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RAINBOW TROUT RESISTANCE TO *Flavobacterium psychrophilum*: A GENOME WIDE ASSOCIATION STUDY IN A FRENCH POPULATION AFTER A NATURAL DISEASE OUTBREAK

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Health management is a major issue for sustainable aquaculture. *Flavobacterium psychrophilum* (Fp), the causative agent of bacterial cold water disease (BCWD) is responsible of important economic losses in rainbow trout farming. Resistance to the disease is heritable and several Quantitative Trait Loci (QTL) with moderate effects have been detected, indicating that selective breeding may be efficient. However, in most studies, the resistance to Fp was assessed after experimental infectious challenges using injection as route of infection, which is not representative of the natural infection as it bypasses external barriers (e.g. skin, mucus) likely to play a protective role. In this study, we aimed at describing the genetic architecture of the resistance after a field outbreak in a French trout population, using a medium-throughput genotyping array (Affymetrix OD Axiom 57K SNP array).

A natural outbreak of BCWD occurred in a farm from *Les Aquaculteurs Bretons*, a French breeding company in a cohort of 2,000 fish derived from 10 factorial mating design (69 dams, 97 sires in total). Dead fish were removed daily. At day 95 surviving fish were euthanized. All fish were stored for further genotyping. The presence of Fp in dead fish was checked at different time points until day 60, when mortality reached a plateau (30%) and Fp was no longer detected. Fish that died after day 60 were thus considered as resistant. Resistance was assessed as STATUS, a binary trait (dead/alive-resistant), and as time to death (TTD), the number of days between the onset of the disease and the day fish succumbed to the disease (value of 61 assigned for resistant fish). Using microsatellite genotyping, 1,733 fish were correctly assigned to a single mating pair. Those fish were used to estimate pedigree-based heritability for the two traits. For the genome wide association study, 720 individuals were sampled (290 resistant and 430 dead fish) and genotyped with the 57K SNP array. After genotype quality control, 706 fish genotyped for 30,030 validated SNP could be used. The association analysis was carried out using BLUPF90 software on TTD and STATUS separately.

Heritability was 0.33 for TTD and 0.27 for STATUS. We detected seven low-effect and two moderate-effect QTL and several relevant candidate genes involved in the inflammatory immune response were located inside those QTL. Our study confirms the main features of the genetic architecture of resistance to Fp (no major QTL, several QTL with moderate effects) and that implementing genomic selection should improve resistance. Moreover, some QTL were the same as the ones detected previously in other trout populations infected experimentally with different bacterial isolates, confirming that they may drive a core set of resistance mechanisms.

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