Geophysical Research Abstracts Vol. 19, EGU2017-318-1, 2017 EGU General Assembly 2017 © Author(s) 2016. CC Attribution 3.0 License.



Soil quality and bacterial community structure: a case study from the mediterranean region

Manuel Anguita-Maeso (1,2), Isabel Miralles* (3,4), Miguel Soriano** (1,2), Raúl Ortega (1), José Antonio García-Salcedo (2,5), and Manuel Sánchez-Marañon (6)

(1) Dpto. Edafología y Q. Agrícola, Escuela Técnica Superior de Ingeniería, Universidad de Almería, Campus de la Cañada, E-04120 Almería, Spain., (2) GENYO. Centro de Genómica e Investigación Oncológica: Pfizer / Universidad de Granada / Junta de Andalucía, PTS Granada, Granada, Spain., (3) Earth and Life Institute, Université Catholique de Louvain, Louvain-La-Neuve, Belgium., (4) Experimental Station of Arid Zones (EEZA-CSIC), Almeria, Spain., (5) Unidad de Enfermedades Infecciosas y Microbiología, Instituto de Investigación Biosanitaria ibs.GRANADA, Hospitales Universitarios de Granada/Universidad de Granada, Granada, Spain., (6) Dpto. Edafología, Facultad de Ciencias, Universidad de Granada, Granada, Spain.

Bacterial communities play a central role in innumerable processes and functions of soils such as decomposition of organic residues, nutrient cycling, aggregation, and formation of humic substances. We investigated the relationships between bacterial communities, soil profiles, and quality parameters in eight benchmark soils of the Mediterranean calcareous mountain sampled on a local scale. The diversity and composition of prokaryotic community was assessed by 16S rRNA gene amplicon pyrosequencing of DNA from samples of topsoil (10 x 10 x 0.2 m). The bacterial profile content resulted in the identification of groups belonging to 16 phyla and 75 genera. Two-dimensional models using multidimensional scaling (Stress < 0.11), correspondence analysis (Inertia > 71%), and principal component analysis (Variance > 60%) showed a decrease in the abundance of acidobacteria Gp4 and Gp3 while actinobacteria flourished with increasing soil profile development (from Leptosol to Luvisol). This can be attributed to inherent changes in soil quality along pedogenesis such as pH (8.3 to 7.8), organic C (20.0 to 45.2 Mg ha-1), macropososity (0.11 to 0.32 cm3 cm-3), and water stable aggregates (365.8 to 963.4 Mg ha-1). Actinobacteria genera like Aciditerrimonas, Nocardioides, and Solirubrobacter also displayed positive correlations (r > 0.90) with the content of clay and free Ferric forms. Other factors like Re-carbonation, loss of organic matter, and soil compaction probably caused by land use and management, led to a decline in the Chao1 richness and Shannon diversity indices (3625 and 6.3) with respect to native soils (7852 and 7.4). Likewise, Firmicutes and Gemmatimonadetes were tripled and the genera of Proteobacteria and Bacteroidetes decreased. Our data indicate that bacterial community structure depends largely on the soil quality status, both inherent and managed and suggest the bacterial group composition also follows the course of soil genesis.

(*) Financial support by Marie Curie Intra-European Fellowship (FP7-577 PEOPLE-2013-IEF, Proposal n° 623393) and (**) by the Ministerio de Economía y Competitividad (MINECO) cofinanced with FEDER funds (project CGL2015-71709-R) is acknowledged.