P-001.

Molecular characterization of a new fish specific chemokine CXCL_F6 in large yellow croaker (*Larimichthys crocea*) and its role in inflammatory response

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Abstract
Chemokines are a superfamily of structurally related chemotactic cytokines exerting significant roles in regulating cell migration and activation. Currently, five subgroups of fish specific CXC chemokines, named CXCL_F1-CXCL_F5, have been identified in teleost fish. However, understanding of the functions of these fish specific CXC chemokines is still limited. Here, a new member of fish specific CXC chemokines, LcCXCL_F6, was cloned from large yellow croaker *Larimichthys crocea*. Its open reading frame (ORF) is 369 nucleotides long, encoding a peptide of 122 amino acids (aa). The deduced *Lc*CXCL_F6 protein contains a 19-aa signal peptide and a 103-aa mature polypeptide, which has four conserved cysteine residues (C28, C30, C56, and C72), as found in other known CXC chemokines. Phylogenetic analysis showed *Lc*CXCL_F6 formed a separate clade with sequences from other fish species, tentatively named CXCL_F6, distinct from the clades formed by fish CXCL_F1-5 and mammalian CXC chemokines. The *Lc*CXCL_F6 transcripts were constitutively expressed in all examined tissues and significantly up-regulated in the spleen and head kidney tissues by poly (I:C) and *Vibrio alginolyticus*. Its transcripts were also detected in primary head kidney leukocytes (HKLs), peripheral blood leucocytes (PBLs), and large yellow croaker head kidney (LYCK) cell line, and significantly up-regulated by poly(I:C), lipopolysaccharide (LPS), and peptidoglycan (PGN) in HKLs. Recombinant *Lc*CXCL_F6 protein (r*Lc*CXCL_F6) could not only chemotactically attract monocytes/macrophages and lymphocytes from PBLs, but also enhance NO release and expression of proinflammatory cytokines (TNF-α, IL-1β, and CXCL8) in monocytes/macrophages. These results indicate that *Lc*CXCL_F6 plays a role in mediating the inflammatory response.
keywords: CXC chemokine, CXCL_F6, Chemotaxis, Large yellow croaker (*Larimichthys crocea*), inflammatory response

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P-002.

Molecular markers associated with antigen presentation process in Atlantic salmon during outbreaks of *Piscirickettsia salmonis* at sea farming centers

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Abstract
Chile is one of the main producers of Atlantic salmon (*Salmo salar*) in the world, with a currently marine culture biomass close to 350,000 tons. This biomass suffers mortalities close to 3,500 tons per month, being the infectious diseases the second primary cause of this problem (19.6%). The major agent of this mortality is the bacteria *Piscirickettsia salmonis* (67.9% of cases). *P. salmonis* is an intracellular facultative pathogen that generates systemic infections evading the immune response of the host by infection of macrophages and avoiding the respiratory burst. To control this pathogen, Chilean aquaculture has used antibiotics, immunostimulants and vaccines. However, no strategy has given optimal results. In this context, more data of immunological parameters in field conditions are necessary for a more accurate characterization of the real state of the fish when is facing a *P. salmonis* infection. In this work, we have focused on quantifying molecular markers associated with the process of antigen presentation, which is crucial to achieve coordination between innate and adaptive immune response. For this, we evaluated the gene expression of interferon gamma (ifng), transforming growth factor beta (tgfb) and interleukins (il-10, il-12 and il-15); markers of cell lineage (cd83 and cd80/86); major histocompatibility complex I and II (mhci and mhcii); T cell receptor alpha (tcra); immunoglobulin M (igm); and annexin1 (anxa1) by qPCR from spleen of *S. salar* at two sea farm centers (Puelche and Punta Islotes). Puelche reported two outbreaks of *P. salmonis*, while Punta Islotes didn't report any fish infected with the pathogen during the sampling time. Gene expression results showed that fish from Puelche increased the gene expression of ifng, tgfb, cd83, cd80/86, mhcii, il-10, il-12, igm and anxa1 at different sampling points. On the other hand, fish from Punta Islotes showed an increase of the gene expression of il-10 and cd80/86, mhcii and il-12. Finally, the correlation of data showed a proportional detection between markers of the same sea farm center and inversely proportional between centers with *P. salmonis* (Puelche) and without *P. salmonis* (Punta Islotes). This work was funded by the Program for Sanitary Management in Aquaculture of the Ministry of Economy, Development and Tourism of Chile (FIE-2015-V014 201708070149). BML is a fellow of Advanced Human Capital Formation of CONICYT, Chile (21151176).
keywords: *Salmo salar*, Chile, gene expression, spleen, Piscirickettsiosis

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P-003.

Evaluation of alpha-lipoic acid anti-inflammatory properties using zebrafish as in vivo model

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Abstract
Chronic diseases remain the primary root cause of death and disability worldwide. It is now well established that several agents (aging, oxidative stress, iron overload, etc,) induce inflammation and dysregulate inflammatory pathways, which lead to the development of chronic diseases. Acute inflammation is a part of innate immunity initiated by the immune cells that persists only for a short time. However, if the inflammation continues, the second stage of inflammation called chronic inflammation commences which instigates various kinds of chronic diseases, including arthritis, cancer, cardiovascular diseases, diabetes, and neurological diseases via dysregulation of various signaling pathways. Therefore reducing inflammation by therapeutic strategies would decrease the risk of various chronic diseases. Alpha-lipoic acid (ALA) is a natural antioxidant compound which is naturally found in plant and animal sources but small quantity of ALA can be absorbed as free ALA. The pivotal action of ALA is the antioxidant activity due to its ability to scavenge and inactivate free radicals, protecting against oxidative damage in several diseases, including neurodegenerative disorders.