**Warheit, Kenneth – Washington Department of Fish and Wildlife**

**Presentation Title: Genome-wide Association Study (GWAS) of (1) Survival of Acoustically Tagged and (2) *Nanophyetus salmincola* Infected Steelhead Smolts from South/Central Puget Sound, Washington**

Abstract for the 2018 Pacific Coast Steelhead Management Meeting

Kenneth I. Warheit1, Megan E. Moore2, Barry A. Berejikian2

1 Washington Department of Fish and Wildlife, Olympia, WA; - kenneth.warheit@dfw.wa.gov

2 National Marine Fisheries Services, NOAA, Manchester, WA

In this study we tested the hypothesis that there is a genomic association with (1) survival of outmigrating steelhead smolts as they transit from either the Green or Nisqually rivers through Puget Sound, Washington to the Pacific Ocean, or (2) *Nanophyetus* *salmincola* (trematode parasite) infestation in steelhead smolts captured in the freshwater, estuary, or offshore areas in the Green or Nisqually rivers. We used RADseq data (8909 SNPs) and mixed linear model procedures in the program *TASSEL* to test for associations between genotypes and survival-index or *Nanophyetus* counts. Genotypes at a large linkage block along chromosome 5 (Omy05) had the strongest association with both survival and *Nanophyetus* infestation, although this association was dependent of source location, and statistical power was weak. In California, loci located on Omy05 have been associated with migratory behavior in *Oncorhynchus mykiss* (residence versus migratory behaviors). We do not know if the Omy05 genotypes in Puget Sound are also associated with juvenile migration life histories. Fish used in this study were smolts, all of whom we assumed would eventually migrate to the ocean if they had not died in route (acoustic-survival) or euthanized for the *Nanophyetus* study. In addition to Omy05, loci that were significantly associated with steelhead survival included two circadian clock genes and one locus identified as part of the immune system. We concluded that how far a naïve steelhead smolt can migrate through Puget Sound as or how many *Nanophyetus* that smolt contracts is dependent of the smolt’s genome. However, this study did not clarify the relative importance of the genome, compared with environmental factors, or how the genome interacts with these environmental factors to affect survival or prevalence of *Nanophyetus*. Adding genome-association and functional genomic components to any experimental study that relates smolt performance with the prevalence of *Nanophyetus* will contribute to understanding the relationship of the genome to smolt survival.