

Genome-wide association analysis for body weight identifies candidate genes related to development and metabolism in rainbow trout (*Oncorhynchus mykiss*)

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Growth is one of the most important traits from both a physiological and economic perspective in aquaculture species. Thus, identifying the genomic regions and genes underpinning genetic variation for this trait is of particular interest in several fish species, including rainbow trout. In this work, we perform a genome-wide association study (GWAS) to identify the genomic regions associated with body weight at tagging (BWT) and at 18 months (BW18M) using a dense SNP panel (57 k) and 4596 genotyped rainbow trout from 105 full-sib families belonging to a Chilean breeding population. Analysis was performed by means of single-step GBLUP approach. Genetic variance explained by 20 adjacent SNP windows across the whole genome is reported. To further explore candidate genes, we focused on windows that explained the highest proportion of genetic variance in the top 10 chromosomes for each trait. The main window from the top 10 chromosomes was explored by BLAST using the first and last SNP position of each window to determine the target nucleotide sequence. As expected, the percentage of genetic variance explained by windows was relatively low, due to the polygenic nature of body weight. The most important genomic region for BWT and BW18M were located on chromosomes 15 and 24 and they explained 2.14% and 3.02% of the genetic variance for each trait, respectively. Candidate genes including several growth factors, genes involved in development of skeletal muscle and bone tissue and nutrient metabolism were identified within the associated regions for both traits BWT and BW18M. These results indicate that body weight is polygenic in nature in rainbow trout, with the most important loci explaining as much as 3% of the genetic variance for the trait. The genes identified here represent good candidates for further functional validation to uncover biological mechanisms underlying variation for growth in

rainbow trout.