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Interaction of exogenous microbial inoculum with soil organic matter fractions

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In a previous study (Zaccone et al., 2018. Appl. Soil Ecol. 130, 134-142), we evaluated the potential ecological partition of microbial and plant DNA across soil organic matter (SOM) fractions linked to conceptual stabilization mechanisms. We found that different microbial taxa (bacterial and fungal) seem to be specifically associated to SOM fractions. In the present work we investigated the short-term distribution of exogenous microbial population in SOM fractions following inoculation, in order to track the fate of bacterial DNA (in the form of spores) artificially spiked in bulk soils. The main hypothesis was that the colonization of external organisms proceeds from the unprotected fraction (FR) towards those protected physically and/or chemically by soil minerals from decomposition (i.e., into macro and micro-aggregates [MA, MI] or interacting with mineral surfaces [MIN]).

Three different soils with different pH, SOM content and texture were used in the experiment. One aliquot of soil was spiked with approx. 8 Log cfu of spore of Bacillus clausii from a commercial preparation of 4 strains. DNA was extracted from soil and recovered from SOM pools isolated using a physical fractionation method [Plaza et al., 2012. CLEAN-Soil Air Water 40, 134-139] and quantified by fluorescence (Qubit).

DNA recovered from spiked vs. non-spiked samples followed two different patterns of distribution, according to the SOM fractions. Total DNA in the bulk soils varied according to the soil types and the effect of spiking 8 cfu was negligible. In the SOM fractions, while MI and MIN showed different concentration according to the soil type (no apparent influence of spiking), total DNA in FR was clearly higher for spiked samples, while MA had a putative interaction between soil type and spiking. Even if very preliminary, our results point out a possible mechanism of short-term distribution of exogenous DNA (through spores and potential vegetative forms of B. clausii germinated during the incubation) from the free SOM to the macroaggregates, with no apparent influence on MI and MIN yet.

Further analyses (e.g., PCR-ARISA and qPCR) will allow to disclose whether indigenous vs. exogenous bacterial DNA are differentially distributed in SOM, possibly enhancing the description of the mechanisms underlying the distribution of microbial communities in soil, according to the different organization of the SOM in soil aggregates.