

The International Debate on Microbiota of the Rhizosphere of Native Plants from Desert Areas of North-Central Algeria

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Intensive land use and increased industrial emissions of greenhouse effect pollutants have caused a negative impact on non-renewable natural resources such as the soil itself. The desertification process represents the main cause of the impoverishment of ecosystems in terms of productivity and biodiversity. To date, arid lands represent 45% of the earth's surface and are continuously increasing. Water loss and poor agricultural management cause soil salinization. The adaptation of agriculture to soils subject to water and salt stress is a topic of great interest for scientific research. Rhizosphere microorganisms play a central role in survival and resistance to abiotic and biotic stresses. Each plant builds its own specific microbiota, which will be different in relation to the type of soil, the environmental components and its genetics. The study of microbial communities associated with plants living in desert soils can provide new information for stress prevention. However, the enormous diversity of microorganisms in the soil, the multiple relationships they establish with the environment, the impossibility of cultivating many species and the lack of identification methods with adequate specificity and sensitivity, The aim of this work is to study the composition of the microbiota associated with indigenous plants of Algeria (*Cleome arabica*, *Reseda villosa*, *Arthrophytum scoparium*, *Astragalus armatus*, *Retama raetam*, *Salsola tetragona*, *Atriplex halimus*, *Peganum harmala*, *Suaeda fruticosa* and *Thymelaea microphylla*), to then identify the potential PGPR (Plant Growth-Promoting Rhizobacteria) and produce biostimulants to be applied to crops sensitive to water and salt stress. Following the sampling of the rhizosphere, DNA was extracted and the library was built. Using the NGS technology,

which uses the 16S ribosomal RNA gene as target, amplicons were sequenced. The data analysis was performed using MicrobAT, Microbiome Analyst and StatView4.5 software. The results obtained agree with many other studies and demonstrate a low bacterial biodiversity. The desert soils are very dry, low in nutrients, generally have a basic pH, higher than other biomes and the lack of plant biomass reduces the inputs of organic carbon useful for bacterial metabolism. The greater the amount of organic matter, the greater the stability and diversity of the microbiota. Sequences assigned to *Bacillus*, *Streptomyces* and *Pseudomonas* genera normally present in most of the soils, occurred with percentages between one and zero. Since only few microbial species can survive in the desert, the shape of the microbial community is driven more by resistance to abiotic stress than by competition. This explains the low prevalence of species usually implicated in biocontrol such as *Bacillus*, *Streptomyces* and *Pseudomonas*. To arrive at the production of biostimulants, further studies are needed, including the tests of functional activities and the isolation of culturable PGPR.

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 Genoa 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 Diagnostic in Microbiology. (AA 2013-2014) Professor of Environmental Microbiology and Professor of Agri-Environmental Microbiology..