O-120.

Integrated transcriptomic and functional immunological approach for assessing the invasiveness of bivalve alien species

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Abstract
Biological invasions started when humans moved species beyond their normal geographic limits. Bivalves are the most notoriously invasive species in subtidal aquatic environments. Next-generation sequencing technologies are applied to understand the molecular mechanisms involved in the invasion. The ecological immunology focuses on the role of immunity in invasion, and its magnitude could help to predict the invasiveness of alien species. A remarkable case of invasion has been reported in the Ría de Vigo (Spain) by the black pygmy mussel *Xenostrobus securis*. In Galicia, the Mediterranean mussel *Mytilus galloprovincialis* is the predominant cultured bivalve species. Can we predict the invasiveness of alien bivalve species by analyzing their immune response? Can *X. securis* represent a risk for the autochthonous mussel? We evaluated the suitability of the immune-related hypotheses in our model by using an integrated transcriptomic and functional immunological approach. Our analysis suggests lower immune capabilities in *X. securis* compared to *M. galloprovincialis*, probably due to the relocation of energetic resources from the immune response to vital physiological processes to cope with salinity stress. This multidisciplinary approach will help us understand how the immune response can be influenced by the adaptive process and how this immune response can influence the invasion process.
Keywords: Ecological immunity, invasive species, immune response, mussel, transcriptome.

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Transcriptomic analysis of clam extra pallial fluids reveals immunity and cytoskeleton alterations in the first week of brown ring disease development

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Abstract
The Brown Ring Disease is an infection caused by the bacterium Vibrio tapetis on the Manila clam *Ruditapes philippinarum*. The process of infection, in the extrapallial fluids of clams, involves alteration of immune functions, in particular on hemocytes which are the cells responsible of phagocytosis. Disorganization of the actin-cytoskeleton in infected clams is a part of what leads to this alteration. This study is the first transcriptomic approach based on collection of extrapallial fluids on living animals experimentally infected by *V. tapetis*. We performed differential expression analysis of transcripts from healthy against infected clams by *V. tapetis*. We highlighted, in infected clams, a downregulation of transcripts implied in immune functions that might suggest an important role of deregulation of lysosomal activity and complement- and lectin-dependent PRR pathways during infection. We have also shown a deregulation of transcripts coding for proteins involved in actin cytoskeleton regulation such as an overexpression of b12-Thymosin (which are actin sequestration proteins) or a downregulation of proteins that closely interact with capping proteins such as Coactosin that countercare action of capping proteins or Profilin. According to our results we made the hypothesis that *V. tapetis* might be able to force hemocytes to stay in a "resting state" to inhibit its phagocytic power.
Keywords: Brown Ring Disease, Hemocytes, Actin cytoskeleton, b-thymosin, Coactosin, Resting cells

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O-122.

***Vibrio aestuarianus* virulent traits : Insights from in vitro interaction with oyster hemocytes**

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Abstract
Oyster mortalities associated with pathogenic vibrios are a major concern for the sustainability of oyster farming. Since 2001 and notably since 2011, one bacteria has been regularly detected in France and recently in Ireland: Vibrio aestuarianus. Its implication in oyster mortalities has been validated through experimental pathology and field survey in France4. Moreover, its pathogenesis has been recently elucidated: after a quick colonisation of hemolymph, *V. aestuarianus* virulent strain proliferates and colonizes connective tissues in gills, digestive gland and mantle.
However, shared virulence properties, specific to virulent strains, allowing bacterial proliferation in presence of hemocytes are still poorly described. This study aimed to determine *V. Aestuarianus* virulence strategies, exploring in vitro interactions between bacteria and hemocytes. Adulte oysters hemocytes were exposed to virulent or non-virulent strains. Firstly, to identify commun phenotypic trait we compared hemocyte response face to 8 virulent and non-virulent strains. And secondly, in a more targeted approach, a virulent strain (12/016) and its non-virulent mutant (12/016dVars, previously described) were also compared. Kinetics of hemocytes responses (phagocytosis, mortality and ROS production) were mesured by flow cytometry. Moreover, bacterial proliferation in hemolymph was also estimated for virulent and non-virulent strains and will be presented.
Keywords: Vibrio aestuarianus, oysters, hemocytes, in vitro, phagocytosis

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O-123.

Immune response of common carp to presporogonic development of myxozoan *Sphaerospora molnari*

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