
Overall Mean (1999-2015) = 2.4 R/S
 10 Yr Mean (2006-2015) = 2.4 R/S
 4 of 17 years < 1 R/S

Intrinsic Productivity

(Beverton-Holt modeled = 4.5)

BY1999-2015





Diversity

1. Genetic

- Structure of upper Columbia River summer Chinook and evaluate the effects of hatchery supplementation programs
 - * Objective
 - Determine if genetic diversity, population structure and effective population size have changed in natural spawning populations as a result of the conservation and hatchery programs
 - Hatchery and wild groups from upper Columbia basin
 - Okanogan, Methow, Chelan Falls, Entiat, Wenatchee and Hanford Reach
 - Make comparisons between pre-supplementation (1993) to post-supplementation (2008)

2021 Evaluation

- * Assess the genetic effects of the hatchery program on natural populations
- * BY17 and BY18 Analyses
 - * natural- and hatchery-origin baseline samples (1982-1994)
 - * natural- and hatchery-origin contemporary samples (2017-2018)
- * Genotype samples from upper Columbia programs with appropriate SNP panel
 - * Okanogan included 100 baseline samples (n=50 each from Similkameen and Okanogan) genotyped
 - * Contemporary samples genotyped from CRITFC PBT analyses

2021 Results

- * Measures of genetic diversity showed little differentiation among populations for summer Chinook
 - * Hatchery programs not led to decrease in genetic diversity
 - * F_{ST} was higher among baseline than contemporary collections
 - * Suggests genetic drift and homogenization among stock has occurred over time
 - * Pairwise comparisons of F_{ST} statistically non-significant both for baseline and contemporary collections
 - * Similar to previous evaluations, appears to be little evidence for neutral genetic divergence between contemporary hatchery programs in the upper Columbia watershed and baseline samples collected in the late 1980's and early 1990's

2021 Results

- * Limitations
 - * Not able to evaluate potential differentiation contemporary hatchery and natural origin individuals due to lack of data on individual origin
 - * Not able to evaluate potential shifts in adaptive genetic diversity using genetic techniques
 - * possible for adaptive genetic diversity (i.e., run-timing, age at maturity) to change in response to selection (i.e. domestication) while neutral genetic diversity remains the same
 - * Phenotypic metrics can serve as proxy for adaptive genetic variation

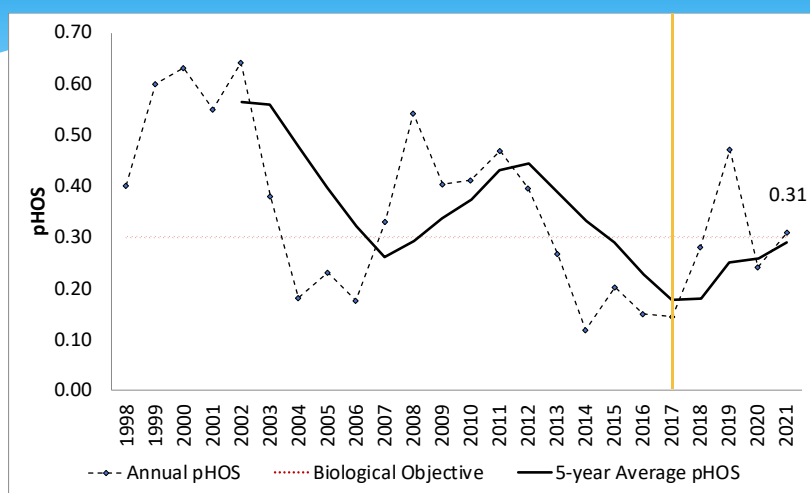
Diversity

2. Phenotypic (morphology and life history traits)

- * Adult run timing
- * Spawn timing
- * Age structure
- * Morphometrics (length, fecundity, others)
- * Juvenile rearing strategies
 - * Natural yearlings?
 - * Transient rearing
 - * True subyearling migrants

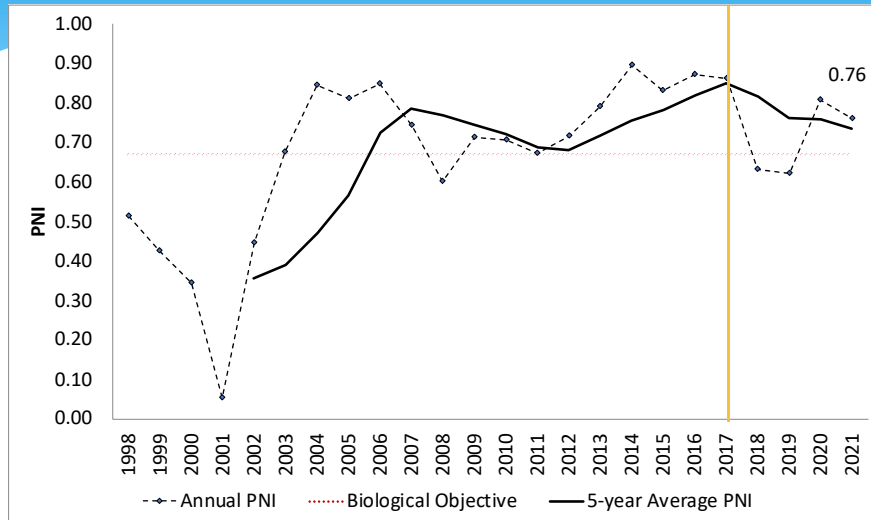
Diversity

3. Risk factors (spawner composition; pHOS)



Diversity

Risk factors (spawner composition; PNI)



Conclusions

- Abundance: below the objective for total escapement and natural origin spawners and trending down
- Productivity: a bit lower than our EDT assumptions
- Spatial Structure: see a redistribution of upper basin between S1 and O6 but not unusual, increase in the O2 reach below the Malott bridge
- Diversity: Last year we saw pHOS levels below the objective, but in 2021 the level was above the .30 objective (5-year avg. has gone up). PNI has gone down a bit but still above objective (5-year avg. starting to come down)

Conclusions

- Diversity: Results from the 2021 Upper Columbia region wide genetic evaluations showed that measures of genetic diversity had little differentiation among summer Chinook populations
 - Suggests that hatchery programs have not led to decrease in genetic diversity
 - Similar to previous evaluations
 - Management strategies in selective harvest and broodstock collection have contributed to this lack of neutral genetic change