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Genetic investigations on two commercially important strains of Arctic charr (*Salvelinus alpinus*), the Tree River and Nauyuk Lake

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Arctic charr (*Salvelinus alpinus*) have the most northerly distribution of all salmonid species and are an inherent part of northern culture. As a food product, they are valued for their mild, orange colored flesh, attractive appearance and high concentration of omega-three fatty acids. As a subject for genomic research, they represent one of three principle groups in the Family Salmonidae and as such, play an essential role in the comparative analysis of Atlantic salmon (*Salmo salar*) and rainbow trout (*Oncorhynchus mykiss*) genomes. Our program is focused on two commercial strains of Arctic charr, the Tree River and the Nauyuk Lake. Microsatellite markers are being used to monitor and maintain the genetic diversity of inbred lines and avoid inbreeding depression. High-density linkage maps are being constructed using AFLP and microsatellite markers. These maps will include QTLs for commercially important traits such as growth, sex, disease resistance, upper temperature tolerance and flesh color. Genetic markers associated with these traits are being developed for use in a marker-assisted breeding program. In addition, fosmid libraries have been constructed and are being screened for markers that are associated with phenotypes as well as genes of known protein function such as metallothionein, growth hormone and lysozyme. Selected fosmids are being sequenced in order to further characterize the regions that surround important traits or genes. These fosmids can also be used as probes to perform FISH analysis and determine the physical location of these regions in the Arctic charr genome. This information can be compared to the physical maps for rainbow trout and Atlantic salmon.