



Gorgan University of Agricultural
Sciences and Natural Resources

J. of Utilization and Cultivation of Aquatics, Vol. 9(2), 2020

<http://japu.gau.ac.ir>

DOI: 10.22069/japu.2020.17399.1526

Investigation of quantitative trait loci (QTLs) variations for growth-related traits in farmed rainbow trout (*Oncorhynchus mykiss*)

***S. Nazari¹ and H. Paknejad²**

¹Assistant Prof., Shahid Motahary Cold-Water Fishes Genetic and Breeding Research Center, Iranian Fisheries Sciences Research Institute, Agricultural Research, Education and Extension Organization (AREEO), Yasouj, Iran,

²Associate Prof., Faculty of Fisheries and Environmental Sciences, Gorgan University of Agricultural Sciences and Natural Resources, Gorgan, Iran

Received: 12.01.2019; Accepted: 02.16.2020

Abstract

The application of genomic technologies of molecular markers specially identification of single nucleotide polymorphism (SNP) and quantitative trait loci (QTLs) towards the genetic improvement of rainbow trout aquaculture is expected to facilitate selective breeding and development of strains of rainbow trout via breeding programs. Thirty male and female broodstock of rainbow trout (n=30) for generating full sibling collected in cold-water fishes Genetic and Breeding Research Center. Then, juveniles were raised at the ponds until 6 months of post-hatching. Genome extracted based on standard method and these individuals randomly selected for molecular analysis. Fin clips were cut and specimens were kept at -20 °C until use. Four specific primers were used for rainbow trout and all the four QTL loci screened in this study were successfully amplified in all families. Statistical analyses including linkage disequilibrium (LD), association between genotypes and two quantitative traits including body weight (BW) and total length (TL) were performed using MapChart 2.1, GDA 1.1. General Linear Model (GLM) was performed with software SPSS 21.0. The results demonstrated that mean observed heterozygosity (H_o) and expected heterozygosity (H_E) varied between 0.354 to 0.699 for locus OMM5140 and 0.568 to 0.836 for locus OMM1268, respectively. No significant epistatic interactions were identified between QTL markers. Proportion of phenotypic variation explained by each QTL (PV) for body weight at age of 30 and 180 were 18.48 and 31.24, respectively. Hardy-Weinberg departure was observed for most loci from all farms and were disequilibrium ($P < 0.05$). The four QTL loci variation in rainbow trout is important to gain a better understanding of the genetics of production traits and for transferring genetic information and improved selective breeding program to farms in Iran.

Keywords: Marker Assisted Selection, QTL, Rainbow Trout, Selection