

TITLE: A multi-omics approach provides a deeper understanding of the immune response of sea cucumber coelomocytes to lipopolysaccharides

AUTHORS: Noé Wambreuse^{1§}, Jérôme Delroisse¹, Vanessa Tagliatti², Igor Eeckhaut¹,
Laura Borrello¹, Guillaume Caulier¹

AFFILIATIONS: *University of Mons – UMONS*

¹ *Biology of Marine Organisms and Biomimetics Unit – Pentagone 2B, 6 Avenue du Champ de Mars, 7000 Mons, Belgium*

² *Human Biology and Toxicology Laboratory – Pentagone 2A, 6 Avenue du Champ de Mars, 7000 Mons, Belgium*

Abstract

Sea cucumbers are curious organisms belonging to echinoderms – a basal phylum of deuterostomes, relatively close to our early vertebrate ancestors. Their primitive appearance might suggest that their defence mechanisms against pathogens are limited. On the contrary, these animals have a very efficient immune system, capable of neutralizing a wide spectrum of invaders. Moreover, sea cucumbers are of great interest in many areas: they have a crucial ecological function by playing much the same role as earthworms but in seas and oceans, and some species have a high economic value due to their commercial exploitation as seafood and traditional pharmacopoeia in the Asian market.

The present research aims to further our knowledge of the coelomocyte immune response in these particular animals. Coelomocytes are circulating cells constituting the main cellular actors of immunity in sea cucumbers and many other organisms. In echinoderms, they are particularly abundant in two body fluids: the coelomic fluid (i.e., the fluid of the perivisceral cavity) and the hydrovascular fluid (i.e., the fluid of the water vascular system). Here, we used a combined transcriptomic and metabolomic approach to study the response of coelomocytes to lipopolysaccharides (LPS).

Our results show both a differential expression of genes and a differential abundance of metabolites, in response to the LPS challenge. First, regarding the transcriptomic response, 945 genes were differentially expressed, of which 673 were up-regulated and 272 down-regulated in the LPS-treated individuals. Some of them were annotated as immune genes, with most falling into the category of pathogen recognition receptors. Then, regarding the metabolomic response, out of the 19 metabolites identified, 6 metabolites increased in abundance while 3 decreased after the LPS challenge. Interestingly, some characteristic metabolites of bacteria were differentially abundant between the two conditions, suggesting a microbiome response to the LPS challenge. In addition, glutamate-glutamine metabolism appeared to be strongly decreased after immunostimulation.

This multi-omics approach should help to better understand how sea cucumbers cope with bacterial infections and could also be a first step for preventing bacterial diseases in sea cucumber aquaculture facilities while providing valuable data for comparative immunology.

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§Corresponding author. E-mail address: noe.wambreuse@umons.ac.be (N. Wambreuse)