POSTER AND SELECTED SHORT TALKS

1 - Environmental Microbiology and Biotechnology

P1 1
Contrasting effect of diet shift on the gut microbiota of two amphipods species Orchestia montagui and Talitrus saltator
K. F. A. Abdelrahman1 G. Bacci2 A. Mengoni1 A. Ugolini1
1Department of Biology, University of Florence, via Madonna del Piano 6, I-50019 Sesto Fiorentino, Firenze, Italy. 2Museum of Natural History, Sezione Zoologia “La Specola” University of Florence, via Romana 17, I-50125, Firenze, Italy.

Talitrid amphipods are among the most important detrivorous living in the supralittoral environment of sandy beaches. We have previously reported that different talitrid species may host different gut bacterial communities. However, it is unclear if such differences arose because of some species-specific physiological features of host origin or in relation to possibly different foraging behavior. Consequently, we wanted to investigate the resilience of gut bacterial communities of talitrid amphipods, to shed some light on the effect that different alimentary sources feeding habits may have on species-specific gut microbiota patterns. We choose as model species two species contrasting food preferences and gut microbiota: Talitrus saltator (Montagu) and Orchestia montagui (Audouin) and challenged them with artificial food for two months to evaluate the resilience and the effect of dietary changes over the gut microbiota. Results, obtained by 16S rRNA gene metagenomics and analysis of cellulase-encoding genes, along five time points samples: natural habitats (T 0), after 24 hours (T 1), after 7 days (T 2), after 23 days (T 3) and after 1 day (T 4) showed a contrasting behavior of gut microbiota dynamics in the two talitrid amphipod species with T. saltator being more affected than O. montagui in terms of diversity of the microbiota. Concerning the taxonomic profiles, in O. montagui members of the class Bacilli resulted the most variable over time, while in T. saltator most of the variability was due to Enterobacteriaceae. Finally, cellulose-encoding genes (GH48 family) were strongly increased in their abundance in O. montagui gut microbiota compared to T. saltator, mirroring the increase of Actinobacteria over time. In conclusion, we provide evidences that changes in food sources (in natural environments related to the availability of stranded organic material) may have a contrasting impact over the gut microbiota of different talitrid amphipod species, which could determine mid- or long-term changes in animal’s physiology and on species’ fitness in the environment.

P1.3
Identification of FDA-approved compounds targeting the pqs quorum sensing system of Pseudomonas aeruginosa
F. D’Angelo, Y. Halldeli, L. Leoni, and G. Rampioni
Department of Science, University Roma Tre, Rome, Italy.

Hampering bacterial adaptability to the host environment is considered a promising strategy for the eradication of infections caused by drug-resistant pathogens. Quorum sensing (QS), a communication system that controls virulence factors production and biofilm formation in several pathogens, is an ideal target for the development of anti-virulence drugs. Here we describe the identification of new inhibitors of the pqs QS system of Pseudomonas aeruginosa, relying on 2-alkyl-4-quinolones (AQs) as signal molecules. Briefly, a reporter system based on the co-culture of P. aeruginosa PA01 and of an AQs biosensor, in which light emission depends on AQs produced by the PA01 strain, has been used for the screening of a library of 1,600 FDA-approved drugs. Three hits specifically inhibit the pqs QS systems, and hence the expression of pqs-controlled virulence traits in P. aeruginosa. Preliminary analyses suggest that the newly identified inhibitors hamper the pqs system by targeting the transcriptional regulator PqsR. Further analyses proving the ability of the pqs-inhibitors to reduce P. aeruginosa pathogenicity in animal models of infection are in course.

P1.4
Fungal treatment for recalcitrant compounds removal in raw leachate and synthetic mixtures
A. Bardi1 Q. Yuen2 V. Tigni1 F. Spina1 G.C. Varesi1 F. Spennati2 S. Becarelli1 S. Di Gregorio2 G. Petroni1 G. Munz1
1Dep. of Biology, University of Pisa, Via Luca Ghini 13, 56126, Pisa, Italy. 2Dep. of Civil Engineering, University of Manitoba, 15 Gillson Street, R3T 5V6, Winnipeg, Canada. 3Dep. of Life Sciences and Systems Biology, University of Turin, viale Mattioli 25, 10125, Torino, Italy.

Recalcitrant compounds represent a serious concern in wastewater treatment since biological processes, based on bacterial degradation, are not suitable for their removal. Recently, the capability of white-rot fungi (WRF) in transforming recalcitrant pollutants generated a significant interest among bio-based industries. This study focused on the treatment of 3 effluents with the white-rot fungus Bjerkandera adusta MUT 2295 in batch tests. B. adusta MUT 2295 was selected during a previous experiment due to its ability to act towards a raw leachate sample (Italy). Treatment efficiency of B. adusta was evaluated on a) landfill leachate (Canada) and b) two synthetic recalcitrant solutions prepared with 1) tannic and 2) humic acid. Different parameters such as the pH of the treated effluent, its chemical oxygen demand (COD) enzymatic activities and glucose consumption of B. adusta during the treatment were monitored for 10 days. COD removal was up to 49%, 61% and 49% in raw leachate and the two synthetic solutions. Moreover, color removal between 25% and 49% was achieved in 1 week. Results obtained encouraged further investigations on the use of the selected white-rot fungus.