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medium (CM) showing a 2.5-fold increase in the exponentially growing cells supplemented with CM compared to the control cells. The identification of genes that respond to different growth stages and the characterization of signal molecules involved in this process will help to understand the nature of the molecular mechanism of cellular communication used by the haloarchaea in extreme environmental conditions. Supported by UNMDP, ANPCyT and CONICET. *Enrique Madrid y Micaela Cerletti contribuyeron en igual proporcion.*

**MM-P11**

**EFFECTS OF GENOMIC CONTEXT ON *Escherichia coli* DNA MUTATION RATE**

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In *Escherichia coli* the transitory hemimethylated state of adenines in GATC sequences provide the strand discrimination signal to direct the DNA mismatch repair system (MRS). Strains deficient in any of the principal components of the MRS (MutS, -L, -H, and Dam proteins) are mutators. It has been reported using plasmid heteroduplexes that a decrease in the number of GATC sequences within these vectors lowered the efficiency of mismatch repair *in vitro* and *in vivo*. We analyzed the effect of genomic GATC density on mutation rate in *E. coli*. We introduced a mutated copy of a gene able to confer antibiotic resistance within a genome region with a high or low density of GATC sequences and analyzed the reversion rate of the mutation. Our results show, unexpectedly, that the reversion rate was lower in strains containing the mutated gene in a genomic region with a low density of GATC sequences, than those located in a high density context. Moreover, the reversion rate of the mutated gene located in the low GATC density region of a MRS deficient strain was lower than the reversion rate of the mutated gene located in the GATC high density region of a wild type strain. Two possibilities are discussed: 1- Other(s) *cis* or *trans* acting factor(s) influence the mutation rate; 2- The high and low GATC density genomic regions differently affect the transcription rate of the reporter gene.

**MM-P12**

**CONDITIONED MEDIUMS MODULATE EXPRESSION OF THE RCSB-REGULON GENES IN *S. typhimurium***

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The Rcs is an unusual phosphorelay system composed of the inner membrane proteins RcsC and RcsD as sensors, and the response regulator RcsB. At the present, the signals that lead to activate the Rcs phosphorelay system remain unknown. Even though, a wide range of conditions have been described as Rcs system activation state. The growth at low temperature or on solid surface; the polymyxin B exposition; the DjlA overproduction, the *rcsC11* constitutive mutation; mutations that affect cell envelope like *tolB* and *pmrA*, or *rcsB* overexpression are some examples of this activation states. Previously, we reported that the *rcsB* gene is transcribed from two promoters: i) $P_{rcsDB}$ located upstream of *rcsD*, and ii) $P_{rcsB}$ located within the *rcsD* coding region. The first promoter is induced during the exponential growth phase while the last one it does at lower levels in stationary phase. We also reported that the RcsB overproduction repressed the *rcsD* expression by directly binding to the $P_{rcsDB}$ promoter. The repression, resulting in a differential rate of *rcsD* and *rcsB* genes expression levels, was also observed using *rcsC11* mutant or polymyxin B to induce the system. Under these conditions an increased level of RcsB was observed when the bacteria reach the stationary growth phase and the regulator began to be also transcribed from $P_{rcsB}$. In addition, the $P_{rcsB}$ is physiologically required to maintain the repression on swarming behavior. The subject of the present work was to determine if an Rcs stimulation factor is excreted to the supernatant of *tolB* and *pmrA* mutant culture. This finding would allow us to identify the Rcs system signal. Here, the supernatant obtained from the above mutants' cultures, as "conditioned mediums", was used to determine the reporter expression levels. The *cps* and *flhDC* operons were the reporter of the factor presence in the conditioned mediums. We demonstrated that the *cps* and *flhDC* operons were modulated under the growth on these mediums. As RcsB regulator is expressed exponential and stationary phase and the above reporters are exponentially controlled, we looking for reporter RcsB-depended gene that are transcribed in stationary phase like *bapA* gene. Here we report that *asr* is a new member of the RcsB regulon, which was reported as an stationary phase expressed gene. Additionally, we studied the expression modulation of *asr*, *bap*, *cps* and *flhDC* using conditioned medium harvested from both different growth phase in order to relate with expression of RcsB regulator. Under this condition we observed a growth phase-dependent expression mediated by RcsB. These results increase the Rcs system knowledge on regulon and ligand identification issues.