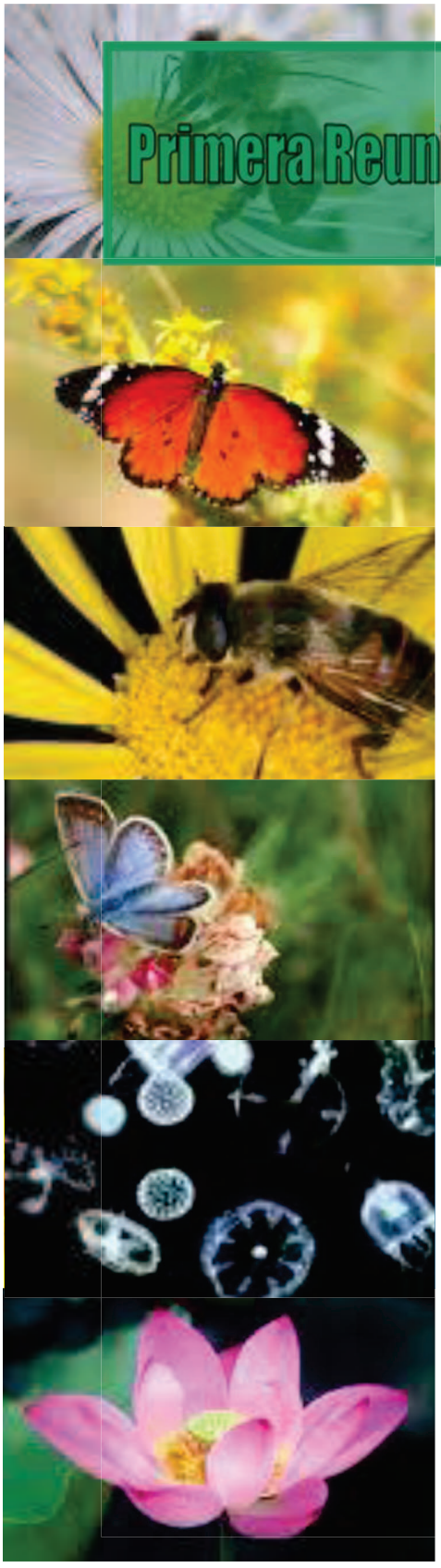

Primera Reunión de Fotobiólogos Argentinos

LIBRO DE RESUMENES

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CONFERENCIAS

Extremophilic *Acinetobacter* strains from High-Altitude Lakes in Argentinean Puna: UV-B resistance and DNA repairing mechanisms involving photolyases.

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High-Altitude Andean Lakes (HAAL) at the northwest of Argentina (from 3,000 to 6,000 masl) are extreme environments of biotechnological interest. A collection of 200 extremophilic strains which displayed multiple resistance profiles to diverse environmental stress: hipersalinity, high UV-B irradiation and arsenic. has been built. The aim of this work is to study the UV-resistance profile of four extremophilic strains from the genus *Acinetobacter* by partially characterize their photorepairing mechanisms upon UV-B DNA damage. In addition, we present *Acinetobacter* sp. Ver3 whose recent genome sequencing revealed the presence of interesting and novel photoreceptors such as photolyases.

Acinetobacter spp. N40, Ver3, Ver5, Ver7 and sensitive strains *Acinetobacter baumannii* DSM 30007 and *Acinetobacter jhonsonnii* DSM 6963 where exposed to UV-B light (38 kJ) in liquid media. The control strains were not able to maintain their population after the UV-B exposure while *Acinetobacter* sp. Ver7 showed 100% survival after the irradiation, *Acinetobacter* sp. Ver5, 50% and *Acinetobacter* sp. Ver3 and N40 20% and 1% respectively. After the DNA damage, the strains were exposed to light (PR) and dark repair (DR) during 2 h and DNA photoproducts in total genomic DNA after each treatment was measured using HPLC-MS/MS. *Acinetobacter* sp. Ver3 and Ver5 were able to completely recover their initial population after PR. *Acinetobacter* sp. N40 also was able to increase their population thanks to the PR (60%). In contrast, *A. baummanii* was not able to recover after PR, while *A. jhonsonnii* recovered partially in a 15%. DR was not efficient for recovering the initial population for all strains. The most efficient strains to deplete TT-CPD and CT-CPD under PR were *Acinetobacter* sp. Ver3 and Ver7 with a reduction of 90% and 100% compared to the controls non-PR, respectively.

Genome analyses (performed after pyro-sequencing and RAST annotation) revealed the presence of two different photolyase-coding sequences in Ver3. Upon BLAST analysis the nearest matches of one of them (PL1) was found to be the photolyase (ZP06727183) from *A. haemolyticus* ATCC 19194 (62% identity) and the photolyase (ZP06062937) from *A. johnsonii* SH046 (61% identity). In turn, the nearest matches for the second photolyase (PL2) were the deoxyribodipyrimidine photolyase-related protein (ZP06693260) from *Acinetobacter* sp. SH024 (70% identity) and the photolyase (ZP06066462) from *A. junii* SH205 (61% identity). The conserved domain architecture retrieval tool from the NCBI database revealed a different domain structure for the studied photolyases. Based on homology modeling, a strong three-dimensional similarity to the photolyase from *E. coli* (PDB 1DNPA) was observed for the PL1. Overexpression of the PL1-coding sequence revealed it can be functional and improve UV-B resistance profiles in *E. coli* cells. Functional characterization of the purified photolyase proteins is ongoing.