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Dissolved organic matter dynamic and resident microbiota evolution in soil amended with fresh and composted olive mill wastes

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The disposal of olive mill wastes represents a problem of environmental relevance particularly in the Mediterranean countries where olive oil is mostly produced. Among the several valorisation and recycling methods proposed, interesting for its operational simplicity and convenience is land spreading, either directly or after composting. However, the agriculture use of the water-saturated husk produced by the new two-phase oil extraction systems may be hampered by its consistency and its high content of phenolic compounds, which may finally lead to phytotoxicity. Humid husk may indeed modify the dynamic of soil organic matter (SOM) and the structure and function of microbial communities. On the other hand, organic amendments are known to positively affect SOM fractions, particularly by increasing the concentration and quality of dissolved organic matter (DOM), which may eventually lead to an increase in microbial activity.

The aim of this work was to investigate, during a 90-day field trial, the modifications in soil DOM composition and the effects on the soil microbiota induced by a humid husk, obtained from a new generation two-phase oil extraction plant, spread in an olive orchard either as a fresh amendment or after a composting process.

With respect to the control, the soil amended with either fresh or composted husk showed an increase in water extractable organic carbon (WEOC). Interestingly, while during the first 30 days the soil amended with the composted husk showed a WEOC content higher than the one amended with the fresh husk, after that time only in the latter the WEOC remained significantly higher than in the control. The total content of phenolic compounds showed a similar trend, with the only difference that their concentration in the soil amended with both treatments remained higher than the control for the entire trial. Similarly, both treatments induced an increase in soil reducing sugars, with an higher effect observed in the soil amended with the composted husk. FT-IR spectra and SUVA254 data confirmed the changes in DOM composition caused by the amendments.

Denaturing gradient gel electrophoresis (DGGE) analyses of 16S and 18S rRNA genes was used to characterize the microbiota in both amendments and soils. Interestingly, the DGGE profiles changed after composting the humid husk, indicating how the organic matter transformations occurring during this process profoundly altered the microbial communities of the OMW. Soil bacterial communities were very complex and presented a high species richness throughout the entire trial. In particular, the fresh and the composted husk appeared to have only a slight effect on the bacterial community structure. This effect was observed only during the first 60 days, while after 90 days no differences with the control plot were present. On the contrary, the fungal communities presented a lower biodiversity and more variable DGGE profiles than the bacterial communities. Both treatments clearly altered the structure of the soil fungal community throughout the entire trial. Interestingly, the fungal communities profiles were different when the fresh or the composted husk was used, with the former showing more profound and stable effects.