**The common bean (*Phaseolus vulgaris*) –*Rhizobium etli* N-fixing symbiosis: unraveling novel plant regulators through genetic/genomic approach**

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The symbiotic N2-fixation process (SNF) in the legume-rhizobia interaction, relevant for sustainable agriculture, is a complex process that is tightly regulated in both symbionts. Advances in legume genomics and genetics, mainly the characterization of symbiotic mutants, have been instrumental for the understanding of legume genes required for effective symbiosis with rhizobia [1].

Common bean (*Phaseolus vulgaris*) is the most important grain legume for human consumption in the world. The focus of our current research is to characterize or decipher relevant symbiotic genes in common bean using genetic approaches.

Only one common bean EMS symbiotic mutant has been genetically/molecularly characterized [2]. It is evident that isolation, characterization and mapping of symbiotic common bean mutants is required to expand the knowledge of the fine regulation (SNF) in this important crop. To this end, we have screened 1,692 M4 lines of an EMS-generated common bean mutant population derived from the BAT93 genotype [3]. After the population screening, we aim to characterize three stable non-nodulating *(nnod*) mutant lines, that appear to be recessive and monogenic. Microscopic analysis of inoculated mutants revealed that each line is altered in a different early step of rhizobial infection: effective root hair deformations, formation of infection chambers and infection thread formation and development [4]. Comparative whole genome sequence analysis was undertaken for the prediction of responsible mutated genes in each mutant. In this talk we will present advances aiming to decipher mutated genes as well as further genetical/molecular characterization of selected common bean mutants.

***References:***

[1] Roy S. et al, Celebrating 20 Years of Genetic Discoveries in Legume Nodulation and Symbiotic Nitrogen Fixation. The Plant Cell. Vol.32, 2020, p. 15.

[2] Ferguson BJ. et al, The Soybean (Glycine max) Nodulation – Suppressive CLE peptide, GmRIC1, Functions Interspecifically in Common Bean (Phaseolus vulgaris) but Not in a Supernodulating Line Mutated in the Receptor PvNARK. Plant Biotechnology Journal. Vol. 12, 2014, p. 1085.

[3] Porch TG. et al, Generation of a Mutant Population for TILLING Common bean Genotype BAT93. Journal of American Horticultural Science. Vol. 134, 2009, p. 348.

[4] Reyero-Saavedra R, et al. Identification and Characterization of Common Bean (Phaseolus vulgaris) Non-Nodulating Mutants Altered in Rhizobial Infection. Plants. Vol. 12, 2023, p. 1310.