Geophysical Research Abstracts Vol. 19, EGU2017-322, 2017 EGU General Assembly 2017 © Author(s) 2016. CC Attribution 3.0 License.



Biocrusts role on nitrogen cycle and microbial communities from underlying soils in drylands

Manuel Anguita-Maeso (1,2), Isabel Miralles* (3,4), Bas van Wesemael (3), Roberto Lázaro (4), Raúl Ortega (1), José Antonio Garcia-Salcedo (5), Miguel Soriano** (1,2)

(1) Dpto. Edafología y Q. Agrícola, Escuela Técnica Superior de Ingeniería, Universidad de Almería, Campus de la Cañada, E-04120 Almería, Spain., (2) Centro Pfizer-Universidad de Granada-Junta de Andalucía de Genómica e Investigación Oncológica (GENYO), 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.

Biocrusts are distributed in arid areas widely covering most of the soil surface and playing an essential role in the functioning of nitrogen cycle. The absence of biocrust coverage might affect the soil nitrogen content and the quantity and diversity of microbial communities in underlying biocrust soils. To analyse this mater, we have collected three underlying soils biocrusts samples dominated by the lichen Diploschistes diacapsis and Squamarina lentigera from Tabernas desert (southeast of Spain) at two extremes of its spatial distribution range: one with a high percentage of biocrust coverage and other with a huge degradation and low percentage of biocrust coverage in order to determine differences on the total nitrogen content and microbial communities from these underlying soils. DNA from these samples was isolated though a commercial kit and it was used as template for metagenomic analysis. We accomplished a sequencing of the amplicons V4-V5 of the 16S rRNA gene with Next-Generation Sequencing (NGS) Illumina MiSeq platform and a relative quantity of bacteria (rRNA 16S) and fungi (ITS1-5.8S) were conducted by quantitative qPCR. Total nitrogen was measured by the Kjeldahl method. Statistical analyses were based on ANOVAs, heatmap and Generalized Linear Models (GLM). The results showed 1.89E+09 bacteria per gram of soil in the high biocrust coverage position while 6.98E+08 microorganisms per gram of soil were found in the less favourable position according to the lower percentage of biocrust coverage. Similarly, 1.19E+12 was the amount of fungi per gram of soil located in the favourable position with higher biocrust coverage and 7.62E+11 was found in the unfavourable position. Furthermore, the soil under high percentage of biocrust coverage showed the greatest total nitrogen content (1.1 g kg-1) whereas the soil sampled under depressed percentage of biocrust coverage displayed the fewest quantity of total nitrogen content (0.9 g kg-1). Metagenomic and statistical analysis exhibited different bacteria communities according to underlying soils with unlike percentage of biocrust coverage. Opitutus and Adhaeribacter predominated in soil under high biocrust coverage percentage whereas Chelatococcus was found as prevalent bacteria community in soils under low biocrust coverage percentage. Our data illustrate that the percentage of biocrust coverage influence the total nitrogen content in underlying biocrust soils and also affects the amount and the variety of bacteria communities in these underlying soils.

(*) 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.