Precocious males and genetic resources in coho salmon: what if we remove the jacks?

Photo by Chris Huss
Background

• Most coho in WA spawn at 3 years.
  – Jacks spawn at 2 years, providing gene flow among years

• Divergence among geographic populations >
  divergence among years within sites
  – Populations can generally be described even without
    temporal sampling

• “...If hatcheries exclude jacks from spawning, they are
  effectively propagating three independent
  populations...”

USFWS hatcheries on the Olympic Peninsula

Makah 1981

Quinault 1968

Quilcene 1911
Quilcene NFH

• Propagating coho for ~100 years
• Earliest returning fish used for broodstock
• Jacks excluded from broodstock prior to 1992

Photo credit: Ron Wong
Quilcene NFH

Three different run years have three different return times
Coho salmon microsatellite baseline

Divergence among broodlines at Quilcene NFH

Relative frequency

$F_{ST}$
Genetic diversity in coho salmon from Puget Sound/Strait of Georgia ESU
Genetic diversity in Quilcene NFH coho salmon
individuals
USFWS hatcheries on the Olympic Peninsula

Makah 1981

Quinault 1968

Quilcene 1911
Temporal structure > geographic structure for Quinault and Makah NFH
Summary

• Hatchery populations which excluded jacks exhibit
  – Temporal structure based on divergence among broodlines
  – Loss of genetic variation (lower $N_e$/increased genetic drift)

• Loss of variation is likely due to many interacting factors, but increased temporal structure is probably mostly due to exclusion of jacks.

• Precocious males provide a mechanism through which coho salmon populations can increase their standing genetic variation, and insure against the loss of genetic resources due to catastrophic habitat loss.
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Disclaimer

The findings and conclusions presented here are those of the author and do not necessarily represent the views of the United States Fish and Wildlife Service.