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Whom to let in? A 16S-based analysis of the rhizospheric and root endophytic microbiomes of bean

Francisco Medina-Paz^{1, 2}, Cei Abreu-Goodger¹ and Martin Heil² ¹National Laboratory of Genomics for Biodiversity, Mexico ²Center for Research and Advanced Studies of the IPN (CINVESTAV), Mexico

Plant roots harbor a specific endophytic microbiome, which is largely obtained horizontally from the external (rhizospheric) soil microbiome. Both microbiomes contribute, e.g., to nutrient uptake and plant resistance. Endophytic bacteria colonize the root tissue despite the plant immune system. It remains an open question to which degree the microbiome's stability or dynamism over the lifetime of the plant depends on vertically versus horizontally transmitted bacteria. Here, we analyzed 16S rRNA gene amplicons generated from rhizosphere and endosphere samples of field-grown common bean (*Phaseolus vulgaris*) plants (root samples excluded nodules) and from *in vitro* cultured plants. We detected Firmicutes such as *Paenibacillus* in the *in vitro* samples, indicating a vertical mode of transmission of these putatively plant-growth promoting bacteria. Dominant taxa in the endosphere were Proteobacteria such as *Rhizobium* and *Agrobacterium*, which are suggested to contribute to plant nutrition and hormone synthesis. Overall, the diversity in the root endosphere was approximately 5-10 times lower than in the rhizosphere samples. Interestingly, the endophytic microbiomes did not change significantly over three phenological stages (plants with three true leaves, early flowering phase and during pod filling). We conclude that root microbiomes can reach equilibrium early during the ontogeny of a plant and that vertically transmitted bacteria can contribute to the root microbiome of bean plants. An ongoing project employs metagenomic data to obtain a better understanding of the processes that determine the assembly of the root microbiome of bean plants under field and *in vitro* conditions.

Biography

Francisco Medina-Paz has completed his Master's from Center for Research and Advanced Studies of the IPN. Currently, pursuing his PhD and working on the assembly of the root microbiome of bean at the Center for Research and Advanced Studies of the IPN, Mexico. His major goal is to integrate molecular and bioinformatics tools into field ecological work to understand mechanisms that determine plant-microbe interactions under natural conditions.

fmedina@ira.cinvestav.mx

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