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Transcriptomic and proteomic analysis of splenic immune mechanisms of rainbow trout (*Oncorhynchus mykiss*) infected by *Aeromonas salmonicida* subsp. *salmonicida*

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Furunculosis caused by *Aeromonas salmonicida* subsp. *salmonicida* is an epidemic disease among salmonids including rainbow trout (*Oncorhynchus mykiss*). However, the immune mechanisms that are elicited in rainbow trout against the invasion of *A. salmonicida* are not yet fully understood. In this study, we examined the spleen to investigate the immune response of rainbow trout at 3d post infection by *A. salmonicida* at the transcriptome and proteome levels by using Illumina-seq and iTRAQ methods, respectively. A total of 1036 genes and 133 proteins were found to undergo differential expression during the immune response of the spleen against *A. salmonicida* infection. Gene ontology and KEGG analysis were conducted among the differentially expressed genes and proteins revealing that immune system process and response to stimulus were the top two biological processes and immune system, signaling molecules and interaction and immune diseases were the differential pathways activated. Correlation analysis of transcriptomic and proteomic results showed 17 proteins (11 up-regulated and 6 down-regulated) having consistent expression at RNA and protein levels. Moreover, protein-protein interaction analysis showed that diseases, proteasome, aminoacyl-tRNA biosynthesis and nucleotide metabolism were the main interactions among the consistently expressed proteins. Consequently, these up-regulated proteins namely ferritin, CD209, IL13Ra1, VDAC2, GIMAP7, PSMA1 and two ANXA11s could be considered as potential biomarkers for rainbow trout immune responses.

Biography

Aihua Li is currently a Professor in Institute of Hydrobiology, Chinese Academy of Sciences, China.

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