DNA-based stock-of-origin assignment of Chinook salmon (*Oncorhynchus tshawytscha*) smolts outmigrating past Chandler trap (Yakima River) for years 2004-2008: computational error, methodological concerns, and outmigration trends

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Since 2001, the WDFW Molecular Genetics Laboratory has been genetically assigning to stock Chinook salmon smolts that pass the Chandler Trap. Beginning 2004, the lab has used a standardized set of genetic markers (GAPS markers) for both the baseline and smolt genetic fingerprints, enabling year-to-year comparisons of results. In addition, since 2004 a host of analytical tools have been developed to evaluate the efficacy of the baseline data sets and to enhance statistical confidence of both mixture analyses and individual assignments. In this talk we will introduce some of these tools, evaluate the baseline data used for assigning Chandler smolts to stock, provide new estimates of stock proportions based on five years of data (2004-2008), and compare the stock composition of the outmigrating Chinook smolts in the Yakima River system from 2004-2008.