

— Metallothionein gene identification and expression in the cockle (—



Among benthic organisms, bivalves are often used as bioindicators of environmental pollution because of their high bioaccumulation capacities for heavy metals leading to metallothioneins (MT) induction. MT are small cytosolic metal-binding proteins involved in metal homeostasis and detoxification in living organisms. These proteins can also be induced by a wide range of factors, such as hormones, physical stress, parasitism. MT quantification in relation to parasitism is rarely reported in literature, while parasites are omnipresent and have deleterious impacts on bivalves. Moreover, only a few number of MT genes have been characterized in molluscs. This study describes the partial sequence of the MT gene (Cemt1) in the edible cockle *Cerastoderma edule*. The cockle's MT cDNA was sequenced and showed over 80% homology to several other bivalve MT sequences. This sequence was then used to determine MT specific primers which can be used in quantitative real time PCR. MT protein and gene expression levels were quantified for individuals selected under different conditions: free from or infected by the digenean trematode

Himastha elongata, and under cadmium exposure at 15 µg Cd L⁻¹. Results evidenced that MT concentrations were significantly increased by both treatments; parasite infection and Cd exposure. Moreover, congruent results between MT protein and gene expression levels were obtained.

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