XIX CONGRESO DE LA SOCIEDAD ARGENTINA DE MICROBIOLOGÍA GENERAL

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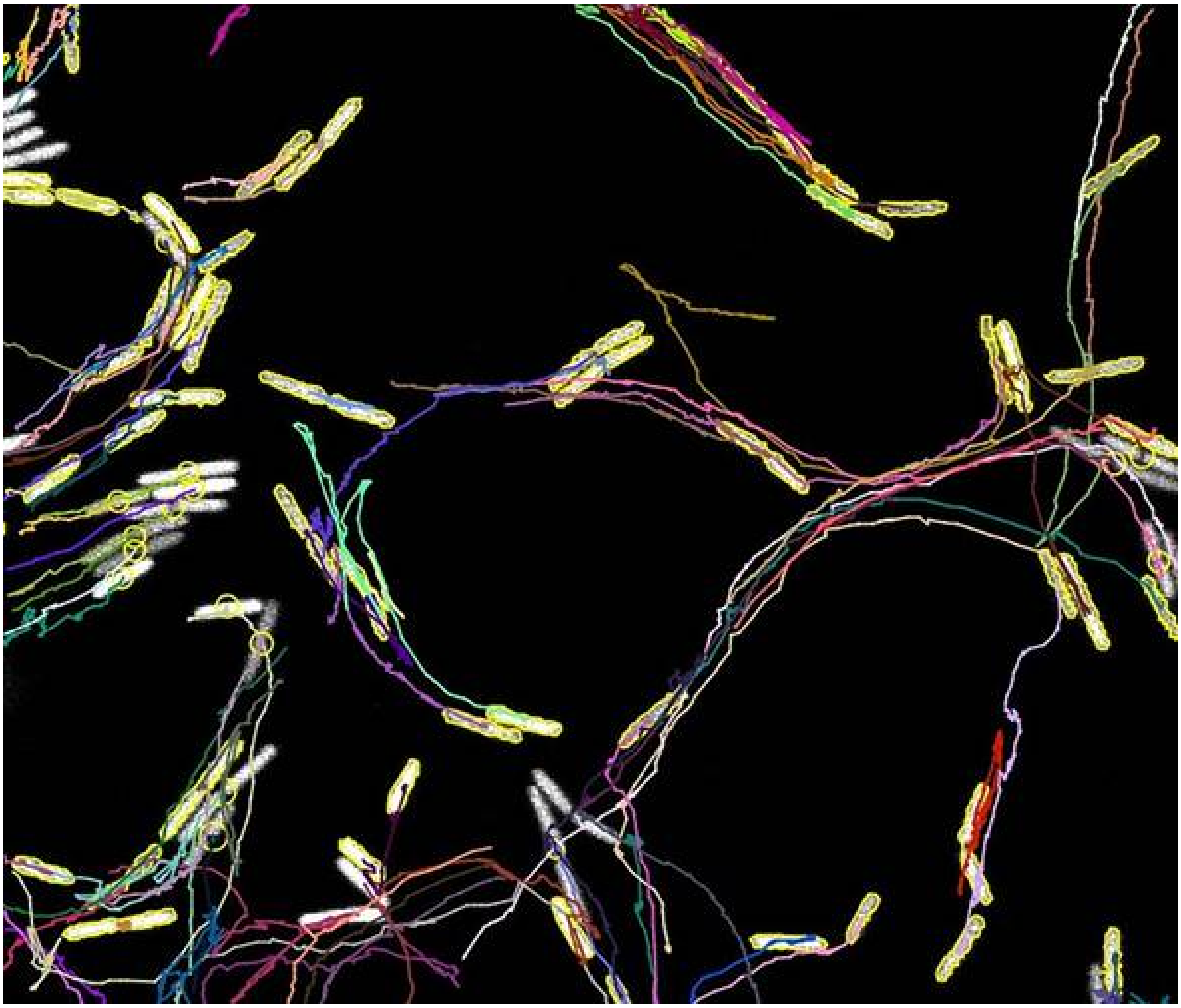

Foto: Se hace camino al andar. Celeste Dea. 1er puesto. Concurso fotográfico SAMIGE 20 años.

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SYSTEMIC APPROACH FOR THE DETECTION OF GENES INVOLVED IN THE GENERAL STRESS RESPONSE IN Sinorhizobium meliloti

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Bacteria collectively known as rhizobia are proteobacteria capable of establishing interactions with plants, mainly legumes. In this context of interaction, rhizobia with the capacity to fix atmospheric nitrogen supply it to plants as a nutrient source, in exchange for the supply of carbon sources to maintain the fixation system in operation. The establishment of the symbiosis is finely regulated in its different stages, from recognition between symbionts to nodular development, and all these stages are susceptible to be affected by the different abiotic stresses present in the soil. The action of these factors leads to the failure of the establishment and/or functioning of the symbiosis and, therefore, to the loss of nitrogen supply to the plant. Bacteria activate cellular responses to the abiotic stresses they face in nature. Sometimes these responses not only enable them to cope with the stresses that affect them, but also allow them to enhance their performance against other environmental stresses, an effect known as cross-stress response. This type of response shares common genetic factors that can be integrated into a general stress response by bacteria. To expand the understanding of stress defense in rhizobia, systems biology techniques were used to recognize the cellular components involved in general stress defense. For this purpose, transcriptomes of *S. meliloti* growing under stress conditions deposited in the EMMA2 database (Rhizogate) were selected. From them, studies of *S. meliloti* in exponential growth phase and subjected to different abiotic stresses (salinity, high osmotic pressure, acidity, iron deficiency) were selected. From the genes showing differential expression for each experiment, matrices were generated and, using Geneck software, coexpression networks were created using the available algorithms. From these networks, a consensus network was generated using Cytoscape software, which allowed the detection of possible central genes (hubs or nodes) that determine the topology of the network. Based on the results obtained, the gene SMa1241, which encodes the NapE protein, part of the periplasmic nitrate reductase complex (Nap), was selected. The deletional mutant Sme2011?*napE* was generated for phenotypic characterization, evaluating its growth under different stress conditions. So far, the results obtained showed an altered growth of the mutant strain under conditions of salt stress, osmotic stress and P deficiency. Notably, this gene did not show significant differences in any of the studies performed with the individually applied stresses, validating the systemic approach as a sensitive approach to detect macromolecular components of *S. meliloti* involved in the general defense against abiotic stresses.

Palabras clave: System Biology - Sinorhizobium meliloti - Stress