Genetic diversity of *Saprolegnia* isolated from salmonid fish in Canada, Chile, Japan, Norway and Scotland

*Saprolegnia* species are oomycetes (watermolds), which are fungal-like filamentous eukaryotes, that are closely related to chromophyte algae (Baldauf 2003), and are capable of infecting multiple hosts (Sarowar et al. 2013). The amplified fragment length polymorphism (AFLP) and sequence data of the internal transcribed spacer (ITS) methods were used to study the genetic diversity and relationships of *Saprolegnia* spp. collection from Canada, Chile, Japan, Norway and Scotland. AFLP analysis of 37 *Saprolegnia* spp. isolates using six primer combinations gave a total of 163 clear polymorphic bands.

Cluster analysis using genetic similarity divided the isolates into three main groups suggesting that there are genetic relationships among the isolates. ITS analyses of 48 *Saprolegnia* sequences resulted in five well defined clades. Principal Coordinate analysis (PCO) confirmed the pattern of the cluster analyses. Analysis of molecular variance (AMOVA) revealed greater variation within countries (91.01%) than among countries (8.99%).

We were able to distinguish the *Saprolegnia* isolates according to their species, ability to produce oogonia with and without long spines on the cysts and to their ability to cause mortality or not in salmonids. AFLP markers and ITS sequencing data obtained in the study, were found to be an efficient tool to characterize the genetic diversity and relationships of *Saprolegnia* spp. Comparison of AFLP analysis and ITS sequence data using the Mantel test showed a very high and significant correlation ($r^2 = 0.8317$). Further studies on *Saprolegnia* spp. using genome sequencing, are recommended in order to identify genes responsible for disease development and to study the taxonomy of *Saprolegnia* species.

**References**
