

47th World Congress on Microbiology

September 10-11, 2018 | London, UK



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Vitis vinifera rhizosphere microbiome: Metagenomic and metaproteomic approaches

Vitis vinifera is a Mediterranean crop with relevant impact on the Italian landscape, culture and economy. The rhizosphere is a hotspot where the release of root exudates modulates bacterial density and diversity. Despite the high bacterial number found in rhizosphere, only 1-10% of the soil bacteria are able to grow on laboratory media, so that the majority of the bacterial cells in soil results to be viable, unculturable, but active; even more, this percentage change according to the host plant. Thanks to culture-independent methods (metagenomics) the complexity of the soil/rhizosphere microbial community has been explored. However, metagenomics doesn't provide information regarding the activity and the molecular interactions between the bacterial communities and roots. Proteins are the drivers of cellular activities encoded by the genome. Therefore, proteomic tools could be useful to gain information about microbial community activity and to better understand the real interactions pathways between roots and soil. A comparison between the microbial community structure in rhizosphere and bulk soil using metagenomics (pyrosequencing of 16S rDNA) and proteomics (MS/MS analysis of the total protein occurring in soil samples) was performed. Actinobacteria were the dominant class in all the soil samples, followed by Proteobacteria, Gemmatimonadetes and Bacteroidetes. While Actinobacteria and *Proteobacteria* are well known as dominant in soil, for the first time, members belonging to Gemmatimonadetes have been observed in vineyard soils. Bacteria belonging to *Streptomyces*, *Bacillus*, *Bradyrhizobium*, *Burkholderia* and *Pseudomonas* genera were the most active. Concerning the biological activity of these genera, in the rhizosphere, we observed the exclusive presence of phosphorus metabolic process and the regulation of: biosynthetic, cellular, macromolecule, nitrogen compound and primary metabolic process. Our results underlined the difference between the metagenomic and metaproteomic approaches and the potentiality of proteomics in describing the environmental bacterial communities and their activity.

Biography

Dr. Elisa Bona. Researcher in Microbiology at the Università del Piemonte Orientale. She holds a Specialization degree in Microbiology and Virology (2010) at the Università di Genova and a Ph.D. (2006) in Environmental Science at the Università del Piemonte Orientale. She is teacher in different courses at UPO University: since 2015, Professor of General Microbiology, Professor of Applied Bacteriology and Professor Diagnostic in Microbiology. (AA 2013-2014) Professor of Environmental Microbiology and Professor of Agri-Environmental Microbiology.

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