O-045.

Involvement of myticins in tissue injury in Mediterranean mussels

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Abstract
Mediterranean mussels (*Mytilus galloprovincialis*) are sessile filter feeders that live in close contact with numerous marine microorganisms. As all invertebrates, they lack an adaptive immune response and how these animals are able to respond to a bacterial infection and discriminate it from their normal microbiome is difficult to understand.

The analysis of mussel hemocytes transcriptome before and after the animals being infected with *Vibrio splendidus* revealed an important reaction against a tissue injury, even without bacteria, in which the myticins, the most expressed antimicrobial peptides in mussel, appeared significantly up regulated. Functional experiments with flow cytometry confirmed these transcriptomic results, seeming that myticins would be involved in the response to a danger signal such as a simple injection in the adductor muscle.

Moreover, mussel hemocytes stimulated with myticin C (*in vitro* approach) showed a transcriptomic response basically related to cytoskeleton and contraction, as well as maintenance of tissues and cell structures integrity. All results suggest a new role of myticin C, an antimicrobial peptide traditionally related to immune response and defense against pathogens, which seems to be important after a tissue damage.

Keywords: Mussel, tissue injury, myticin C, RNAseq, hemocyte

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O-046.

The sydney rock oyster microbiome is influenced by local environmental parameters and QX disease resistance

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Abstract
Sydney rock oysters, (SRO: *Saccostrea glomerata*) are a native species in Australia and the most important aquaculture species in the state of New South Wales (NSW). However, production of this species has declined significantly since the mid-1970s, in part due to the impacts of mortality events associated with QX (Queensland unknown) disease. QX disease is caused by a spore-forming protozoan parasite called *Marteilia sydneyi* however, the presence of the parasite does not necessarily result in QX disease indicating the role of environmental and/or host-specific factors in disease progression. Another potential factor in QX disease is the microbiome of the SRO, however, little research has been conducted into the microbiome of this oyster species. In this study, we examined the microbiome of six families from the SRO breeding program with differing resistance to QX disease (two highly resistant, two with intermediate resistance and two susceptible) deployed in two different locations using 16S rRNA (V1 − V3 region) amplicon sequencing. The broad aim of this study was to determine the effect of local environmental parameters and disease resistance on the microbiome of the SRO. Our results show that microbiomes of SRO families significantly differed between the two deployment locations of Port Stephens and Wallis Lake (NSW), and between our two sampling points in the Austral summer and winter. Additionally, the SRO microbiome was influenced by QX disease resistance at Port Stephens at both time points with the susceptible lines significantly differing from the resistant and intermediate families. However, in Wallis Lake, the influence of host-specific QX disease resistance was not consistent over the two seasons suggesting that environmental factors can overcome the influence of host genetic factors.

Keywords: Microbiome, Sydney rock oyster, QX disease resistance, selective breeding, Port Stephens, Wallis Lake

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O-047.

Β-glucan immuno-modulation in common carp intestine: A role for microbiota and its metabolites

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Abstract
Dietary supplementation of fish with β-glucans has been widely associated with immunomodulation and commonly accepted as beneficial for fish health. However, to date the exact mechanisms of immunomodulation by β-glucan supplementation in fish are still largely unknown. In mammals a clear relation has been observed between high fibre diets and immunomodulation via intestinal microbiota and its metabolites. In this study, we first described the normal microbiota of common carp intestine by 16S rRNA sequencing. Based on the abundance of the genus *Bacteroides*, well known for their capacity to degrade and ferment carbohydrates, we hypothesized that common carp intestinal microbiota could ferment dietary β-glucans. Indeed, two different β-glucan preparations (curdlan and MacroGard®) were both fermented *in vitro* albeit with distinct fermentation dynamics and significant differences in production of short chain fatty acids (SCFA). MacroGard® more than curdlan lead to production of propionate, a SCFA with immunomodulatory properties. Subsequently, *in vivo* treatment effects of a single oral gavage with MacroGard® were analysed. Intestinal microbial composition seven days post-treatment showed a significant shift towards the family *Rhodocyclaceae*, including *Propionibacterium* sp, known to synthesize propionic acid by using unusual transcarboxylase enzymes. Coinciding with the shift in microbial composition, an overall immunomodulation could be observed as inhibition of expression of several pro-inflammatory genes (*il1β*, *il6*, *tnfα*). Based on our data, we discuss the possibility that fermentation of MacroGard® by specific bacteria part of the normal microbiota of common carp intestine can lead to a shift in microbial composition and associated production of the SFCA propionate, the increased presence of which could possibly explain (part of) β-glucan-induced immunomodulatory effects.

Keywords: Microbiota, β-glucan, SCFA, *Cyprinidae*, 16S rRNA sequencing

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