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their nutritional nitrogen requirements, constitutes a tool that could help the researchers and professionals of alimentary industries to produce foods with optimal qualities. Phenotype Microarray (PM) analysis, which is a high throughput method for microbial characterization, has been applied to the chemical sensitivity and carbon metabolism analysis of LAB. Nevertheless, such approach failed when nitrogen metabolism was investigated. Consequently, the aim of the present research is to define an efficient protocol for analysing LAB nitrogen metabolism using PM, evaluating appropriate tetrazolium dye, used as a reporter of metabolic activity, carbon sources, and buffer conditions. The results obtained will be showed and discussed.

P1.15

Anti-virulence activity of niclosamide in *Pseudomonas aeruginosa* isolates from cystic fibrosis patients

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The antibiotic-resistant chronic lung infection caused by *Pseudomonas aeruginosa* is the major cause of death in cystic fibrosis (CF) patients. The anti-helminthic drug niclosamide (NCL) inhibits the *P. aeruginosa* quorum sensing (QS) pathways based on *N*-3-oxododecanoyl-homoserine lactone (3OC12-HSL) and *N*-butanoyl-homoserine lactone (C4-HSL) as signals, hence reducing virulence *in vitro* and in an insect model of infection. However, since *P. aeruginosa* CF isolates show high genetic variability, the effect of NCL must be assessed in clinical isolates in order to support repurposing of this drug for CF therapy. Here 100 *P. aeruginosa* isolates from intermittent and chronic CF infections were collected and analyzed. Results showed that 63 strains produced both QS signals, while 22 and 6 strains produced only C4-HSL or 3OC12-HSL, respectively. QS proficient strains were found to be overall sensitive to NCL, with no effect on growth. However, great variability in the extent of NCL-mediated QS inhibition was observed among strains. Our results highlight that anti-QS molecules such as NCL have a good potential for CF therapy, though upon strain-specific susceptibility analysis.

P1.16

Immobilization of *Aspergillus niger* Cellulase on epoxy beads

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Cellulase (E.C. 3.2.1.4) is an important enzyme useful to obtain glucose from biomass and, thus, it is important for the circular economy, also known as bioeconomy. In fact, biomass can be used as substrate for the enzyme with the aim to obtain biofuel. Microorganisms provide powerful enzymes for different application. In this work *Aspergillus niger* cellulase has been chosen to be immobilized on epoxy beads. Enzyme immobilization is highly desired for industrial application to obtain high efficiency of the process at lower costs. Of course studies are need to find an efficient immobilization method that provides an enzymes exhibiting high performances. In this study we have used beads from ChiralVision (Immobeeds-COV-2), made of a support that immobilizes covalently the enzyme. To quantify enzymatic activity we have used the 3,5-dinitrosalicylic acid based method (Ghose, 1987), while to determine the protein concentration, BioRad method was used (Bradford, 1976). Immobilization yield was equal to 42% while protein loading was in average 1 mg of enzyme per gr of beads. Experiments are in progress to establish the stability of the immobilized enzyme over the time.

P1.17

Environmental spread of antibiotic resistance genes (ARGs) in aquatic systems with different level of microbial contamination

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Aquatic ecosystem is considered as a significant reservoir of antibiotic resistance genes (ARGs), which could potentially be transferred from environmental microorganisms to human pathogens. In order to mitigate possible health problems, the environmental spread of the ARGs should be characterized and monitored. The purpose of the study was the assessment of ARGs occurrence in various water environments in Italy with different levels of microbial contamination (i.e. raw and treated wastewaters, surface waters and groundwaters). By using PCR and qPCR, the presence and/or abundance of 13 ARGs, selected on the basis of their environmental spread and clinical relevance, were investigated in comparison to total bacteria (16S rDNA gene) and a fecal contamination indicator (*E.coli uidA* gene). ARGs, comprising clinically relevant extended spectrum beta lactamases, were frequently detected in water environment. Overall, higher ARGs levels were associated to more contaminated waters (e.g. wastewater or contaminated surface water). Instead, limited or no correlation was found among the ARGs levels and *E.coli* levels, indicating different contamination sources and fate in the environments.

P1.18

Biodegradable films and containers from bitter vetch (*Vicia ervilia*) seed proteins

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Bitter vetch (*Vicia ervilia*; BV) seeds were analyzed as source to produce protein-based edible films and properly shaped biodegradable containers. Seed protein concentrates were prepared and analyzed for proteins, carbohydrates, phenols and other organic compounds, and protein film forming solutions were cast in the presence of different glycerol concentrations. Both lower plasticizer concentration and lamination by additional corn zein layer were found to reduce film moisture content and elongation at break, while both film tensile strength and water vapor barrier properties resulted enhanced. The obtained bioplastics were finally processed by a new laboratory plastic moulding equipment specifically designed and fabricated to convert films to shaped containers. The use of either lower glycerol concentration or zein lamination gave rise to satisfactory vacuum thermoformed containers with acceptable resistance and stability. These findings open new perspectives in using BV proteins as a sustainable alternative to fossil fuel based plastics to produce a variety of properly shaped biodegradable articles. Supported by "Ministero degli Affari Esteri e della Cooperazione Internazionale"

P1.19

Profiling microbial communities in hyperalkaline waters of the Kizildag ophiolite complex (Turkey)

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It has recently been hypothesized that life on Earth could have been originated in hyperalkaline waters related to serpentinization of ophiolitic rocks, despite their extreme conditions (high pH and very low levels of nutrients). Five hyperalkaline springs of the Kizildag

ophiolite complex (Turkey) were characterized. The dominant gases are either H₂, CH₄ or N₂. Bacterial diversity, analysed by RISA (Ribosomal Intergenic Spacer Analysis) revealed different profiles for each spring. Sequencing of excised DNA bands allowed to identify the presence of *Bacillus*, *Ralstonia*, *Pseudoalteromonas*, *Ureibacillus*, *Alicyciphilus*, *Anaerococcus*. 16S ribosomal DNA sequencing by Illumina is in progress. Three samples were also positive for the presence of *pmoA* (encoding the key enzyme of methane oxidation) confirming the presence of methanotrophs in accordance to gas analyses that showed clues of microbial methane oxidation in the isotopic ratio. The presence of methanotrophs in these hyperalkaline springs highlights the extraordinary capability of the methanotrophs to adapt to extreme conditions.

P1.20

Allosteric control in the synthesis and sensing of cyclic-di-GMP, a master regulator of bacterial growth and physiology

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Cyclic-di-GMP (c-di-GMP) is one of the most important regulators of bacterial adaptation strategies including biofilm formation and persistence. C-di-GMP is able to interact with a large variety of macromolecules via deeply different binding modes; the combination of c-di-GMP affinity and binding mode(s) along a complex signaling pathway leads to a wide variety of allosteric control mechanisms, yet to be identified and characterized in detail biochemically. Here we present mechanistic data on the protein domain involved in c-di-GMP synthesis (GGDEF domain) as i) a isolated catalytic unit or ii) a modulator of other domains. Our model systems belong to proteins (YfiN and PA0575) from *P. aeruginosa*, which are involved in biofilm formation during chronic infections. The mechanisms of single-domain regulation by domain-domain interactions have been investigating, integrating advanced biochemical and molecular biophysics methodologies with structural biology. We aim at defining the structural determinants required to "handle" c-di-GMP in biological systems to ultimately being able to predict the mode of action of a given GGDEF-containing protein in different bacterial species.

P1.21

Microbial terroir of red and white wines from Tuscia

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Grapevine (*Vitis vinifera*) represents one of the most economically and culturally important fruit crop worldwide. The *V. vinifera* phyllosphere is colonized by bacteria and fungi that substantially modulate vine growth, berry development and grape and wine quality (Barata *et al.*, 2012). Thus, metagenomic approaches that can reliably analyze the microbial community structure are essential for studying microbial "terroir" and developing tailored strategies to improve wine quality. Next-generation sequencing (NGS) of nucleic acids has facilitated major advances in our understanding of microbial ecology and it is now widespread in biotechnological applications from medicine to foods. In this work, NGS analysis and conventional techniques (culture-dependent methods) were used to analyze microbial systems inhabiting two Italian grape varieties (Grechetto and Sangiovese) from the same Tuscia vineyard. Results demonstrated that the importance of indigenous microorganisms on wine's "terroir" could be only evaluated using NGS analysis of both bacteria and yeast populations.

P1.22

Recovering dredged sediments contaminated by total petroleum hydrocarbon to productive soils: the mycoremediation approach in the Bioresnova project

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Chemo-physical treatments to remove salinity and metal contamination from dredged sediments were applied in combination to bio-based approaches. New fungal specimen were isolated from the contaminated sediments and re-inoculated to remove the Total Petroleum Hydrocarbon (TPH) contamination. Toxicological assays were exploited to estimate the effectiveness of the process. In fact, the only chemical characterization of polluted matrices does not allow to predict its real toxicity eventually related to the original pollutants, their degradation intermediates and the synergic actions of the both. Higher plants were exploited as indicators of toxicity of the process and for the evaluation of the eco-safety of the final product. Genotoxicity and clastogenicity were monitored by the detection of chromosomal aberrations in mitotic cells and of micronuclei formation, detectable in interphase cells of root tips. The combination of the Chemo-physical and the Bio-based approach was able to remove the organic contamination (TPH) and the excess of sodium salts. The sediments were detoxified and converted in a humified productive soil, suitable for a safe re-allocation in the environment.

P1.23

Annurca apple (*M. pumila* Miller cv Annurca) extracts act against stress and ageing in *S. cerevisiae* yeast cells

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Over the years, a number of studies on the relationship between diet and ageing are growing and it was demonstrated that calorie restriction and some antioxidants extend lifespan in yeast and also in others model organisms. In particular, fruit and vegetable consumption has been related with improving health thank to polyphenols that have been demonstrated to possess a wide range of biological activities which may contribute to health beneficial effect against diseases including cancer, cardiovascular disease, diabetes, pulmonary disorders, Alzheimer's disease and other degenerative diseases. In particular it has been demonstrated that apples and derivatives have a role on ageing, cell stress and on different diseases such as cancer, degenerative and cardiovascular diseases. We used yeast, a unicellular eukaryotic organism, as a model to study the effect of apple supplement on ageing and cells oxidative stress and we showed that apple extract increases lifespan, reduces the accumulation of reactive oxygen species, and protect cells from regulated cell death.

P1.24

Improvement of actinorhodin production yield in *Streptomyces coelicolor* by immobilized-cell cultivations by using PCL- and PLA-based films

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