

Impacts of managed gene flow on disease resistance in hatchery Chinook salmon

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Abstract:

Incorporating wild-origin individuals into hatchery broodstock has been shown to reduce genetic divergence of hatchery populations from their natural source populations. Such managed gene flow – or “integration” - may reduce potential genetic risks of hatchery rearing to wild populations. However, the effects of managed gene flow on disease resistance in hatchery individuals is unknown. Strict disease management practices may limit exposure of hatchery fish to pathogens thus making them more susceptible to disease when released. Additionally, hatchery populations are typically smaller than wild populations, and the reduced genetic diversity may limit the ability of hatchery fish to respond to selection following disease exposure. Alternatively, high rearing densities found in hatcheries could possibly increase exposure and resistance to disease. Disease resistance may also increase in small hatchery populations through genetic drift. Here we use genomic data from segregated and integrated hatchery lines of Chinook salmon in Washington State to 1) identify genetic markers associated with traits linked to disease resistance, and 2) assess the effectiveness of two different hatchery strategies in mitigating disease risk in hatchery individuals. We challenged 1,125 juvenile Chinook salmon from integrated and segregated lines with *Vibrio anguillarum* and measured mortality for 14 days. DNA from challenged individuals were sequenced using RADseq, and genomic data was used to identify genetic markers associated with traits linked to disease resistance and determine whether lines had diverged at these loci. This study will help inform best management practices for disease mitigation in hatcheries, as well as provide insight into the genetic mechanisms for disease resistance in at-risk salmon populations.