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MI-P09
STABILITY OF THE POINT MUTATION OF THE *Salmonella thyphimurium rcsC11* ATTENUATED STRAIN

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The foodborne diseases are usually caused by *Escherichia coli*, *Shigella*, *Listeria* and *Salmonella*, which is the most prevalent bacterium in Argentina. The *Salmonella* infection involves many steps where the modulation of genes located in different pathogenesis islands are coordinately controlled. The RcsCDB system of *Salmonella* controls the colanic acid, flagellar and biofilm synthesis, as well as others virulence processes. Previously, we have studied the *rcsC11* mutant harboring a point mutation in the histidine kinase domain of RcsC sensor. This change produces the RcsCDB system constitutive activation, resulting in a mutant with mucoid phenotype and attenuation of virulence. Here, we evaluated the ability the *rcsC11* mutant to infect non-phagocytic and phagocytes eukaryotic cells. We also investigated the reversion degree of the *rcsC11* mutant to wild-type state by loss of the mucoid phenotype, by means of temperature changes, crop aging and chemical mutagenic agent challenges. We found that the *rcsC11* mutant produced strong immunogenic response and it was unable to replicate in macrophages. Moreover, no revertant strains were isolated in any of the treatment analyzed, strongly suggesting that the *rcsC11* mutation would be fairly stable. The results of this study represent a significant contribution that supports the use of the *rcsC11* mutant as candidate for vaccines development.

MI-P10
Lactobacillus reuteri CRL1098 SOLUBLE FACTORS EXERT *IN VITRO* AND *IN VIVO* ANTI–INFLAMMATORY EFFECTS

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Soluble factors produced by probiotic bacteria such as lactobacilli can modulate immune system responses. The aims of this study were to determine whether *Lactobacillus reuteri* CRL1098 soluble factors (LrS) were able to modulate *in vitro* the inflammatory response triggered by LPS in murine macrophages (RAW 264.7) and to evaluate *in vivo* their capacity to exert anti–inflammatory actions in acute lung injury (ALI) induced by LPS in mice. *In vitro* assays demonstrated that LrS significantly reduced the production of pro–inflammatory mediators (NO,COX–2,Hsp70) and pro–inflammatory cytokines (TNF–α, IL–6) caused by the stimulation of macrophages with LPS. Results from flow cytometry assays revealed that LrS reduced apoptosis of LPS–challenged RAW cells. Bax expression was reduced while no significant difference was observed in Bcl–2 expression levels. In addition, the effect of LrS on NF–κB pathway was evaluated by immunofluorescence microscopy: inhibition of NF–κB translocation to the nucleus in LrS–treated macrophages exposed to LPS was detected, as well as a reduction of Akt and increase of ERK phosphorylation. *In vivo* assays proved that the LPS–induced secretion of the pro–inflammatory cytokines, inflammatory cells recruitment to the airways and inflammatory lung tissue damage were reduced in LrS treated mice, providing a new way to reduce strong pulmonary inflammation.

MI-P11
CHOLINE CONTRIBUTES TO INCREASE SOME PATHOGENIC FACTORS IN DIFFERENT *Pseudomonas syringae* STRAINS

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P. syringae infects a wide variety of plants and causes necrotic symptoms in leaves, stems, and fruit. It is considered a hemibiotrophic pathogen because it is able to obtain nutrients from living host cells in order to multiply in the apoplast and infect close tissues. Choline (Cho), an alkylammoniun compound, is a normal constituent of plant tissues and in the apoplast is found as a component of phosphorylcholine (Pcho). *P. syringae pv. tomato*, *P. syringae pv. tabaci*, and a local strain that we isolated and named S5, use Cho as nitrogen source. These strains produce the enzyme phosphorycholine phosphatase (PchP), capable to generate free Cho from Pcho. In S5, Cho increases at least two virulence factors: tabtoxin and swarming mobility. S5 was isolated from oat leaves from a south field of Córdoba, and the strain was characterized in our laboratory by bioinformatic, microbiology, biochemical and molecular approaches. By the analysis of *ARN16S*, S5 was classified as *P. syringae pv. atropurpurea*. The BOX fingerprint of S5 resulted similar to those of *P. syringae* isolated from different host plants of our area. We conclude that S5 is a potentially dangerous bacterium, able to obtain nutrients from host and enhance the production of