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Validation of the use of soil bacterial 16S rDNA markers for sediment fingerprinting in a small endorheic lagoon in southern Spain

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Several studies have shown the effect of soil management on the soil microbial community in olive orchards, and how these can be identified using DNA markers (Landa et al., 2014). DNA markers of soil bacteria seems to have the potential to differentiate between different areas, particularly in those might not present differences in other chemical or geochemical soil properties.

In a previous study (Gómez et al., 2016) two lagoons (Zoñar and Dulce) in southern Spain with a small contributing area were selected for a preliminary analysis of sediment tracing by DNA markers. In May 2015, two small subcatchments within each of the lagoon's contributing area were sampled. Previously, three homogeneous zones per subcatchments were delineated based on soil management, visual indications of soil erosion, soil color, and landscape position. At each area several composite soil samples (differentiating between 0-20 and 20-40 cm depth) were taken. Deposited sediment samples were taken in the sedimentation area where the stream draining the subcatchments reached the lagoon (0-20 cm depth). The bulk community of DNA was extracted from 250 mg of the soil samples. The bacterial 16S rRNA gene V1-V2 hypervariable regions were amplified in polymerase chain reaction (PCR). The next generation sequencing (NGS) procedure was performed according to the manufacturer's recommendations using MiSeq Reagent Kit v3 for 600 cycles on MiSeq desktop sequencer.

The raw dataset for each sample consisted of the number of counts for each of the 6640 operational taxonomic units (OTU) identified. Then, the OTUs that were present in all of the sampled areas and the sediments, but were significantly different in the number of counts among areas, were used to solve several over-determined mixing models.

Preliminary results show that 0.2 to 0.6 % of the searched OTUs (i.e. 14 to 42) had the potential for being used in the mixing models after the four-step screening process allowing the quantification of the sediment contribution from each of the three zones within each subcatchment to the lagoon.

In January 2016 we visited the same areas of one of the lagoons (Dulce), sampling the same areas with a similar strategy, and complemented this sediment sampling with more detailed sampling up to 0.35 m depth at 0.075 m intervals and the collection of suspended sediment samples. The samples were analyzed for DNA markers using the same NGS approach than in the previous year and the analysis of sediment contribution from each of the three homogeneous zones in the subcatchment was repeated to evaluate:

1 - The stability of soil and sediment DNA profiles with time.
2 - The stability of the sediment contribution attributed using soil DNA profiles made in a relatively short (7 months) period.
Preliminary results on this analysis are presented in this communication.
Key words: sediment, fingerprinting, soil, microbial, DNA, lagoon

References
Gómez, J.A., et al. Geophysical Research Abstracts Vol. 18, EGU2016-5185.
Landa, B. B., et al. 2014. Environmental Microbiology Reports 6: 196 – 207.