UNRAVELING THE MICROBIAL COMMUNITY ASSOCIATED WITH SYMPTOMATIC AND ASYMPTOMATIC GERANIUM

da Silva, T.F.¹, Vollú, R.E.¹, Salles, J.F.² and Seldin, L.¹ ¹ IMPPG - Instituto de Microbiologia Paulo de Góes (Av. Carlos Chagas Filho 373, Ilha do Fundão, Rio de Janeiro, RJ), ² Groningen Institute for Evolutionary Life Sciences, University of Groningen (Linnaeusborg, 5th floor, Nijenborgh 7, AG Groningen)

Pelargonium graveolens also known as geranium is an essential oil producing plant widely used for geraniol production which is one of the main compounds of its essential oil. Geraniol is largely used in cosmetics and perfumery industry. P. graveolens crops throughout the world are affected by a plenty of diseases. One of these diseases is Anthracnose, a group of fungal diseases that affect a variety of plants in warm and humid areas. One of its causative agents is the fungus known as *Colletothrichum acutatum*, which can bring huge yield losses to the crop. Taking this into consideration we intend to understand the ecological interaction between this fungal phytopathogen and the microbial community within the plant and in the soil surrounding this plant and ultimately fight the phytopathogen and decrease the yield losses. Our hypotheses are: (i) The fungal phytopathogen is distributed all over the plant, also in asymptomatic leaves and throughout the soil, but in different abundances; (ii) Some bacterial groups are related to the presence and abundance of the phytopathogen in the different parts of the plant. In order to do that we sampled bulk soil, rhizosphere soil, root, stem, symptomatic and asymptomatic leaves from Pelargonium graveolens infected by Colletothrichum acutatum harvested from Natal-RN, Northeast Brazil. Besides we used High-throughput sequencing (Illumina-MiSeq platform/primers: 515F-806R) to unravel the bacterial diversity and gPCR to detect the presence and abundance of C.acutatum and bacterial 16SrRNA encoding genes in our samples. The preliminary results indicate that the phytopathogen is located mainly in the rhizosphere. Also, the bacterial community seems to be influenced mainly by the plant location than by the presence or absence of the phytopathogen.

Keywords: bacterial communities, Colletothrichum acutatum, geranium.

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