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αβ DEFENSIN ANTIMICROBIAL PEPTIDE (BPDEF) FROM THE INVASIVE RED SEA MUSSEL *BRACHIDONTES PHARAONIS* (P. FISCHER, 1870)

The immune system plays a major role in determining host fitness in the wild, i.e. under the constraints imposed by ecology and life history. Permanent conflict interactions with the environment are the natural situation for a living creature but the immune system is characterized by an enormous variety of mechanisms and effectors, including the Antimicrobial peptides (AMPs). These compounds, in fact, are extremely successful in dealing with a huge range of pathogens, including bacteria, fungi, protozoa and viruses. In the present study, using primers designed from coding sequences from *Mytilus galloprovincialis*, the cDNA sequence of the Defensin was cloned and characterized from the Red Sea mussel *Brachidontes pharaonis* living along the rocky shores of the Mediterranean. Analysis of the sequence of 262 nucleotides revealed in the *B. pharaonis* defensin (BpDef) the presence of an ORF coding for 81 amino acids consisting of a signal peptide of 23 aa in the amino terminal portion followed by the mature peptide of 35 a.a. and a carboxy-terminal extension position. Alignment with the sequences of *M. galloprovincialis* indicate high similarity with the antimicrobial peptide MGD1 and MGD2 of Mediterranean mussel. *In situ* hybridization analysis revealed BpDef mRNA expressed in circulating hemocytes with small intra-cytoplasmic granules and with large granules. Sequence identity and the common conserved sequence characteristics show that BpDef belongs to the αβdefensin family AMPs with a typical domain structurally characterized by α helix and two sheets αβ. Two predicted bactericidal stretches were found in correspondence of the mature peptide and the Boman index value indicated the strong antibacterial feature of defensin of *B. pharaonis*. This is the first report on the AMP of defensin family in lessepsian species *B. pharaonis*. The results enrich the basic research on the AMPs gene family in mussels, providing improved understanding of the immune system in invasive mollusks. The study is also a first step for further practical application of bioactive peptide derived from lessepsian species as alternative and/or complementary bioactive compounds in the vast reservoir of marine invertebrates antimicrobial peptides (AMPs).