LVII SAIB Meeting - XVI SAMIGE Meeting

SAIB - SAMIGE Joint Meeting
2021 *on line*

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Phobius predicted that CACHE domain is present in periplasmic space, probably sensing extracellular signals. Although CACHE domains are widespread in bacteria, they present high variability and can sense different ligands. Comparison of BdcA CACHE to CACHE domains with known ligands did not give us a strong idea of a putative ligand for BdcA. BB2109 is a membrane, dual protein involved in motility regulation in *B. bronchiseptica*. Our analysis indicates that EAL and GGDEF domains have degenerated, hence PDE or DGC activity are not expected. PHYRE2.0 analysis yielded structural similarity to WalK protein from *Lactobacillus plantarum*. The histidine that is phosphorylated in WalK is also present in BB2109, suggesting a role for this amino acid in BB2109 function. *In silico* description of these proteins involved in the regulation of cdG in *B. bronchiseptica* is important to design new strategies and experiments to understand the role of this second messenger in the *Bordetella* pathogenesis.

MI-P122-202

PLASMID PREDICTION IN *Micrococcus* BACTERIAL STRAINS

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Plasmids are circular or linear extrachromosomal DNA molecules that replicate autonomously and occasionally provide their guests with bacterial extra genetic material important for their survival and adaptation. The sequencing of bacterial genomes has generated a vast wealth of data that can be processed by different computational tools to identify plasmid sequences. This would allow expanding the knowledge about plasmids and their diversity in most prokaryotic taxa. We tested this idea in a barely studied bacterial genus such as *Micrococcus*. These are environmental bacteria, and the best-known species is *M. luteus*, sometimes associated with skin and opportunistic infections. Other species show potential for biotechnological applications, as they can produce antibiotics, biofuels, enzymes and could be applied as biofertilizer or in bioremediation processes. Draft genomes were obtained from sequencing reads of 20 strains of *Micrococcus.* The combination of different methods on these genomes allowed us to detect the presence of sequences associated with plasmids in 17 of the selected strains. The predictions are not complete plasmids, but rather a set of fragments. In these sequences, genes directly associated with plasmid functions (replication and segregation) were detected, as well as accessory genes related to resistance to toxic compounds, oxidative stress, and antibiotics. To test the novelty of these predictions, they were analyzed with the software Copla to identify plasmid taxonomic units (PTUs). Only one set was classified in a PTU containing a diverse set of plasmids that could be involved in horizontal gene transfer between different phyla. Thus, most of the predictions might represent "novel" plasmids. In addition, a bipartite bacterial network was constructed with the plasmid predictions and known as actinobacterial plasmids. These networks include two types of nodes: "genomic" nodes representing each plasmid or genetic unit, and "protein" nodes representing clusters of protein sequences encoded by the different plasmids. Our network included 833 actinobacterial plasmids, 17 predictions, and 112878 proteins. The network had poor connectivity, with most of the nodes consisting of single elements related to isolated plasmids. 80% of the nodes were hypothetical proteins and 69% included only one protein sequence. From the non-hypothetical proteins, 1438 were annotated as transposases, an abundant element in plasmids, and they formed the largest clusters. This suggests that most actinobacterial plasmids are "unique" and highlights the lack of knowledge on the biology and roles of these mobile genetic elements in Actinobacteria. Still, this represents a significant addition to the *Micrococcus* plasmid sequences pool and the first step in a study over the whole phylum.

MI-P123-210

MODULATION OF ACIL-COA CARBOXYLASE ACTIVITY IN *Mycobacterium tuberculosis*: CHARACTERIZATION OF MAF PROTEIN

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Mycobacterium tuberculosis is the etiological agent of tuberculosis, an infectious disease with the highest cause of death in the world. Currently, it has been reestablished since the breach of extensive treatments with antibiotics, the continuous appearance of strains resistant to specific antimycobacterial drugs, and the HIV epidemic. In actinobacteria, a group of enzymes called acyl-CoA carboxylases complexes (ACCasa) catalyzes an essential step in the synthesis of fatty acids, the carboxylation of acetyl-CoA to produce the precursor malonyl-CoA. These enzymes can also carboxylate other substrates and have an important role in the synthesis of membrane lipids and cell wall. The cell walls of mycobacteria are unusually rich in lipids and have a huge variety of components that are essential for their viability, and the pathogenicity of these microorganisms. In *M. tuberculosis* and *M. leprae* the ACCasas enzymes produce malonyl-CoA, which is the precursor for the synthesis de novo of fatty acids and to produce meromycolic acids. Furthermore, these pathogens are capable to synthesize mycolic acids, mycocerosic acids, and methyl-branched fatty acids, for which they need other precursors such as methylmalonyl-CoA, formed by the carboxylation of propionyl-CoA. *M. tuberculosis* genomic analyses revealed that 3 genes encode the subunits α (accA1-3), and 6 genes encode the subunits β (accD1-6). Thus, *M. tuberculosis* might have 6 putative different ACCasa complexes. Mutagenesis studies postulate that the subunit α, AccA3, 3 subunits β, AccD4, AccD5 y AccD6, and the subunit ε, AccE5, might be essential for the viability of the microorganism. Even though some of these complexes are well characterized in many aspects, there is little information about their transcriptional and post-transcriptional regulation. The complex ACC5, formed