The microbial community of the coelomic fluid of the sea urchin *Paracentrotus Lividus*

T. Faddetta¹, E. Palazzotto², F. Faillaci², C. Catania³, F. Strati³, C. De Filippo³, G. Spinelli², A. M. Puglia¹, G. Gallo¹, V. Cavalleri¹

1. STEBICEF Department, University of Palermo, Viale delle Scienze, ed. 16, 90128 Palermo
2. Research and Innovation Centre - Fondazione Edmund Mach Via E. Mach 1, 38010 San Michele all'Adige
3. IBIMET CNR, via Giovanni Caproni 8, 50145 Firenze
4. ATEN Center, University of Palermo, Viale delle Scienze, ed. 18, 90128 Palermo

teresa.faddetta@unipa.it

The occurrence of bacteria into the coelomic fluid of sea urchins has not been explored so far, although this liquid is the main circulatory medium of these echinoderms. In the present work, we describe the culture based and culture-independent investigations on the microbiota residing in the coelomic fluid of the Mediterranean sea urchin *Paracentrotus lividus*. Culture-dependent analysis allowed the isolation of 8 Gramnegative bacterial strains, all belonging to the Proteobacteria phylum. In particular, the isolated strains were classified as the following genera: *Vibrio, Pseudoalteromonas, Idiomarina, Alteromonas, Halomonas* and *Loktanella*. Next Generation Sequence analysis (NGS) of the 16S rDNA from samples extracted from the coelomic fluid lead to the identification of 168 Operational Taxonomic Units. Proteobacteria, Bacteriodetes and Fusobacteria were the most abundant taxa. At the genus level, the most represented ones are Propionigenium, *Vibrio* and Photobacterium. The predominance of Proteobacteria perfectly agrees with the identification of the bacterial isolated strains. In order to provide data on the possible metabolic activity and the function of the microbial communities, we performed PICRUSt (Phylogenetic Investigation of Communities by Reconstruction of Unobserved Statest) analysis, a computational approach used to predict the functional composition of a metagenome using marker gene data and a database of reference genomes. Among the 27 gene functional families identified, the most conserved one is cellular processes and signaling which underlines the crucial importance of bacteria-host association.