



State of Washington
Department of Fish and Wildlife

Mailing Address: 600 Capitol Way N, Olympia WA 98501-1091, (360) 902-2200, TDD (360) 902-2207
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From: Maureen P. Small PhD, WDFW Molecular Genetics Laboratory

Comments on proposal# 200751100 - DNA typing to identify native inland *Oncorhynchus mykiss*, Thorgaard, Nordquist and McMahon, Washington State University

I found this proposal highly innovative and timely. Developing a DNA marker that distinguishes inland from coastal *O. mykiss* will be a valuable tool for management on several levels. At WDFW we seek to protect and foster native biodiversity by identifying native diversity in all the species we manage. Non-native, coastal-origin hatchery *O. mykiss* have been widely planted throughout the state for over 100 years. In our microsatellite DNA study in the Spokane drainage (Small et al. 2007) we found that any tributary where hatchery fish have been planted or where there were no barriers to hatchery fish moving through tributaries, genetic evidence suggested that hatchery fish had interbred with native fish. We would like to collaborate with Dr. Thorgaard's laboratory by sharing tissue samples from some collections in this study to test the efficacy of their markers under development. Our collections range from pure native *O. mykiss*, to varying degrees of introgression, as well as collections of all coastal-origin hatchery *O. mykiss* planted in Washington State.

These markers will provide all managers of inland *O. mykiss* in the Columbia drainage with the ability to screen their populations for hatchery introgression. This will save money and effort for all inland fish managers since fish populations under their jurisdiction could be screened to determine if they are native fish, introgressed by hatchery fish, or are populations of naturalized hatchery fish, allowing managers to set priorities for protecting native diversity.

At WDFW Molecular Genetics Laboratory we are developing SNP technology that we currently use for Chinook and chum salmon. Once developed, SNPs are an inexpensive technology that can be applied to high-throughput that we use at our lab. Currently, for *O. mykiss* we use microsatellite DNA. A SNP that distinguishes inland and coastal *O. mykiss* could easily be added to our suite of microsatellites, giving us the ability to routinely screen for hatchery introgression as part of our population genetics studies and *O. mykiss* baseline development in the Columbia River.

Small, M. P., J. G. McLellan, J. L. Loxterman, J. Von Bargen, A. Frye, and C. Bowman (2007). Fine-scale population structure of rainbow trout (*Oncorhynchus mykiss*) in the Spokane River drainage in relation to hatchery stocking and barriers. Transactions of the American Fisheries Society 136:301-317.



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