

## Characterization of bacterial communities and functions of two submerged soils from San Vitale park (Italy)

Stefano Mocali (1), Carolina Chiellini (1), Alessandra Lagomarsino (1), Chiara Ferronato (2), Livia Vittori Antisari (2), and Gilmo Vianello (2)

(1) Consiglio per la Ricerca e la Sperimentazione in Agricoltura, Centro di Ricerca per l'Agrobiologia e la Pedologia (CRA-ABP), Firenze, Italy (stefano.mocali@entecra.it), (2) 2Dipartimento di Scienze Agrarie-DipSA, Alma Mater Studiorum-Università di Bologna, Bologna (Italy)

Subaqueous soils has been introduced in the last edition of the Keys to Soil Taxonomy (Soil surveystaff, 2014), to describe soils covered by a water column of up to 2.5 m where different pedogenetic processes can be recognized. However, the role of bacterial community structure and function in such environments and its potential use as pedogenetic indicator is still largely unknown.

Two submerged soils (WAS-2 and WAS-4) were collected from San Vitale park (Italy), a site where the evolution of the landscape from subaqueous wetland to interdunal and dunal system, and the interfacing of freshwater with saltwater, made this site particularly suitable for examining the pedogenetic indicators which can characterize and predict the soil hydromorphism in trasitional ecosystems. The two soils were classified and their physicochemical and morphological features were investigated. Selective media were used to isolate both culturable aerobic and anaerobic (microaerophilic) bacteria associated with each horizon. In WAS-2 seven horizons were identified (depths 4-0, 0-6, 6-13, 13-20, 20-36, 36-59/60, and 59/60-83 cm) while in WAS-4, five horizons were identified (depths 0-14, 14-20, 20-40, 40-45, 45-100 cm) for a total of 12 horizons (samples). For each sample, aerobic bacterial plate count was performed on solid LB medium, coupled with microaerophilic bacterial plate count either on SA500 minimal medium and AYE medium (0.5% soft agar each). Molecular identification (16S rRNA gene sequencing) of  $\sim 100$  strains isolated from each of the three used medium was performed, for a total of  $\sim$ 300 strains for each sample. To complete the characterization of the microbial communities in all horizons, Next Generation Sequencing (NGS) analysis was carried out with 454 platform on each of the 12 samples. Moreover, the N2O and CH4 emissions were determined from each pedon. All the parameters were used to highlight the similarities and the differences between and within the pedons. The results will potentially help to highlight some features related to the origin and morphogenesis of submerged soils, and also to clarify the process of differentiation of soil horizons from a biological point of view.