Keywords: Mollusc; Immune recognition; Pattern recognition theory; Novel patter receptors; Mucosal recognition

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Hematopoiesis and regulatory signaling in molluscs

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Abstract
Hematopoiesis is a complex process by which different blood cells are formed and released from hematopoietic tissues. Due to lack of oxygen-carrying erythrocytes and blood cells of the lymphoid lineage, which are participating in adaptive immune defense, hematopoiesis in invertebrates offers a simple model system to study regulation of the blood cells of the innate immune system. Several transcription factors have been characterized as hemocyte-specific markers in molluscs, such as Tal-1/SCL, GATA2/3, Runx, CBFβ, ETS, and c-Myb, and are conserved across taxonomic groups from molluscs to chordates. They were highly distributed in the hemocytes as well as potential hematopoietic tissue gill, and the RNAi of Tal-1/SCL, GATA2/3 and Runx significantly reduced the hemocyte renewal rates in the hemocytes and gill tissue. The temporal and spatial expression pattern revealed the potential developmental events of hematopoiesis during ontogenesis of oyster, which initially occurred early in blastula stage and definitively resided in the dorsal region in trochophore larvae. A cytokine-like factor astakine was identified from Pacific oyster *Crassostrea gigas*, which could induce the regeneration of oyster hemocytes either receiving an injection of r*Cg*Astakine *in vivo*, or incubation with r*Cg*Astakine *in vitro*. Furthermore, critical components in signaling pathways, such as Notch signaling pathway, Wnt signaling pathway, were restricted to the potential hematopoiesis sites in the adult oyster, which hints at a possible role for them during the hematopoiesis. In oyster, three types of hemocytes were morphologically identified and separated as agranulocytes, semi-granulocytes and granulocytes by flow cytometry and Percoll® density gradient centrifugation. The granulocytes were proved to be the main immunocompetent hemocytes, and there was potential differentiation relationship among these three sub-population hemocytes. Several hemocyte-specific molecules, such as *Cg*AATase, *Cg*SPSB3, *Cg*CD-9 were identified, which could be employed as a potential marker for the isolation of each subtype hemocytes. Above researches of molluscan hematopoiesis may shed light on the study regulation of the blood cells of the innate immune system in invertebrates.
Keywords: Hematopoiesis; Mollusc; Transcription factors; Cytokines; Hemocyte-specific molecules

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Deep transcriptome profiling sheds light on key players in nucleus implantation induced immune response in the pearl oyster *Pinctada martensii*

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Abstract
Immunological rejection of the pearl oysters following nucleus implantation is a major issue limiting the successful rate of cultured pearls. To date, the molecular mechanism of immune tolerance during pearl formation in the pearl oysters is still largely unknown. Through the RNA sequencing platform and comparative transcriptomic analysis, we investigated the chronic gene expression changes at seven time points (0, 5, 10, 15, 20, 30, 60 days post implantation or dpi) over a period of 60 days following nucleus implantation in the pearl oyster Pinctada martensii. A total of 81,390 unique transcripts (or unigenes) with a combined length of 96.8 million bp and a N50 value of 2,227 bp were obtained. When compared with sequences in the nr, nt, Swiss-Prot, KEGG, COG and GO databases, 36,380 unigenes can find homologous genes. Pairwise comparison of gene expression among all the samples showed that the largest number (or 6,846) of differentially expressed genes was observed at 10 dpi. The number then decreased to below 5,000 at 15, 20 and 30 dpi and increased again to 6,679 at 60 dpi. PCA analysis further showed that the seven time points can be roughly divided into four groups. Comparative transcriptomic analysis between the four groups identified a variety of genes showing differential expression at different time points, including many immune-related genes such as those encoding for toll-like receptor, lectin, scavenger receptor, and peroxidase. In addition, GO and KEGG enrichment analysis revealed that these differentially expressed genes were mainly associated with metabolism, ribosome function, immune response, signaling transduction, and cytoskeleton organization. Notably, two KEGG pathways, namely “cell adhesion molecules” and “primary immunodeficiency” were significantly enriched during the whole process. This finding indicates that genes in these pathways are likely to play critical roles in the immune tolerance of the pearl oysters. To conclude, the data obtained contribute to a better understanding of the molecular mechanisms of allograft induced immune response in the Pearl oysters, and will facilitate the development of effective measures to improve the performance of pearl culture.
Keywords: Pearl oyster, *Pinctada martensii*, Nucleus implantation, Allograft, Transcriptome

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Immune responses of American oysters to bacterial and parasitic challenge

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Abstract
The American oyster Crassostrea virginica is an ecologically and economically important species in the Northwest Atlantic and the Gulf of Mexico. Wild and cultured populations of this organism are impacted by a variety of bacterial and parasitic pathogens. Taking advantage of the recently assembled sequence of the American oyster, we have performed a transcriptomic characterization of the immune responses of oysters to bacterial and parasitic challenge. Evaluation of the response of *C. virginica* larvae to probiotics *Bacillus pumilus* RI0695 and *Phaeobacter inhibens* S4 showed