

Influence of biocrusts coverage on microbial communities from underlying arid lands soils

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In regions where the water availability limits the plant cover, biological soil crusts are especially essential in the development of an almost continuous living skin mediating the inputs and outputs across the soil surface boundary. However, the entire area is not covered equally and microbial communities from underlying soils might be influenced by biocrust type and the percentage of biocrust coverage. To clarify this question, we have collected underlying soils from biocrusts samples dominated by i) incipient colonization by cyanobacteria, ii) cyanobacteria, biocrusts formed by the lichens: iii) *Diploschistes diacapsis* and *Squamarina lentigera* and iv) *Lepraria issidiata* from Tabernas desert (southeast of Spain) so as to determine the differences in the microbial communities from these underlying soils at two extremes of its spatial distribution range: one with a high percentage of biocrust coverage and fewer degradation and other with a huge degradation and less percentage of biocrust coverage. DNA from these samples was isolated by using a commercial kit and it was taken as template for metagenomic analysis. We conducted 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 and fungi were accomplished by quantitative qPCR of rRNA 16S and ITS1-5.8S, respectively. The high biocrust coverage position revealed the highest number of bacteria per gram of soil (1.64E+09 in *L. issidiata*, in 1.89E+09 *D. diacapsis* and *S. lentigera*, 1.63E+09 in cyanobacteria and 2.08E+09 in incipient colonization by cyanobacteria) whereas the less favourable position according to the percentage of biocrust coverage showed fewer amount (1.16E+09 in *L. issidiata*, 6.98E+08 in *D. diacapsis* and *S. lentigera*, 1.46E+09 in cyanobacteria and 7.92E+08 in incipient cyanobacteria biocrust). Similarly, the amount of fungi per gram of soil presented identical correlation ranging from the favourable position of biocrust cover (1.59E+12 in *L. issidiata*, in 1.19E+12 *D. diacapsis* and *S. lentigera*, 2.71E+12 in cyanobacteria and 2.15E+12 in incipient colonization by cyanobacteria) to the unfavourable state (8.94E+11 in *L. issidiata*, in 7.62E+11 *D. diacapsis* and *S. lentigera*, 1.30E+12 in cyanobacteria and 5.49E+11 in incipient cyanobacteria biocrust). Clearly, it is observed that the percentage of biocrusts coverage influences the number of bacteria and fungi in underlying biocrusts soils. Furthermore, metagenomic and statistical analysis displays the variability of microbial communities depending on the percentage of biocrusts coverage. *Segetibacter* (5.28%), *Rubrobacter* (3.12%) and *Blastopirellula* (0.77%) tend to be present in advantageous state of biocrust coverage while *Rubellimicrobium* (1.17%), *Arthrobacter* (0.35%) and *Gp16* (0.65%) lean towards the adverse positions. Our results concluded with the idea that different microorganisms have a tendency to be located at certain percentage of biocrust coverage, which playing an essential role in the maintenance of microbial communities structure in underlying soils.

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