

PROTEOMIC STUDIES OF MARINE ORGANISMS

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Several features make marine organism interesting animals to study; as their sensitivity to environmental changes in seawater ecosystems makes them excellent models to study marine pollution, or their common biological features with ancient progenitors give the possibility to study living fossils. Our work first focuses on the proteome characterization of the haemolymph of *Limulus polyphemus*, a very ancient marine arthropod dating back to ca. 440 million years; it has been explored in depth via capture by combinatorial peptide ligand libraries [1]. Whereas barely a dozen proteins had been known up to the present, we have increased this number by more than one order of magnitude, up to 160 unique gene products, identified by nLC MSMS [2], by consulting the dbEST_limulus database as well as via comparison with the other members of the Chelicerata sub-phylum to which *Limulus* belongs, namely scorpions, ticks, mites and spiders. This further reinforces the notion that these are truly ancestral proteins, scarcely represented in present times. These data might represent the true birth of paleo-proteomics [3]. In addition our study is focused on the proteomic analysis of the cell free coelomic fluid from the sea urchin and the haemolymph of mussels in order to understand and characterize the molecules involved in important biological processes like organism's defense against bacterial infection and adaptation at marine habitat changing.

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[2] A. D'Amato, A. Bachi, E. Fasoli, E. Boschetti, G. Peltre, H. Sénéchal, P.G. Righetti, *J. Proteome Res.*, 8, 3925-3936 (2009).

[3] D'Amato A, Cereda A, Bachi A, Pierce JC, Righetti PG. In depth exploration of the haemolymph of *Limulus polyphemus* via combinatorial peptide ligand libraries. *J. Proteome Res.* 9:3260-3269 2010.