

P39 - Breeding for resistance to soil-borne pathogen impacts rhizosphere microbiome functions in common bean

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Over the past century, plant breeding programs have substantially improved plant growth and health, but have not yet considered the potential effects on the plant microbiome. Here, we conducted a metatranscriptome analysis to determine if and how breeding for resistance of common bean against the root pathogen *Fusarium oxysporum* (*Fox*) affected gene expression in the rhizobacterial community. Our data revealed that rhizobacterial community assembly of *Fox*-resistant and susceptible bean cultivars follows niche-based mechanisms, presenting lower diversity and distinct community structure compared to the bulk soil. The microbiome of the *Fox*-resistant bean cultivar presented a significantly higher expression of bacterial genes associated with nutrient metabolism, motility, chemotaxis, and the biosynthesis of the antifungal compounds phenazine and colicin V. Network analysis further revealed a more complex community structure for the *Fox*-resistant cultivar and indicated that *Paenibacillus* is a keystone genus in the rhizosphere microbiome. Collectively, our data suggest that resistance breeding in common bean has unintentionally co-selected for plant traits that strengthen the rhizosphere microbiome network structure and enrich for specific beneficial bacterial genera that express specific antifungal traits involved in plant protection against infections by root pathogens.
