FATTY ACID BINDING PROTEIN FAMILY PREVALENCE IN TRANSCRIPT LEVELS FROM DIFFERENT TISSUES IN OYSTER CRASSOSTREA GIGAS.

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The oyster *Crassostrea gigas* is the most cultivated, consumed and studied marine bivalve mollusk in the world. In addition, many ecotoxicological studies use *C. gigas* as sentinel organisms, since they are sessile and filter feeding with great capacity to accumulate contaminants. Fatty acid binding proteins (FABPs) are a group of proteins that respond to environmental stressors and are involved with development of oysters in aquaculture farms. FABPs may promote gene expression regulation of lipid and carbohydrate metabolism and are involved in lipid droplet deposition, membrane synthesis, oxidation on mitochondria and peroxissome organelle. In this work it was analyzed the transcript levels from FABPs family in different *C. gigas* tissues to identify the prevalence and function of each isoform. *C. gigas* genome was used to locate all *FABP* gene regions in a parallel study being developed by our research group. Total RNA of 10 oysters was extracted from digestive gland, gills, labial palps, mantle, adductor muscle and heart. Eight putative FABPs isoforms were analyzed by qPCR. Three isoforms were prevalent in digestive gland compared to other tissues. These isoforms are probably involved with lipid uptake and metabolism in this tissue. One isoform was prevalent in labial palps and another one in gills. It could be associated with the biotransformation and detoxification of lipophilic compounds absorbed during the filter feeding process. One isoform was prevalent in muscle and mantle, and another one in mantle only, suggesting a role in lipid storage in these tissues, as well as an enhanced energy demand associated with the valve drive mechanism. Differences between transcript levels of FABPs isoforms in *C. gigas* suggest distincts functional specializations of proteins codified by these genes. We are now analyzing the differences between isoform structures in order to infer about its function and trying to find new biomarkers of contaminant exposure.

Keywords: FABPs, oyster tissues, qPCR.