Title: Statewide Washington steelhead SNP baseline development

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Abstract:

Many different genetic resources of *Oncorhynchus mykiss* are found in Washington State. As stewards of these resources, one of our responsibilities is to characterize these genetic resources, including establishing baseline collections, evaluating relationships among collections, and describing standing genetic diversity. This kind of work has been ongoing since the days of allozyme loci, and the work we will present is, in part, a continuation of those efforts, updated with single nucleotide polymorphism (SNP) markers. In this presentation, we will describe the current understanding of the full suite of genetic lineages of *O. mykiss* found in Washington State, the spatial extent of our collections to date, with concomitant data gaps, the genetic relationships among our baseline collections, descriptions of the genetic diversity, describe some interesting and unexpected results, and discuss the ongoing efforts to fill in significant data gaps. Ultimately, our goal is to provide a baseline of use to many different management applications, including monitoring and evaluation of hatchery programs or genetic stock identification, and of use to researchers interested in studying particular populations or groups of populations.