

measuring different cytokine expression and biochemical parameters, as well as phagocytic activity.

**keywords:** *Dicentrarchus labrax*, fish cytokines, head-kidney macrophages, cameline oil, sea bass serum

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#### P-057.

##### Characterization and expression analysis of *Salmo salar* heat shock proteins in response to *Piscirickettsia salmonis* infection under a cohabitation challenge

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#### Abstract

Heat shock proteins (HSPs) comprise several families of highly conserved proteins which function mainly as chaperonins that refold proteins in response to stressful stimuli (changes in pH, salinity, temperature, radiation, among others) and are players in the host immune system activation during infection. The different HSP families are roughly grouped according to their molecular weights (such as Hsp110, Hsp100, Hsp90, Hsp70, Hsp60 and small HSPs). HSPs have been widely characterized as being modulated by the aforementioned stimuli, and many have been linked to processes like signaling, apoptosis and regulation of homeostasis, in addition to their chaperonine functions. In previous studies exploring the modulation of gene expression for HSPs, results have been varying, mostly depending on the kind of stressing agent and host organisms. Infection by virus and bacteria show mostly an up-regulation of small HSPs and down-regulation of some constitutively expressed HSPs (cognates). The present study aims to characterize several HSPs (4 in the Hsp30 group, Hsp60, 2 Hsp70 proteins and 6 Hsp90-like proteins, for a total of 13 HSPs) in *Salmo salar* in terms of phylogenetic relationships, conserved synteny, basal gene expression in several tissues and modulation of gene expression at the transcript level in response to infection (via cohabitation challenge for 7 weeks) using two field strains of the bacterium *Piscirickettsia salmonis* (which is the most relevant pathogen in Chilean aquaculture and the etiological agent of Piscirickettsiosis) and under two different salinities (5 and 20%). The field strains used (AUS005 and AUS111) belong to two different genogroups (LF-like and EM-like) and were isolated from differing marine environments in terms of salinity (freshwater and estuary). Results show distinct patterns of gene expression for hsp in each tissue, with most of them expressed predominantly in liver and kidney. During infection, differential expression patterns were observed for most of the HSPs studied, generally showing a sharp up-regulation of *hsp30* genes in the initial phases of the challenge, up-regulation of *hsp90* genes and, interestingly, a slight down-regulation of *hsp60* and *hsp70* genes. These data demonstrate that *Salmo salar* HSPs possibly play a role in the immune response of fish against a bacterial infection and encourage further research in order to elucidate their concrete roles in those processes.

**keywords:** Heat shock proteins, *Salmo salar*, *Piscirickettsia salmonis*, cohabitation challenge, stress.

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#### P-058.

##### De novo assembly, characterization of tissue-specific transcriptomes and identification of immune related genes from the scallop *Argopecten purpuratus*

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#### Abstract

The scallop *Argopecten purpuratus* is one of the most economically important cultured mollusks on the coasts from Chile and Peru but its production has declined due, in part, to the emergence of mass mortality events of unknown origin. Driven by this scenario, increasing progress has been made on recent years in the comprehension of the immune response mechanisms in this species. However, it is still not entirely understood how different mucosal interfaces participate and cooperate with the immune competent cells, the hemocytes, in the immune defense. Thus, in this work we aimed to characterize the transcriptome of three tissues with immune relevance from *A. purpuratus* by next generation sequencing and de novo transcriptome assembly. For this, 18 cDNA libraries were constructed from hemocytes, gills and digestive gland tissues of scallops from different immune conditions, and sequenced by the Illumina HiSeq4000 platform. A total of 967.964.884 raw reads were obtained and 967.432.652 clean reads were generated. The clean reads were *de novo* assembled into 46.601 high quality contigs and 32.299 (69.31%) contigs were subsequently annotated. In addition, three de novo specific assemblies were performed from clean reads obtained from each tissue cDNA libraries for their comparison. Gene ontology (GO) and KEGG analyses revealed that annotated sequences from hemocytes, gill and digestive gland could be classified into both general and specific subcategory terms and known biological pathways, respectively, according to the tissue nature. Finally, several immune related candidate genes were identified, and the differential expression of a mannose receptor, C-type lectin, C1q, MPEG-1, IL-17 and a scavenger receptor CD163 genes was established as tissue-specific, suggesting they could display specific roles in the host defense. The data presented in this study provides the first insight into the tissue specific transcriptome profiles of *A. purpuratus*, which should be considered for further research on the interplay between the hemocytes and mucosal immune responses. WORK FUNDED BY FONDECYT 11150009.

**keywords:** RNA-seq; tissue-specific immune genes; scallop; mucosal interfaces; antimicrobial effectors

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#### P-059.

##### Cellular and humoral immune responses of meagre (*Argyrosomus regius*) juveniles to bacterial infection with *Photobacterium damsela* piscicida

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