Sociedad Argentina de Microbiología General

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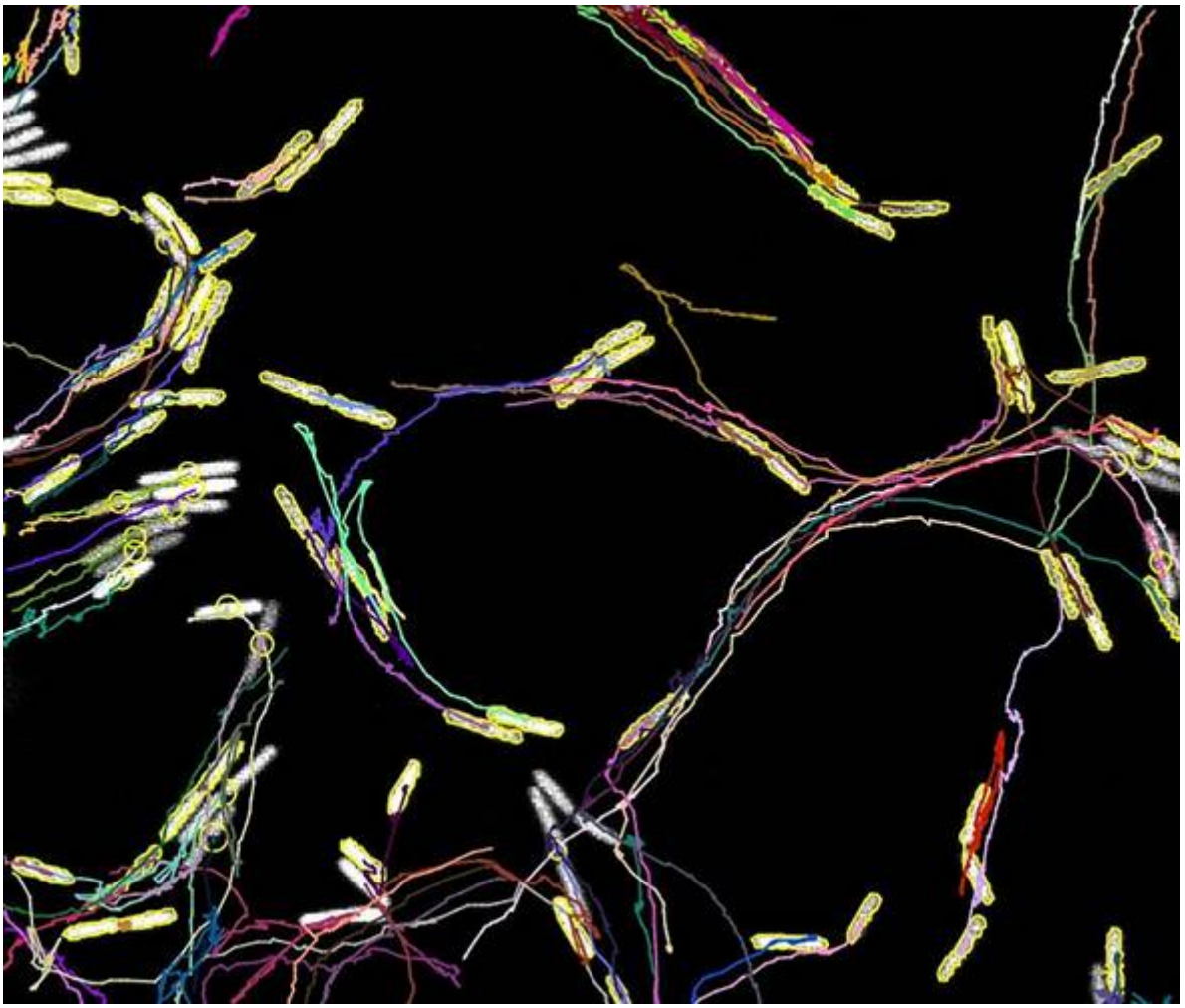

Foto: Se hace camino al andar. Celeste Dea. 1er puesto. Concurso fotográfico SAMIGE 20 años.

IDENTIFICATION OF TRANSCRIPTION FACTORS INVOLVED IN *Rhizobium favelukesii* LPU83 RESPONSE TO ACID CONDITIONS

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The sustainable agriculture is a green-friendly practice, which its objective is to reduce the damage of conventional techniques, like the extensive use of chemical fertilizers. One sustainable agriculture strategy to replace those fertilizer is the use of symbiotic microorganisms capable of Biological Nitrogen Fixation (BNF) with legumes. In the symbiotic interaction between *Sinorhizobium meliloti*-alfalfa this microsymbiont fixes nitrogen. However, moderately low pH (around 5.5) particularly affects *S. meliloti*, thereby negatively impacting the symbiotic interaction. Our group has characterized a new rhizobium, designated *Rhizobium favelukesii* LPU83, which can nodulate alfalfa but cannot fix nitrogen efficiently. Notably, *R. favelukesii* can grow at a pH as low as 4.6 and also nodulates in moderately acidic conditions. These characteristics make *R. favelukesii* LPU83 a valuable model for studying different mechanisms of acid tolerance. In previous studies, our group conducted transcriptomic and proteomic analyses of *R. favelukesii* LPU83 growing in minimal medium at pH 7 and 4.6. The results showed that 844 genes and 120 proteins were overexpressed under acidic conditions. Among these differentially expressed genes and proteins, we are particularly interested in studying those annotated as Transcription Factors (TFs). TFs play a crucial role in the survival of cells in various environments by regulating gene expression, enabling them to control different regulatory mechanisms. Our goal is to elucidate and study the TFs that are important for the acid tolerance response of *R. favelukesii* LPU83. To achieve this, we analyzed the transcriptomic and proteomic data mentioned earlier. We first filtered these data to identify proteins annotated as TFs in *R. favelukesii*. A set of 121 TFs where identified, from which 15 and 11 were over-expressed and under-expressed under acid condition, respectively. A second step implicates searching for those 15 TFs its homologs in S. meliloti. Finally, we continued working only with those *R. favelukesii* TFs whose *S. meliloti* homologs were either under-represented or showed no change in expression levels under acidic conditions. The TFs that met all these criteria are: LPU83_0133 (annotated to allow RNA polymerase to continue transcription beyond a termination site); LPU83_0873 (related to iron deficiency and nitric oxide); LPU83_2879 (regulates amino acid pathways); LPU83_3154 (involve in signaling mechanisms); LPU83_3442 (possibly modulates the rate cellular DNA-templated transcription.); LPU83_4045 (hypothetical transcription factor); and LPU83_pLPU83c_0540 (reported to repress genes associated to sialic acid metabolism). Further work will focus on

obtaining deletional mutants of the genes mentioned above to be analyzed in free living conditions, and then identify their regulome.

Palabras clave: Rizobios - Alfalfa - Acidez - Factores - Transcripción