



## **Small-scale distribution of bacterial and fungal communities in soil cultivated with cranberries**

Thiago Gumiere (1), Silvio Gumiere (2), Jonathan Lafond (2), Modeline Jean (2), and Alain Rousseau (1)

(1) Institut national de la recherche scientifique, Centre Eau Terre Environnement, 490, rue de la Couronne, Quebec City, QC, Canada (thiago.gumiere@ete.inrs.ca), (2) Department of Soil and Agricultural Engineering, 2480 Hochelaga Boulevard, Laval University, Quebec City, QC, Canada

The production of cranberries is mostly concentrated in the USA and Canada, which are responsible for 98% of the global production. The drainage system in cranberry soils is composed by multiples drain pipes (varying between 60 and 90 cm of depth). The drains control the height of the water table (important in the sub-irrigation system) and also the flood/drain of water during the harvest. The drains promote an internal variation of soil water and soil elements of cranberry fields, which could develop a small-scale distribution of the soil microbial communities. Here we evaluated the distributions of bacterial and fungal communities in soils cultivated with cranberry. We evaluated two sides (east and west) of two cranberry fields. A total of 18 soils samples were collected disposing of a transect, crossing the irrigations drains. The results indicated that significant differences (ANOVA,  $p$ -value  $< 0.05$ ) of soil moisture (UR) between the field sides (east and west), and also between the soils samples located on the drain and inter-drains. The environmental factors (Fe, Ca, K, Zn, Rb, Sr, UR, and pH), drain pipe location (samples disposed under the drain or inter-drain) and geographical coordinates (Latitude and Longitude) explained 63% of the bacterial community and 77% of the fungal community. For both microbial communities, the soil elements, UR and pH were identified as the main driver, explaining 42% (bacterial community) and 36% (fungal community) of their variation. Random Forest model was used to predict the occurrence of the most abundant groups of bacterial and fungal communities. The model used the parameters of the soil microbial composition and the environmental factors. The five most abundant bacterial phyla showed a considerable percentage of prediction distribution (Actinobacteria = 42%, Proteobacteria = 66%, Acidobacteria = 76%, Chroloflexi = 71%, and Planctomycetes = 58%). *Arthrobacter* genus, which it has been related to agricultural pesticides degradation, and *Burkholderia* genus, which it has been described as an important plant growth promoting rhizobacteria, showed 70% and 84% of prediction distribution, respectively. For the fungal community, the models predicted 64% of the Ascomycota phylum and 52% of the Basidiomycota phylum distribution. Surprisingly, the Entomophthoromycota phylum, which is composed by pathogens of insect pests and soil invertebrates (e.g., Nematoda phylum), showed 78% of prediction distribution. At the genus level, the *Trichoderma*, known as an important biological control of plant pests, showed the best prediction of 65%. Therefore, the bacterial and fungal communities showed a small-pattern distribution in soils cultivated with cranberry promoted by the drainage system. The Random Forest model showed potential results on the prediction of soil microbial community, especially for microorganisms related to plant growth promoting and biological control. These findings compose an effort to increase the knowledge of the soil microbial community, which could further help to increase crop production and maintain the system sustainability.