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GENOME-WIDE ASSOCIATION STUDY OF HYPOXIA STRESS TOLERANCE IN RAINBOW TROUT

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Introduction

Hypoxia is one of the most critical threats for future aquaculture sector due to the global climate changes. Global warming decreases dissolved oxygen leading to decline of health and welfare of cultured aquatic organisms and has also deleterious impacts on growth, reproduction, immunity and other energy demanding activities (Farrel and Richards, 2009; Gallage et al., 2016). Although many studies have revealed that there is an adaption strategy in low oxygen tolerance for fish species (Zhu et al., 2013), Genome-Wide Association Studies (GWAS) of hypoxia stress tolerance in aquaculture species are rare (Li et al., 2017; Wang et al., 2017).

Rainbow trout (*Oncorhynchus mykiss*) is one of the most commonly farmed salmonid species that requires high level of dissolved oxygen in comparison to other fish species. However, GWAS of hypoxia stress tolerance in rainbow trout is still missing. Therefore, objectives of this study were to estimate heritability and to detect quantitative trait loci (QTL) associated with hypoxia tolerance.

Materials and methods

The experimental stock was established from 190 dams and 98 sires of a commercial selected diploid population of Milin Nevez breeding company (Bretagne Truite Group, France). The stock was reared under commercial conditions until the experiment. Fish were then transported to the ANSES-SYSAAF Fortior Genetics platform and acclimatized before acute hypoxia challenge test. 1,320 individuals were P.I.T. tagged and fin-clipped for later DNA extraction and genotyping. The challenge to hypoxia was sub-divided into seven batches (one per day) and in each batch a random sample of fish (app 188 fish per batch) was challenged. At the beginning of each batch the initial oxygen level was recorded. Gradual decline of oxygen was conducted by bubbling nitrogen. When fish lost their equilibrium, they were removed from the tank, identified (PIT-tag reading), weighed (mean weight 50.8 g) and euthanized in Eugenol. The corresponding time and oxygenation level were recorded. The challenge ended when the last fish lost its equilibrium and was removed of the tank.

All individuals were genotyped for 57,501 SNPs with the Axiom™ Trout Genotyping array at the INRAE genotyping Platform Gentyane. After quality controls and imputation of missing genotypes approximately 28,875 SNPs and 1,297 individuals were used in the statistical analysis. Tolerance to hypoxia was analysed as time to loss equilibrium (TLE) with the day of trial as a fixed effect in the final model. Using BLUPF90 package (Misztal et al., 2014) GBLUP analysis was performed to estimate heritability of the trait with AIREMLF90 program and to detect QTL with POSTGSF90 program (Aguilar et al., 2014).

Results

Genomic heritability of hypoxia tolerance was moderate (0.37 ± 0.04). We also identified a few QTLs with the most significant one on chromosome 31 with possible candidate genes in the region spanning approximately from 20 Mb to 23 Mb on the Arlee genome reference assembly (USDA_OmykA_1.1.).

Discussion and conclusion

Preliminary results revealed that the tolerance to hypoxia is a heritable trait. In addition, a significant QTL was identified on chromosome 31 with several putative QTLs detected on other chromosomes. However, further statistical analyses including more dense genotypes and Bayesian approach need to be conducted to precise our preliminary results.

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