

12<sup>th</sup> International Congress on**Microbial Interaction and Applications of Beneficial Microbes**

July 17-18, 2017 Munich, Germany

**Ecological assessment of ammonium transformation in a facultative pond for domestic wastewater treatment**Sara Victoria Morales-Cortés, Andres Mauricio Zapata, Janeth Snabria and Miguel Peña-Varón  
University of Valle, Colombia

Although nitrogen removal processes in facultative ponds for domestic wastewater treatment have been extensively investigated, microorganism role in nitrogen transformation processes in these systems remain unclear. This research aimed to determine the factors that influence the dynamics of ammonium transformation in a facultative pond located in Ginebra, Valle del Cauca, and Colombia. Physicochemical parameters (temperature, pH and dissolved oxygen) and microbiological (nitrates, ammonium, total nitrogen, biochemical oxygen demand and chemical oxygen and total suspended solids) parameters were measured in-depth ranges of between 0-0.20 m, 0.50-0.80 m and 1.80 m sediments. Result analysis showed the stratification of temperature, pH and OD and the existence of significant differences in these variables in relation to depth. The other variables including the concentrations of metabolic intermediates and density of microorganisms linked to ammonium transformation showed no significant difference distribution along the profile. Correlation analysis between these variables indicated that although biomass assessed in terms of cultivable functional group is not a determining factor in the ammonium transformation throughout the profile, there are differential transformation dynamics of ammonium in the different depths, and they are not just explained by the impact of stratified variables. They could instead be strongly influenced by the microbial community structure in the profile as well by microbial associations between nitrogen-fixing and nitrogen anammox microorganism whose presence was verified with molecular biology techniques.

sara.morales@correounivalle.edu.co

**The impact of breeding for pathogen resistance on the rhizosphere microbiome assembly in common bean (*Phaseolus vulgaris* L.)**Siu Mui Tsai<sup>1</sup>, Lucas William Mendes<sup>1,2</sup>, Jos M Raaijmakers<sup>2,3</sup>, Mattias de Hollander<sup>2</sup> and Rodrigo Mendes<sup>4</sup><sup>1</sup>University of Sao Paulo, Brazil<sup>2</sup>NIOO-KNAW, Netherlands<sup>3</sup>Leiden University, Netherlands<sup>4</sup>Brazilian Agricultural Research Corporation, Brazil

The rhizosphere microbiome plays a key role in plant growth and health, providing a first line of defense against pathogen root infection. Here, we investigated how breeding for resistance of common bean (*Phaseolus vulgaris* L.) to the soil borne pathogen *Fusarium oxysporum* (Fox) changes the composition and functional potential of the bacterial community when present in a bean rhizosphere. Rhizobacterial abundance was positively correlated with Fox-resistance, tested in four different bean cultivars grown in two contrasting soils. *Pseudomonadaceae*, *Bacillaceae*, *Solibacteraceae* and *Cytophagaceae* showed highest abundance in the rhizosphere of the resistant cultivar. Network analyses showed a non-modular topology of the rhizosphere microbiome of the Fox-resistant cultivar, suggesting a more complex and highly connected bacterial community when compared to the Fox-susceptible cultivar. Further metagenome analyses revealed that specific functional traits such as protein secretion systems and genes involved in the biosynthesis of antifungal phenazines and rhamnolipids were more abundant in the rhizobacterial community of the Fox-resistant cultivar. In conclusion, our findings suggest that breeding for Fox-resistance in common bean co-selected for other unknown plant traits that support a higher abundance of specific beneficial bacterial families in the rhizosphere with functional traits that may reinforce the idea of being as a first line of the plant defense in the soil.

tsai@cena.usp.br