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Null mutation but not catalytic inactivation of AGO2 leads to ectopic expression of *nht* and downstream spermatogenesis genes. Depletion of either AGO2 or LaminB results in reduced looping interactions within the nht TAD as well as ectopic inter-TAD interactions, as detected by 4C-seq analysis. In the second half of this presentation, we show that AGO1 works as a coactivator of estrogen-induced enhancers. In brief, ChIP-seq analysis showed that AGO1 modulates Estrogen Receptor function onto such enhancers. Overall, our findings reveal that AGO proteins dictate genome architecture and thereby regulate gene expression with a concomitant impact on disease.

YI-S02

THE HITCHHIKER'S GUIDE TO THE GALAXY OF CSR/RSM RNA-BINDING PROTEIN FAMILY IN THE GENUS *PSEUDOMONAS*

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Cells can adjust its protein dosage by the modulation of multiple genetic circuits operating at different levels of the genetic information flow. In Bacteria, the regulation on gene expression at the post-transcriptional level by RNA-binding protein and small non-coding RNAs (sRNAs) offers an interesting mechanism, optimized to the adjustment of mRNA stability or translation rate involved in tight-control on costly phenotypes or synchronization of gene expression in a clonal population. The members of the Csr/Rsm family are small dimeric proteins with heterogeneous distribution across the bacterial tree of life, that act as global regulators of gene expression because they recognize characteristic sequence/structural motifs present in hundreds of mRNAs. This regulatory output is counteracted in most cases by molecular mimicry, non-protein coding RNAs that titrate the Csr-Rsm dimers away from the target mRNAs. In this talk, I will focus on the evolution of the Csr/Rsm protein family by comparative genomics approach. We shall explore the phylogenetical distribution of this particular RNA-binding protein family and some structural and functional aspect in Bacteria. Interestingly, bacterial genomes may possess from 2 to 6 paralogues of theses RNA-binding protein. In particular, within the *Pseudomonas* genus, we described, at least, 9 different subfamilies of Csr-Rsm based on sequence, structural and syntenic parameters. In average, we found 3 paralogues per genome, always belonging to different subfamilies. Finally, I will describe a specific subfamily, denominated RsmM, associated with lytic and temperate phages infecting representative of the *Pseudomonas aeruginosa* complex.

YI-S03

MALIC ENZYME FAMILY: STRUCTURAL-BIOCHEMICAL ANALYSIS TO IMPROVES CATALYTIC PROPERTIES

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Structure-function studies contribute to deciphering how small modifications in the primary structure could introduce desirable characteristics into enzymes without affecting its overall functioning. Malic enzymes (ME) are ubiquitous and participate in different biological functions as diverse as lipogenesis, photosynthesis and organic acid metabolism. In the presence of a divalent cation, this enzyme catalyzes the oxidative decarboxylation of malate to pyruvate, NAD(P)H, and CO_2. MEs of several sources including humans, pigeons, nematodes, bacteria, phytopathogens and plants have been kinetically and structurally characterized. Our results, which combine structural, biochemical, phylogenetic and functional analysis, show that this family have members with: different structural conformation (like homo/hetero-dimers, tetramers, oligomers, bifunctional enzymes), post-traductional modifications and specie-specific regulation. In relation to this, we recently gained novel information provided by the crystal structural analysis of the photosynthetic ME of maize and sorghum, and of the minimal functional ME structure known until now, from Candidatus *Phytoplasma mali*. Currently, we started applying all the knowledge obtained to perform rational design modification of two groups of enzymes: i. the bifunctional MEs, which have high potential to produce new generation of biofertilizers; and ii. the photosynthetic ME isoform, that is a key candidate to improve crop yields. By these strategies, we try to improve photosynthetic efficiency of agronomic crops that has not reached their maximum potential and will not be enough to feed the world´s population in the near future.

YI-S04

ASSESSING THE POTENTIAL OF *Rivularia halophila* FOR ARSENIC REMOVAL

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Rivularia halophila (*R. halophila*) is a filamentous cyanobacteria isolated from microbial mats of the Laguna Negra Lake (LN), Catamarca, Puna-Argentina. The LN is a high-altitude hypersaline lake, where extreme environmental conditions (i.e., high UV-radiation and extreme temperature, salinity, and water activity) restrict eukaryotic life. Besides, the presence of arsenic (As) has been detected in water, sediments and lithified microbial mats. This particular cyanobacteria is part of a microbial consortium that participates actively in the carbonate precipitation process. Taking this into account, the objective of this study were (i) to evaluate the capability of *R. halophila* to tolerate moderate to high As concentration and (ii) to assess the role of this cyanobacteria in carbonate precipitation with the potential incorporation of As in the carbonate lattice. Tolerance and resistance experiments were perform under different As (III and V) concentration, and evaluated by biomass growth, pigment intensity and chlorophyll a content. Besides, lethal dose 50 (LD 50) was also evaluated. On the other hand, carbonate precipitation experiments were perform under different calcium concentrations and moderate levels of As (similar to LN concentrations). Optical and electronic microscopy images of the precipitates were taken and measured near the cyanobacterial sheaths and from the bottom of the culture flask. DRX analysis were also performed. Preliminary results showed that *R. halophila* tolerates high concentrations of As (III and V), especially As (V), and can accumulate As in the sheath and in the cells. Moreover, *R. halophila* might facilitate carbonate precipitation in culture. The precipitation of amorphous crystals, near the sheath, were observed with the addition of As (V); while without *R. halophila* the minerals were mostly geometric, corresponding to chemical precipitation. All the results obtained until now, give us some clues about the potential of this cyanobacteria for As bio-removal.

YI-S05

CONTRIBUTION OF SOME TRANSCRIPTIONAL REGULATORS TO THE OLEAGINOUS PHENOTYPE IN RHODOCOCCI

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Oleagenicity is a property attributed to some microorganisms capable of accumulating high levels of intracellular lipids within the so-called lipid droplets (LDs). Some species of the *Rhodococcus* genus, such as *R. opacus* and *R. jostii*, are able to accumulate triacylglycerols (TAG) up to 60% or more of their cellular dry weight. For this reason, oleaginous rhodococci are promising microbial cell factories for the production of lipids to be used as fuels and oleochemicals. Although several genes involved in TAG biosynthesis and accumulation have been well described, it is not clear yet how these processes are regulated. In recent studies we have observed that some global and specific transcriptional regulators (TRs) contribute to the oleaginous phenotype in *Rhodococcus*. Between these TRs, three of them, known as GlnR, NlpR and TadR, act at different hierarchical levels and their mutation or overexpression significantly affected the TAG content in *Rhodococcus*. GlnR and NlpR act as putative global TRs, controlling a large set of genes associated with nitrogen, lipid and central metabolism. On the other side, TadR acts at a lower hierarchical level and regulates some specific genes associated with LDs ontogeny and lipid metabolism. Here, we presented some physiological and molecular evidences that confirm their roles on lipid accumulation in these bacteria and how is possible to deregulate this process for the optimization and recovery of these lipids. Based on these results, we proposed a comprehensive and integrative view on the regulatory attributes that explain the extraordinary capacity of these bacteria to synthesize and accumulate TAG at very high levels.

YI-S06

REGULATED CELL DEATH IN CYANOBACTERIA: NEW HORIZONS FOR DEVELOPING METHODOLOGIES TO FACE THE PROBLEM OF CYANOBACTERIAL BLOOMS

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Cyanobacteria are ancient photosynthetic prokaryotes globally widespread, synthesize potent toxins and proliferate massively, forming blooms. Cyanobacterial blooms represent a major ecological and human health problem worldwide. The conditions that promote massive bloom proliferation have been extensively studied but in contrast, mechanisms causing their abrupt termination are poorly understood. Cell death plays a vital role in the dynamics of ephemeral blooms and critically determines the flow and fate of organic matter and nutrients. In recent decades, regulated cell death (RCD) induced by biotic or abiotic stresses stands as a major mechanism to explain the disappearance of blooms. Nonetheless, knowledge of the molecular basis and physiological mechanisms behind RCD in Cyanobacteria is very limited. The present work describes recent advances in regulated cell death in *Synechocystis* sp. PCC6803. Research conducted in our lab has led to the identification of a new cell death program in response to heat stress with biochemical and morphological features resembling eukaryotic ferroptosis. Canonical ferroptosis inhibitors and Calcium (Ca^{2+}) prevent this cell death pathway. Moreover, this cell death process is dependent on iron availability and lipid peroxidation. Besides, cyanobacterial ferroptosis is characterized by depletion of glutathione (GSH) and ascorbic acid (AsA), and can be prevented by GSH or AsA addition. This is the first report of ferroptosis in a prokaryotic organism. Therefore, these results suggest that ferroptosis is an ancient cell death program conserved in