

Distribution of *Ceratomyxa shasta* genotypes in the Pacific Northwest

¹Matthew E. T. Stinson*, ²Stephen D. Atkinson, and ¹Jerri L. Bartholomew

¹Department of Microbiology, Oregon State University, Corvallis, Oregon, USA, stinsonm@onid.orst.edu

²School of Chemistry & Molecular Biosciences, The University of Queensland, St Lucia, QLD 4072, Australia

The myxozoan parasite *Ceratomyxa shasta* is endemic to the Pacific Northwest and causes various degrees of mortality among local salmonid stocks. Recently, a region within the ribosomal DNA, the internal transcribed spacer region-1, was found to have multiple polymorphic loci correlating to four distinct genotypes (I, II, III, and 0) based on a trinucleotide repeat. These different genotypes in turn have been shown to have host-specific virulence and this finding has prompted us to re-evaluate this parasite in other positive drainages. In several rivers dams are proposed to be removed, or upgraded so that fish can migrate beyond the dams, creating the potential for introducing previously isolated genotypes into new habitat. Sentinel exposures in the Willamette and the Deschutes Rivers of the Columbia Basin with a variety of native trout and salmon species were used to assess the effects of these specific genotypes. Analysis of parasite DNA from water samples and returning adult spawners provided additional data from these rivers and other locations in the Pacific Northwest. Data analyzed thus far from the Willamette and Deschutes Rivers supports the previously documented parasite-host interactions. This information can help fisheries managers with stocking strategies, increases our knowledge of the effects of *C. shasta* on different salmonids, including habitat and seasonal effects, and also helps perceive the potential effects of dam removal.