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UNDERSTANDING MOLECULAR MECHANISMS OF DISEASE RESISTANCE IN CONTRASTED RAINBOW TROUT ISOGENIC LINES

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Infectious diseases represent a major threat for the sustainable development of fish farming. It is therefore important to understand the basis of fish natural resistance to infections to help genetic selection and to develop new approaches against infectious diseases. The objective of this study was to achieve a detailed functional annotation analysis of two rainbow trout isogenic lines chosen based on their resistance / susceptibility status to two pathogens, a bacterium (*Flavobacterium psychrophilum*, Fp) and a virus (Viral Hemorrhagic Septicemia Virus, VHSV). The first isogenic line is resistant to Fp infection by injection and susceptible to VHSV infection by immersion; the second is resistant to VHSV and susceptible to Fp. Experimental disease challenges were performed by intramuscular injection for standardisation of the stimulation. Two days post-infection, head kidney of 32 fish (2 lines; 4 experimental conditions: control Fp, injected Fp, control VHSV and injected VHSV; 4 fish per line and per condition) were collected for constructing RNAseq and ATACseq libraries. The 32 RNA-Seq and 32 ATACseq libraries were mapped on the Ensembl rainbow trout genome assembly (strain Arlee) and count tables generated using bioinformatics pipeline nf-core/rnaseq and nf-core/atacseq respectively. Differential gene expression analysis revealed divergent transcriptional responses between the resistant and susceptible lines. In particular, after VHSV infection, higher induction rates of interferon stimulatory genes were detected in the resistant line. The integration between RNAseq and ATACseq data will lead to a better understanding of molecular mechanisms involved in the contrasted response of the two isogenic lines to both pathogens.