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A natural saline soil as a model for understanding to what extent the concentration of salt affects the distribution of microorganisms

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Soils preserve and sustain life. Their health and functioning are crucial for crop production and for the maintenance of major ecosystem services. Human induced salinity is one of the main soil threats that reduces soil fertility and affect crop yields. In recent times, great attention has been paid to the general shortage of arable land and to the increasing demand for ecological restoration of areas affected by salinization processes. Despite the diffuse interest on the effects of salinization on plants' growth, and all the derived socioeconomic issues, very few studies analyzed the ecology of the microbial species in naturally saline soils and the resilience of biological fertility in these extreme habitats. Microorganisms inhabiting such environments may share a strategy, may have developed multiple adaptations for maintaining their populations, and cope eventually to extreme conditions by altruistic or cooperative behaviors for maintaining their metabolism active. The understanding and the knowledge of the composition and distribution of microbial communities in natural hypersaline soils can be interesting for ecological reasons but also to develop new restoration strategy where soil fertility was compromised by natural accidents or human mismanagement.

The aim of this research was to provide specific information on saline soils in Italy, stressing mainly their distribution, the socioeconomic issues and the understanding of the characterizing ecological processes. Moreover, natural saline soils were used as a model for understanding to what extent the concentration of salt can affect some basic microbial processes.

In the present study, physical, chemical and microbiological soil properties were investigated in the shallower horizons of natural salt affected soils in Sicily (Italy), where some ecological contrasting variables acted as strong drivers in fungal and bacterial spatial distribution. Furthermore, the interface between biological and geochemical components in the surface of that peculiar habitat was investigated to evaluate the organization and diversity of the phototrophic and heterotrophic microorganisms. Sixteen soil samples from A horizons were collected according to a random sampling scheme. Bacterial and archaeal communities were characterized by their 16S rDNA genes with T-RFLP method. A total of 92 genera were identified from the 16S pyrosequencing analysis suggesting that cyanobacteria and communities of sulfur bacteria might directly or indirectly promote the formation of protective envelope. Some bacterial phyla appeared spread in the whole area, whatever the salinity gradient, while other groups showed a distribution linked to very compartmentalised soil properties, such as the presence of saline crusts in the soil surface. Results show that saline soils couldn't contain just one single microbial community selected to withstand extreme osmotic phenomena, but many communities that can be variously correlated to one or more environmental parameters having great importance for the maintenance of the overall homeostasis.