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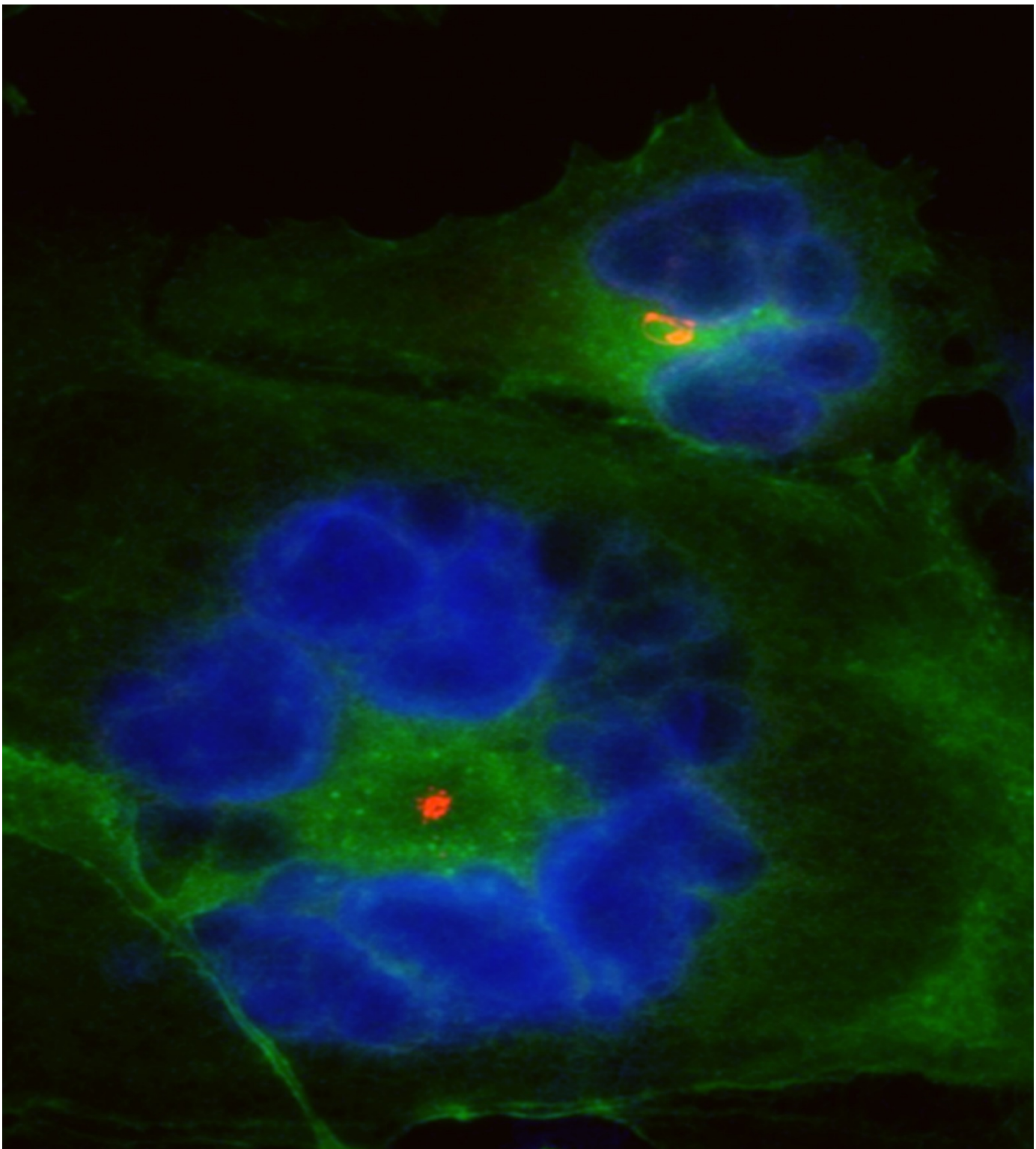

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Cover page: The Synthetic Lethal Rosette

Aberrant mitotic phenotype found in BRCA1-deficient cells treated with the PLK1 inhibitor Volasertib. Cells become giant and multinucleated and acquire a flower shape, with nuclei arranging in a circular disposition around a cluster of centrosomes. Blue (DAPI: nuclei), Green (FITC-phalloidin: actin cytoskeleton), Red (γ-Tubulin: centrosomes).

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MI-P40
CHARACTERIZATION OF THE CELL WALL ASSOCIATED PROTEINASE ACTIVITY FROM *LACTOBACILLUS DELBRUECKII* STRAINS

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Lactic acid bacteria (LAB) have a very long history of use in the manufacturing processes of fermented dairy products. During milk fermentation process, the proteolytic system of LAB plays a key role because it enables these bacteria to grow in milk. LAB are fastidious microorganisms that require an exogenous source of amino acids or peptides, which are provided by the proteolysis of casein, the most abundant protein in milk and the main source of amino acids. The proteolytic system of LAB consists of a cell envelope-associated proteinase (CEP), amino acid and peptide transport systems and various intracellular peptidases. The CEP is the key enzyme of the system and it is responsible for casein initial degradation. In the present work, the goal is to characterize the proteinase activity of 36 *L. delbrueckii* strains belonging to the CERELA culture collection considering the major economic importance of these species as dairy starters. All strains were subjected to genotyping using the rep-PCR technique to group those isolates corresponding to clones of the same strain. One representative of each profile group was selected to further characterize their CEP enzymes. The strains were grown in a chemically defined medium (CDM) and their proteolytic activities were evaluated by two methods: the degradation of the chromogenic substrate succinyl-alanyl-alanyl-prolyl-phenylalanine-p-nitroanilide; and by the degradation profiles of alpha- and beta-casein by SDS-PAGE. Results from the hydrolysis of alpha- and beta-casein degradation evidenced six types of caseinolytic cleavage specificity. Since proteolytic activity is repressed under high peptide content, we next study the inhibitory effect of peptides concentration on the CEP activity by growing bacterial cells in CDM plus Casitone. The proteolytic activity was repressed in the presence of peptides; however the strength of repression was strain-dependent. Finally, the release of these CEPs from the cell envelope was observed after treatment with 2 M NaCl. These results contribute to enlarge the limited knowledge on thermophilic lactobacilli CEP and are important from an industrial point of view since during the manufacture of hard cheeses, high concentrations of NaCl are present, and CEPs would remain active either bound to the cell or released, maintaining the beneficial health effects of the fermented milk products.

MI-P41
ANTIFUNGAL ACTIVITY OF METALS-FLAVONOID COMPLEXES AGAINST PHYTOPHATOGENIC FUNGI WITH AGRONOMIC INTEREST

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Phytopathogenic fungi are organisms that cause disease in plants; they affect agricultural production generating large economic losses in diverse crops. The need to find new environmental-friendly fungicides has led researchers to search for compounds that accomplish this concept. Naringin (NAR) and naringenin (NGE) are flavonoids obtained from wastes of the Citrus industry, with diverse biological properties. These flavonoids can form complexes with ion transition metals. Currently, the study of the antifungal properties of metal-flavonoid complexes is practically unexplored. In this work, the antifungal activity of some metal-flavonoid complexes was evaluated against three phytopathogenic fungi. This activity was quantitatively evaluated by contact assay using potato dextrose agar as culture medium. In *Sclerotium rolfsii*, solutions of Cu(II)-NGE (62 mmol/L), Cu(II)-NAR (32 mmol/L), Ni(II)-NAR (32 mmol/L) and Mn(II)-NAR (14 mmol/L) complexes were tested. Also, flavonoids NGE (124 mmol/L) and NAR (64 mmol/L) were assayed alone. For *Rhizoctonia solani* and *Sclerotinia sclerotiorum,* Cu(II)-NAR (32 and 16 mmol/L), NAR (64 and 32 mmol/L) and $CuSO_4.5H_2O$ (32 and 16 mmol/L) solutions were tested. To prepare these solutions, N, N-dimethylformamide/water 10 % (v/v) have been used as a solvent. The assays were realized with five replicates for each treatment. The results revealed that *S. rolfsii* was highly inhibited by Ni(II)-NAR complex (91 %), followed by Cu(II)-NGE (72 %), Mn(II)-NAR (36 %) and Cu(II)-NAR (3 %), whereas NGE caused only 24 % of inhibition and NAR not manifested antifungal activity. Solutions of Fe(III)-NAR (40 mmol/L), Co(II)-NAR (24 mmol/L) and Cr(III)-NAR (6 mmol/L) were also tested, but they not exhibited activity. *S. sclerotiorum* not presented inhibition by any of the compounds assayed. For *R. solani*, only the solution of $Cu(II)SO_4.5H_2O$ at 32 mmol/L caused significant inhibition (16 %). In conclusion, this study is probably the first reported about the antifungal activity of this kind of compounds, and it demonstrates that some of these coordination compounds have potential as new environmental friendly fungicides.

MI-P42
PROTEOMIC ANALYSIS TO UNDERSTAND CR(VI) HOMEOSTASIS IN *STREPTOMYCES* SP. MC1

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Chromium is a heavy metal widely used in a variety of industrial processes (leather tanning, steel production, metal corrosion inhibition). Hexavalent chromium is carcinogenic and presents higher toxicity than trivalent form since Cr(VI) is more water-soluble and mobile than Cr(III). Industrial effluents containing Cr(VI) are released into water courses, mostly without proper treatment, resulting in anthropogenic contamination. Over the last years, bacteria-mediated removal or stabilization of heavy metal into no or less toxic forms has become in an effective biotechnological process. In this sense, several physiological studies on *Streptomyces* sp. MC1, an actinobacteria isolated from a polluted soil in the province of Tucumán (Argentina), demonstrated be able to grow in presence of Cr(VI) and remove the metal both in liquid medium and contaminated soils. However, the molecular mechanisms involved are unknown in this actinobacteria. MS-based proteomics have become a powerful tool to understand the mechanisms that underlie physiological processes. In the present work, we use MS-based, label-free and