

analysis of *Epinephelus coioides* in metamorphosis stages revealed that dissimilarity in distribution of the individuals in 12dph, 18dph and 50dph. Analysis of immune gene (TLR-3, IL-1 β , IFN- α , IFN- γ , NF- κ B and Mx gene) showed the fish were in pathogen-free environment. The Proteobacteria in intestine microbiome is most abundant microbes at each development stages. In the other hand, NNV-, GIV-, and Vibrio- infected fish exhibit different phylum composition of microbes. The relationship of pathogen and microbiome in grouper will be investigated in the future, which might be the solution for the grouper disease control.

Keywords: Grouper, intestinal microbiota, development stages, disease, 16S metagenomics

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O-136.

Identification of novel biomarkers associated with infection and chronic stress in Russian sturgeon

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Abstract

Acipenser spp (sturgeon) are non-teleost fish species of ecological and economic value due to their exquisite meat and caviar. During 20th century, overfishing and pollution have led to a drastic decline of its natural reserves and nowadays many species are listed as critically endangered. Sturgeon aquaculture is thus an important tool for conservation and restoration of sturgeon populations, representing also an activity with valuable socio-economic impact. *A. gueldenstaedtii* (Russian sturgeon), one of the most cultured sturgeon species worldwide, is successfully farmed in Uruguay. However, for achieving a sustainable development, sturgeon aquaculture has to deal with the adaptation of sturgeon to a warmer climate, since increased mortality rates and economic losses are observed during Uruguayan summer. Our previous work demonstrated that warm temperatures ($\geq 24^\circ\text{C}$) alter fish innate defences by a chronic stress-dependent mechanism. Unfortunately, molecular tools for monitoring chronic stress and innate defences are not commercially available for sturgeons. Therefore, identification of biomarkers associated with inflammation and/or chronic heat stress in sturgeon is crucial for improving sturgeon aquaculture. With this aim, we follow two different experimental approaches: i) analysis of sturgeon acute phase proteins as putative biomarkers of inflammation and ii) analysis by RNA sequencing of differentially expressed genes in sturgeons subjected to chronic heat stress and challenged with pathogenic bacteria. Firstly, we identified several putative acute phase proteins in Russian sturgeon: hepcidin, haptoglobin, hemopexin, transferrin, serum amyloid A protein (SAA) and serum amyloid P protein (SAP). Hepatic expression analysis of these proteins in bacteria-challenged sturgeons showed that SAA could be a good inflammation biomarker candidate. We also obtained specific antibodies against SAA and SAP and analysed their serum protein levels by ELISA or Western blot. We found that SAA, but no SAP levels were significantly increased in serum of bacteria-challenged sturgeons, suggesting that SAA is a positive acute phase protein in Russian sturgeon. However, neither SAA nor SAP showed to be good biomarkers of chronic heat stress. Analysis of differentially

expressed genes in liver and spleen of bacteria-infected sturgeons subjected to chronic heat stress are currently being undertaken by Illumina sequencing in order to identify novel inflammation and chronic stress biomarkers. This identification will open new possibilities for monitoring sturgeon health in farms, contributing to less economic impact from disease outbreaks and favouring aquaculture development.

Keywords: *Acipenser gueldenstaedtii*, infection and chronic-stress biomarkers

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O-137.

A lectin with LDL receptor domain suppress the replication of WSSV

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Abstract

In invertebrates, C-type lectins (CTLs) play important roles in innate immunity against pathogens. Previous studies have focused mainly on the functions of CRD of CTLs in immune recognition, activation, and regulation. Conversely, limited research has been conducted on the relationship of CTLs and low-density lipoprotein (LDL). In this work, a lectin with LDL receptor domain was identified in *Procambarus clarkii* and designated as CTL-R. CTL-R was widely distributed in all tested tissues, and it was induced expression after white spot syndrome virus (WSSV) challenge. The recombinant CTL-R enhanced the anti-virus action of crayfish, whereas the anti-virus action was inhibited after CTL-R knockdown. The expression level of AMPs were suppressed after CTL-R knockdown in crayfish. Furthermore, CTL-R protein induce the activity of dorsal. NF- κ B is associated with anti-virus by regulating the expression of AMPs. Therefore CTL-R plays a key role in immune response of WSSV by positive regulation the activity of dorsal.

Keywords: Lectin; White spot syndrome virus; NF- κ B; *Procambarus clarkii*; Innate immunity

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O-138.

A comparative study on intestinal immune cells in two elasmobranchs species

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Abstract

The immune system of fish is of great relevance as it provides information on the evolution of immunity in vertebrates. All sharks, skates and rays are cartilaginous fish and together form a group called the elasmobranchs.