immunostimulation, as evidenced by high levels of expression of the genes involved in pathogen recognition, immune signaling pathways, apoptosis and effectors such as protease inhibitors, mucins and perforin-2. In contrast, larvae exposed to the bacterial pathogen *Vibrio coralliilyticus* RE22 showed evidence of immunosuppression. Transcriptome analysis of lines of oysters with varying levels of resistance to the bacterial pathogen Aliiroseovarius crassostreae and the protozoan parasite *Perkinsus marinus* yielded information that confirmed the importance of serine protease inhibitors and other immune molecules in disease resistance. Finally, viral, bacterial, and parasite genomes deposited in genetic databases were indexed and used as a reference for the assembly of reads derived from oyster DNA resequencing and transcriptome (RNA) analysis projects. The coverage and expression of these microbial genomes was calculated and compared between samples. Analysis of resequencing data from 96 oysters collected at sites from Texas to Maine for the presence of known (and unknown) parasites of oyster show that genomic data could be used to mine for information on pathogen abundance and distribution. These experiments illustrate the potential of −omic tools to inform host-pathogen interactions in bivalves.

Keywords: bivalves, probiotic, protozoa, transcriptome, vibrio

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Changes in the host microbiota structure and diversity during the immune response of the scallop *Argopecten purpuratus*

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Abstract
Traditionally it has been considered that invertebrates depend mainly on innate immunity mechanisms to defend against pathogens. However, new evidence suggests that the immune capacity of organisms is related with the symbiotic microorganisms. Indeed, all organisms live in close association with a variety of microorganisms, called microbiota, and several studies support a fundamental role of the composition of this microbiota in the health and homeostasis of vertebrates and invertebrates. In this context, the aim of this work was to determine the microbiota composition of the scallop *Argopecten purpuratus,* one of the most important reared bivalve species in northern Chile and Peru, and to assess changes in the scallop bacterial microbiota during the host immune response. For this, adult scallops were immune stimulated by an injection of heat-killed *Vibrio splendidus* and collected 24 h and 48 h after for analysis. The activation of the host immune response was established by the transcript overexpression of several scallop immune response genes in hemocytes and gills, and confirmed by the protein detection of the antimicrobial peptide big defensin in gills of *Vibrio*-injected scallops at 24 h post challenge. Next, the microbiota structure and diversity from pools of scallops were characterized using 16S rDNA deep amplicon sequencing. Results revealed that the injection of *A. purpuratus* with either filtered sea water or *Vibrio* resulted in a noticeable reduction of the order Bacteroidales and an increase in Mycoplasmatales, Clostridiales, Chlamydiales, among others when compared to non-injected scallops. Notably, particular shifts of some bacterial groups were observed between filtered sea water or *Vibrio* injected scallops, both at 24 and 48 hours. Thus, an overall modulation of the microbiota abundance and diversity according the scallop immune status was detected, allowing the prediction of some changes in the functionality of the microbial community. Finally, DGGE analysis was performed to identify any changes in the scallop microbiota at the individual level. Dendrograms constructed from the single scallop DGGE profiles demonstrate that the changes in the predominant bacterial groups are consistently detected according the immune status of scallops and evident changes occurs 48 hours after the immune challenge. Overall, the present study showed that changes in the structure and diversity of the bacterial communities associated to the scallop *Argopecten purpuratus* are detected after the activation of the host immune response. Now, the relevance of the disruption of the microbial balance in the immune capacity of the host remain to be elucidated. WORK FUNDED BY FONDECYT 11150009.

Keywords: Host-microbiota interactions; scallop; innate immune response; antimicrobial effectors; metagenome

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O-114.

Proteomic profile and proteases characterisation of greater amberjack skin mucus after *Neobenedenia girellae* infection

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Abstract
Skin mucus is known for being the first physical and immunological barrier in fish. Skin mucus is composed by a wide range of proteins, like glycoproteins, structural proteins, metabolic proteins and immune related protein-components. Likewise, proteome changes in Atlantic salmon (*Salmo salar*) have been observed due to sea lice infections, demonstrating the importance of protein-immune defenses against ectoparasite infections. Nowadays, greater amberjack (*Seriola dumerili*) pass-through a biosanitary bottleneck on its on-growing period related with monogenean ectoparasites, which could cause a 90% of mortality (Ogawa et al.,1998). For that reason, this study aimed to compare skin mucus proteome of non-infected and experimentally infected greater amberjack juveniles with *Neobenedenia girellae*, as well as to characterize proteases of this skin mucus. Thirty greater amberjack juveniles of 150 ±12 g were randomly distributed in 3 cylindroconical tanks of 500 liters. After 10 days of acclimation, skin mucus of non-infected fish was obtained, pooled and immediately freeze in liquid nitrogen. Cohabitation with *N.girellae* was conducted with 3 previously infected fish stored in cages for 15 days, when all the experimental fish were infected, skin mucus was sampled. The integrative proteomic approach was conducted using a label-free procedure as LC-MS/MS with a 2-DE-PMF-MS/MS. Protease activity was conducted using azocasein hydrolysis assay, while protease characterization was determined combining azocasein hydrolysis with inhibitors of metalloproteases and serine proteases. Results obtained with LC-MS/MS showed the first microbiota analyses in greater amberjack skin mucus, were the most abundant species belonged to gamma-proteobacteria group, and infected and non-infected fish bacterial presence only differed in 6 genus of bacteria.2-DE-PMF-MS/MS analyses showed differences in proteome profile at a qualitative level. Proteins of p/ 5 and molecular weight ranging between 36-66 KD, typically identified as structure proteins, were clearly affected by degradation for *N.girellae* infected fish. Protease activity analysis showed no difference among infected and non-