we describe the generation of SMCs able to establish a "synthetic-to-natural" communication channel with the human pathogen *Pseudomonas aeruginosa*. We demonstrate that SMCs containing *i)* the gene coding for a synthase that catalyzes the production of a *P. aeruginosa* signal molecule, *ii)* the precursors of the signal molecule, and *iii)* a minimal cell-free transcription-translation apparatus, are able to synthesize the signal molecule, thus triggering the expected transcriptional response in *P. aeruginosa*. The generation of SMCs able to respond to signal molecules produced by *P. aeruginosa* is in progress. This further achievement will pave the way for the engineering of SMCs endowed with cognitive capacity, to be used as *softnanorobots* for intelligent drug-delivery approaches.

## P1.10
## Biofilm diversity in cooling towers industrial systems

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Biofilms are usually studied in medical field at biomolecular level and little information is available about multispecies biofilms in industrial settings. Biofilms colonize industrial cooling systems growing as aggregates on the inner surfaces, causing often biofouling with serious equipment damages, even the tower collapse. This study aims to analyze biofilm biodiversity in cooling systems and to understand the main driving adhesion mechanisms. The biodiversity was analyzed in four full scale cooling towers (pharmaceutical and refineries plants in Hungary, Croatia and Italy) by applying CARD-FISH combined with CLSM and Next Generation Sequencing. A complex architecture and diversity (heterotrophic and phototrophic organisms) were found in biofilms from refinery plants (cross-flow type tower). Considering the key-role of the signal molecule "c-di-GMP" in biofilm adhesion mechanism investigated in pure cultures of medical relevance bacteria, the quantification of this molecule in multispecies biofilm is in progress by a HPLC-UV on a lab-scale system designed and constructed to mimic real systems.

## P1.11
## Characterization of the microbiota from coelomic fluid of the sea urchin *Paracentrotus lividus*

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In this study we investigated the bacterial microbiota of *Paracentrotus lividus* coelomic fluid [1, 2] by coupling cultivation independent and dependent analyses and functional tests. Next generation sequence analysis of 16S rDNA from samples extracted from coelomic liquid lead to the identification of 56 bacterial taxa, classified to the genus level. Among these, the most abundant genera were *Propionigenium*, *Vibrio* and *Prolixibacter*. Culture-dependent analysis allowed the isolation of 8 Gram-negative bacterial strains, previously identified by culture independent method. In particular, 7 strains produce extracellular hydrolytic enzymes and 1 strain exhibits antibacterial activity.This research for the first time indicates that the coelomic fluid of a sea urchin does contain bacterial communities, suggesting a functional interaction between sea urchin and marine microorganisms. Moreover, it provides a novel source of biochemical diversity for the production of bioactive compounds and enzymes that can find biotechnological applications.

Remziye Deveci et al. (2015). *Journal of Morphology 276(5):583-8*
Stabili L et al. (1996). *Comp Biochem Physiol B Biochem Mol Biol 113(3):639-44*

## P1.12
## Application of plant-derived protein hydrolysate Trainer stimulates the growth of *Bacillus* with antagonistic activity against phytopathogenic bacteria and fungi

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The use of protein hydrolysates as biostimulant is proposed as an innovative solution to address the challenges to sustainable agriculture, to ensure optimal nutrient uptake, crop yield, quality and tolerance to abiotic stress. In this study we sequenced bacterial communities present on lettuce leaves of treated and untreated plants to evaluate the effect of a commercial plant-derived protein hydrolysate ("Trainer" by Italpollina, Rivoli Veronese- Italy) on the microbial biodiversity. Bacterial communities in the lettuce phyllosphere were dominated by a core microbiome of taxa including Actinobacteria, Bacteroidetes, Firmicutes and Gammaproteobacteria. Data obtained using culture-independent (Next-generation sequencing of 16S rDNA) and culture-dependent approaches indicated that foliar application of "Trainer" altered the composition of the microbial population and stimulated the growth of specific bacteria species of the genus *Bacillus* exhibiting biocontrol activity against *Erwinia amylovora* and several phytopathogenic *Fusarium* species.

## P1.13
## Yeast-based screens to identify natural compounds for Hailey-Hailey disease

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Hailey-Hailey disease (HDD) is a rare and chronic skin disorder, characterized by persistent blisters and skin erosions caused by suprabasal acantholysis. Such dominant autosomic disease has been linked to mutations in ATP2C1 gene encoding an ATP-calcium pump and the *PMR1* gene encodes its functional ortholog in yeast. In line with the notion that yeast represents a useful model for human diseases, *Kluyveromyces lactis pmr1*Δ mutant shows altered $Ca^{2+}$ homeostasis and oxidative stress associated to impaired mitochondrial metabolism/structure and cell wall defects. In this study, *pmr1*Δ strain was exploited to screen a natural compounds library. FDA-approved collection includes inhibitors, activators and antagonists acting on molecular targets involved in different signaling pathways. Initially, the effect on cell wall defects of *pmr1*Δ cells was evaluated and molecules that resulted toxic were discarded. Six compounds showed a recovery of the phenotype and were accepted for further analysis. Their effect on other defects of *pmr1*Δ mutant strain was evaluated, ranging from mitochondrial functionality to sensitivity to the ROS-generator menadione, as well as alteration of $Ca^{2+}$ homeostasis

## P1.14
## Development of a high throughput approach to investigated nitrogen metabolism in Lactic Acid Bacteria

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Lactic Acid Bacteria (LAB) are a heterogeneous group of Gram-positive bacteria, catalase-negative, non-spore-forming, low-GC, either rod-shaped or spherical. The traditional use of many LAB as starter cultures in food and dairy fermentations led to their widespread in human consumption. The knowledge of LAB nitrogen metabolism, including