Comparison of 18s and ITS-1 rDNA of *Myxobolus cerebralis*, the causative parasite of the Whirling Disease

N. Lodh¹, L. Stevens¹, B. Kerans²

¹Biology, University of Vermont, 109 Carrigan Drive, 120A MLS, Burlington, VT 05405; <u>nlodh@uvm.edu</u>

¹Biology, University of Vermont, 109 Carrigan Drive, 120A MLS, Burlington, VT 05405; email: <u>lori.stevens@uvm.edu</u>

²Department of Ecology, 310 Lewis Hall, Montana State University, Bozeman, MT 59717; email: <u>bkerans@montana.edu</u>

Host-parasite interactions in the natural landscape can be understood by studying the genetic structure of both the parasite and the host. The causative agent of whirling disease Myxobolus cerebralis (Myxozoa: Myxosporea) is native to Eurasia but has spread to more than 25 states of the USA. *M. cerebralis* completes two separate developmental pathways involving two hosts, a salmonid fish (several species) and the aquatic oligochaete, *Tubifex tubifex*. The small amount of data available to date suggest that M. cerebralis has little genetic variability and therefore variation in the disease incidence among wild fish populations is not related to genetic variation in the parasite. We examined the genetic variability of parasites from worms collected in the Madison River, Montana, to investigate the genetic variability of a single parasite population. We also compared genetic variability among parasites from with parasites collected in other parts of North America and Europe. Our genetic analysis involved cloning and sequencing of 18S ribosomal DNA and internal transcribed spacer-1 (ITS-1). Five oligochaetes were examined for 18S and five for ITS-1, only one individual was examined for both genes and one to five ITS-1 clones were examined from each individual. Our genetic analysis confirmed no myxozoan parasite other than *M. cerebralis*. We found two different 18S rDNA haplotypes from among the five individuals examined and both intra and inter individual genetic variation for ITS-1, which showed 16 different haplotypes from among 20 clones. Comparison of our sequences with those from other studies reveals M. *cerebralis* from Montana is similar with the parasite from Alaska, Oregon (Lostine +), California and Virginia in the USA and from Munich, Germany based on 18S, whereas parasite sequences from West Virginia are very different. The high haplotype diversity of ITS-1 and uniqueness of these haplotypes illustrate that *M. cerebralis* is more variable that previously thought.