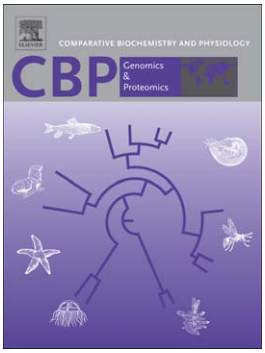

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PII: S1744-117X(15)00052-0
DOI: doi: 10.1016/j.cbd.2015.07.004
Reference: CBD 372

To appear in: *Comparative Biochemistry and Physiology - Part D: Genomics and Proteomics*

Received date: 11 March 2015
Revised date: 13 July 2015
Accepted date: 24 July 2015

Please cite this article as: Bassim, Sleiman, Chapman, Robert W., Tanguy, Arnaud, Moraga, Dario, Tremblay, Rejean, Predicting growth and mortality of bivalve larvae using gene expression and supervised machine learning, *Comparative Biochemistry and Physiology - Part D: Genomics and Proteomics* (2015), doi: 10.1016/j.cbd.2015.07.004

Predicting growth and mortality of bivalve larvae using gene expression and supervised machine learning

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Abstract

It is commonly known that the nature of the diet has diverse consequences on larval performance and longevity, however it is still unclear which genes have critical impacts on bivalve development and which pathways are of particular importance in their vulnerability or resistance. First we show that a diet deficient in essential fatty acid (EFA) produces higher larval mortality rates, a reduced shell growth, and lower postlarval performance, all of which are positively correlated with a decline in arachidonic and eicosapentaenoic acids levels, two EFAs known as eicosanoid precursors. Eicosanoids affect the cell inflammatory reactions and are synthesized from long-chain EFAs. Second, we show for the first time that a deficiency in eicosanoid precursors is associated with a network of 29 genes. Their differential regulation can lead to slower growth and higher mortality of *Mytilus edulis* larvae. Some of these genes are specific to bivalves and others are implicated at the same time in lipid metabolism and defense. Several genes are expressed only during pre-metamorphosis where they are essential for muscle or neurone development and biomineralization, but only in stress-induced larvae. Finally, we discuss how our networks of differentially expressed genes might dynamically alter the development of marine bivalves, especially under dietary influence.

Keywords: RNA-seq; Microarray; Machine Learning; Eicosanoids; Immunity; Fatty acids; Development

1 Introduction

The blue mussel *Mytilus edulis* (Linnaeus, 1758) is a marine organism with fast-evolved adaptive behaviors. For example, immune functions and apoptotic mechanisms are preferentially activated early in development to increase the resistance against benthic pathogens (Xing et al., 2014). However these processes also aid in the elimination of primitive tissue and debris during