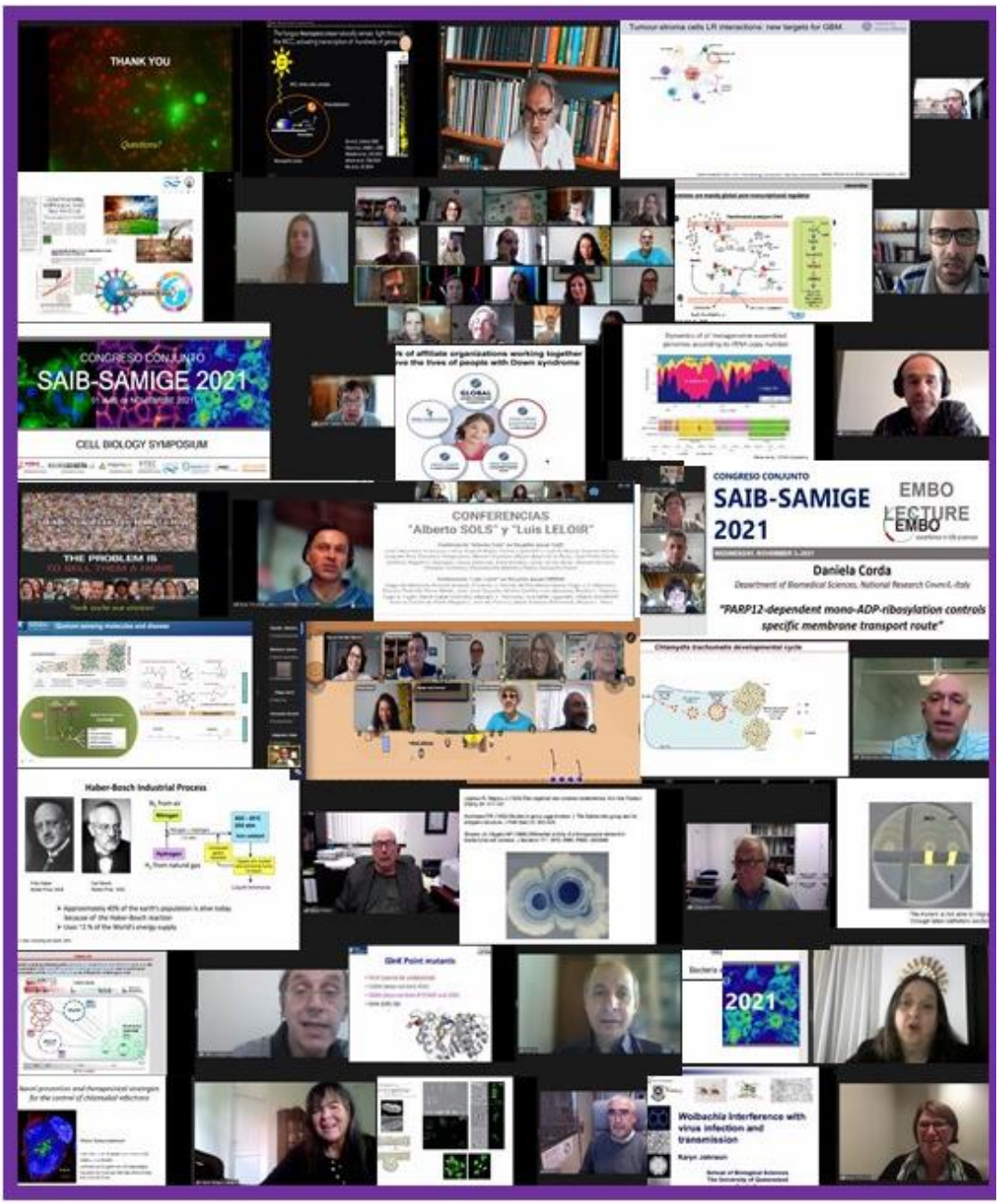
BIOCELL 46 (Suppl. 1), 2022
ISSN 0327- 9545 (printed version)
ISSN 1667-5746 (online version)

SAIB - SAMIGE Joint meeting
2021 *on line*



November 1-5, 2021

BIOCELL 46 (Suppl. 1), 2022
ISSN 0327- 9545 (printed version)
ISSN 1667-5746 (online version)

LVII Annual Meeting of the Argentine Society for Biochemistry and Molecular Biology Research (SAIB)

XVI Annual Meeting of the Argentinean Society for General Microbiology (SAMIGE)

SAIB - SAMIGE Joint meeting 2021 *on line*

triacylglycerols (TAG), diacylglycerols and free fatty acids in comparison to the control cells carrying the empty inducible vector. In addition, quantitative gas chromatography analysis revealed an increase of 1.9-fold in total fatty acid content (8.97% CDW) in ATCC15960 pTipQC2/*nlp*R_{RHA1} in comparison to the control cells, after cultivation in minimal salt medium with glucose (1%, w/v) and nitrogenlimiting conditions (0.1 g/L of ammonium). Unexpectedly, the heterologous expression of $NlpR_{RHA1}$ in *R. erythropolis* ATCC 15960 promoted the production of a co-polymer of 3-hydroxybutyrate-*co*-3-hydroxyvalerate (12.04% CDW), whereas the control cells produced only traces of the copolymer. In contrast, *nlpR*$_{RHA1}$ overexpression in *R. jostii* RHA1 increased only the total fatty acid content in cells and neutral lipid fractions (TAG, DAG, MAG), but it did not promote the PHA biosynthesis. These results demonstrated that the pleiotropic transcriptional regulator NlpR can be considered an interesting tool for genetic modification of rhodococcal species to improve lipid production. Deregulation of cell metabolism by NlpR expression can produce differential phenotypic effects among rhodococcal species.

MI-P052-96
CONTRIBUTION OF A SPECIFIC XRE FAMILY TRANSCRIPTIONAL REGULATOR TO THE OLEAGINOUS PHENOTYPE IN RHODOCOCCI

Hernández MA[1], *Ledesma A*[2], *Alvarez HM*[1]
[1]*Universidad Nacional de la Patagonia San Juan Bosco, INBIOP-UNPSJB-CONICET;* [2]*Universidad Nacional de Santiago del Estero, CIBAAL-CONICET. E-mail: mahernandez@unpata.edu.ar*

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. Global and specific transcriptional regulators (TRs) contribute to the oleaginous phenotype in *Rhodococcus*. Among specific TRs, a XRE family transcriptional regulator (TR) is associated with the lipid droplet ontogeny through regulation of a structural protein coding gene. In this work, we study the role of this specific TR on lipid metabolism in oleaginous rhodococci at the physiological and molecular level. Bioinformatic analysis revealed the occurrence of this regulator only in actinobacteria. In addition, the occurrence of putative TR boxes into the promoters' regions varied between oleaginous *Rhodococcus* strains and non-oleaginous strains. Docking studies revealed putative interactions of this specific TR with palmitic acid. *In vitro* and *in vivo* assays confirmed that the TR binding capacity to DNA is controlled by long chain fatty acids or their acyl-CoA derivatives. Glutaraldehyde (GT) cross-linker assay and limited proteolysis analysis revealed that long chain fatty acids induce oligomerization and conformational changes of TR, respectively. Furthermore, putative binding sites for this TR within upstream regions of genes coding for a lipase, an acyl-CoA dehydrogenase and the fatty acid synthase complex (FASI) were found and validated by EMSA and RT-PCR assays. Finally, deregulation of the TR levels by overexpression of the corresponding gene was used as a strategy to improve TAG biosynthesis and lipid recovery for biotechnological purposes under rich nitrogen conditions. We propose a model in which the activity of this TR is controlled by fatty acyl-CoA pools in cells according to the nutritional conditions of the environment. In addition, this protein participates in the regulatory network controlling lipid metabolism and lipid droplet formation in oleaginous rhodococci.

MI-P053-113
CONTRIBUTION OF UNCHARACTERIZED GENES TO *Acinetobacter baumannii* ENVELOPE FUNCTIONS

Giacone L, Repizo G, Morán-Barrio J
Instituto de Biología Molecular y Celular de Rosario (IBR-CONICET). Facultad de Cs. Bioquímicas y Farmacéuticas (UNR). E-mail: giacone@ibr-conicet.gov.ar

Acinetobacter baumannii (Ab) is a nosocomial pathogen, of major concern due to its multi-drug resistance (MDR) and the recent appearance of hyper-virulent strains in the clinical setting. The World Health Organization included Ab as a critical priority pathogen for the development of novel antibiotics. Ab pathogenesis is associated with a multitude of potential virulence factors (VF) that remain poorly characterized. It is well known that many bacterial envelope components, such as outer membrane proteins (OMPs) and exopolysaccharides facilitate the establishment of a disease state, the persistence in abiotic surfaces and resistance to antibiotic treatment. We previously reported a bioinformatics prediction of *A. baumannii* AB5075 genes coding for uncharacterized OMPs with putative roles in the pathophysiology of Ab. Analysis of mutants in the corresponding genes (1) revealed that four of them showed reduced A549 cell adherence and invasion (2), thus indicating virulence roles for the corresponding proteins. Here, we further analyze the physiology of these four mutant strains. First, *in silico* analysis of the candidate proteins revealed that two of them share high similarity with bacterial domains related to stress response or involved in protein-protein interaction and degradation, with roles in the maintenance of outer membrane integrity. The third protein shares low similarity with a protein involved in biofilm formation in *Escherichia coli*, while no domain similarity was found for the fourth one. In addition, synteny analysis showed that three of the corresponding genes are in proximity to genes related to stress response or other virulence processes like capsule formation, thus suggesting probable regulatory functions. Based on these analyses, we conducted several assays in order to characterize the surface properties of