

Microbiota of the rhizosphere of native plants from desert areas of north Algeria

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Abstract:

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 [1-2]. 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 [3]. Water loss and poor agricultural management cause soil salinization [4]. 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, make the rhizosphere one of the most difficult habitats to analyze. With the advent of metagenomics, which allows genome sequencing, it was possible to characterize microbial populations.

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