

Influence of livestock density on the amount and structure of soil microbial communities in rangelands of SW Spain

Manuel Anguita (1), Manuel Pulido (2), Susanne Schnabel (2), Francisco Lavado-Contador (2), Raul Ortega (3), Miguel Soriano (3,1), Isabel Miralles (4,5)

(1) Centro Pfizer-Universidad de Granada-Junta de Andalucía de Genómica e Investigación Oncológica (GENYO), Granada (Spain), (2) GeoEnvironmental Research Group, University of Extremadura (Spain), (3) Agronomy Department, University of Almería (Spain), (4) Earth and Life Institute, Université Catholique de Louvain, Louvain-La-Neuve (Belgium), (5) Experimental Station of Arid Zones (CSIC), Almería (Spain)

Rangelands (namely dehesas and montados) occupy more than 90,000 km² of land in SW Iberian Peninsula. Their natural pastures are permanently grazed by 13 millions of domestic animals. The persistence of soils of high quality is a key factor for keeping their environmental and economic sustainability. The role of soil microbial communities in the biodegradation processes of organic compounds is essential to ensure soil fertility in this kind of human-induced ecosystems. Nevertheless, there are few studies dealing the effects of livestock grazing on soil microbial communities. The main goal of this study is therefore to assess the amount and structure of soil microbial communities in rangelands of SW Spain by comparing different grazing intensities.

The study was carried out in 4 fenced areas (sampling sites) belonging to privately-owned farms under different grazing intensities: low, moderate and high. One area excluded to grazing for more than 40 years (located in the Monfragüe National Park, Extremadura) was used as reference sampling site. A total number of 30 soil samples (6 each site) were collected in comparable areas with the same lithology and very similar topographical features. Commercial kit to extract DNA from these soil samples was used 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 results showed that soils with a high livestock density had the highest content of bacteria per gram of soil (4.77E+09), followed by soils with moderate (3.32E+09) and low livestock density (2.80E+09). The lowest content of microorganisms was found in soils excluded to grazing (2.38E+09). However, soils with moderate and low livestock density showed the greatest amount of fungi per gram of soil (2.31E+10 and 2.22E+10, respectively) and soils excluded to grazing recorded the lowest fungi amount (1.21E+10). These data suggest that the increase in grazing intensity favour the proliferation of bacteria and fungi due probably to the increase of organic matter via animal excreta.

Taxonomic results revealed a high bacterial presence of phylum Acidobacteria (Gp1, Gp3, and Gp6) and a uniform distribution of the genus *WPS-1_genera_incertae_sedis* in different states of grazing intensity. Thus, the most abundant genus was Gp1 in soils excluded to grazing and in soils with low and moderate livestock density (14.25%, 16.80% and 12.38%, respectively) while Gp3 (8.76%) was the most abundant genus in soils with high livestock density. Curiously, the genus Gp6 tended to be located in moderate and highly grazed areas instead of those with low livestock density. Our results suggest livestock density might influence the edaphic microbial structure affecting the quantity and type of microorganisms.