Talk

The *Sinorhizobium fredii* HH103 double-edged sword

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ABSTRACT

Rhizobia are soil proteobacteria able to stablish an efficient symbiosis with legume plants (Poole *et al*., 2018). In this interaction, bacteria infect the plant roots and penetrate inside through the root hairs. Simultaneously to the infection process, plant develop new organs called nodules, generally located on roots, which hosted the rhizobial cells. Once rhizobia are located in the nodules, they invade the plant cells and differentiate into bacteroids, a morphological and physiological state able to fix the atmospheric nitrogen to ammonium, which is supplied to the plant (Tsyganova et al., 2017). This interaction requires a complex and coordinated molecular signals interchange between two partners, since this event determine the susceptible plants to be nodulate by a specific *rhizobium* and therefore the success of the process (Oldroyd 2013). One of these signals are the molecules called Nod Factors, lipochitooligosaccharides secreted by the bacteria in response to the plant signals and detected by the plant receptors. Several bacterial regulators finely regulate these molecules; however, their overproduction produces changes in the host specificity and the effectiveness of the infection process.

Motivation: Since the host specificity is determined by the bacterial and plant signals, the alteration of some of them could modify the bacterial host range and even increase the efficiency with other plants.

Methods: All the experiments were carried out with *Sinorhizobium fredii* HH103, a rhizobial strain isolated from China and natural symbiont of soybean (*Glycine max* cv. Williams).

Gene expression analysis were carried out by RNA-seq and validated by RT-qPCR.

Nod Factors were extracted from the supernatant culture and analysed by HPLC-HRMS/MS.

Plant assays with *Glycine max* cv. Williams, *Lotus burttii* and *L. japonicus* Gifu were carried out in Leonard jars.

Infection mode analyses were carried out by epifluorescence microscopy.

Results: The mutation of any regulator that finely regulates the Nod Factor production causes an increase of Nod Factor gene expression, among other changes in the gene expression pattern, and in consequence an overproduction of these molecules. These changes provoke a partial impairment in symbiosis with soybean, its natural host, but on the other hand improve the nodulation effectiveness with *L. burttii* and allow the gaining the nodulation capacity with *L. japonicus* Gifu, where the wild type strain is not able to stablish an effective symbiosis. The infection mode analysis revealed that these mutants switched the infection way from intercellular infection, a primitive mode, to infection threads formation, more evolved way.

Conclusions: *S. fredii* HH103 has evolved with its natural host, soybean, to improve their symbiotic performance even though it could diminish or abolish the nodulation effectivity with other legume plants.

REFERENCES

Poole, P., Ramachandran, V., and Terpolilli, J. (2018). Rhizobia: from saprophytes to endosymbionts. *Nat Rev Microbiol*, **16**, 291-303.

Tsyganova, A. V., Kitaeva, A.B., And Tsyganov, V.E. (2017) Cell differentiation in nitrogen-fixing nodules hosting symbiosiomes. *Funct Plant Biol,* **45**, 47-57.

Oldroyd, G.E. (2013) Speak, friend, and enter: signalling systems that promote beneficial symbiotic associations in plants. *Nat Rev Microbiol*, **11**, 252-263.