IMMUNE RESPONSE OF GILTHEAD SEABREAM (*Sparus aurata*) AFTER EXPERIMENTAL INFECTION WITH LYMPHOCYSTIS DISEASE VIRUS (LCDV-SA)

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ABSTRACT

Lymphocystis disease (LCD) is caused by the lymphocystis disease virus (LCDV), a double-stranded DNA virus belonging to the genus *Lymphocystivirus* (family *Iridoviridae*), affecting more than 150 fish species from both marine and freshwater environments. A few studies have been focused on the immune defensive mechanisms of fish against LCDV, but only one was conducted during a natural LCD outbreak in gilthead seabream, which is one of the most important cultured fish species in the Mediterranean and the European Atlantic coasts. The aim of this study was the analysis of 23 genes related to the immune response in gilthead seabream specimens after experimental infection with LCDV-Sa using real-time PCR (qRT-PCR) in samples of head kidney and intestine at 1, 3, and 8 dpi. To study the progression of LCDV-Sa infection in gilthead seabreams, the number of viral DNA copies and the expression of *mcp* were determined in samples of caudal fin, head kidney and intestine. LCDV-Sa was detected by qPCR in all the samples from inoculated fish analysed, whereas no amplification was obtained in samples from the control group. Regarding the gene expression following LCDV-Sa infection, a total of 22 of the 23 genes studied were differentially expressed in head kidney or intestine samples at some time points analysed. The *pkr* was the only gene showing no differential expression compared to control samples through the entire experiment. Different gene expression profiles were obtained between the organs studied, detecting 18 differentially expressed genes (DEGs) in head kidney samples, four of them exclusively up- or down-regulated (*nccrp1*, *il10*, *mhcII*, and *tnfα* genes), and 5 genes with a significant change in the expression tendency from 1 to 8 dpi (*irf3*, *isg15*, *il10*, *ck10*, and *c3*). In the intestine, 18 DEGs were also detected (14 shared with head kidney), being *mx1*, *casp1*, *ck3* and *tlr9* genes exclusively detected in these samples, and *mx1*, *mx3*, *irf9* and *ighm* differentially regulated over time. The results obtained allow us to understand which genes are essential for host-pathogen interactions and could be used as molecular markers for vaccine efficacy evaluation.

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KEYWORDS

Sparus aurata, LCDV-Sa, experimental infection, immune response, differentially expressed genes

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