

PREVIEW

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Microbiome structure and interconnection in soil aggregates across conservation and conventional agricultural practices allow to identify taxa related to soil functioning

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Under conservation agriculture (CA), soil aggregates physically protect soil organic C, creating microhabitats with heterogeneities in nutrient availability. These may become rich in microbial taxa with structured interconnections, and thus maintain the equilibrium between C sources and sinks. A long-term experiment on tillage and N fertilization located in the Mediterranean was used to investigate the microbiota within small macroaggregates (sM), and occluded microaggregates (mM). At surface layer N fertilization was the main driver of diversity of prokaryotes and fungi in soil aggregates, whereas at subsurface layer tillage intensity was the primary driver. Moreover, although along the soil profile a conserved core microbial community was found across managements in soil aggregates, some taxa were unique to certain managements. At surface layer, N fertilization significantly modified the prokaryotic community structure in sM and mM under conventional tillage, whereas in the subsurface layer, tillage modified the community structure of prokaryotes in both soil aggregates, and of fungi in mM. The fungal community structure in sM was strongly modified by the interaction between tillage and N fertilization at both soil layers and in mM only at surface layer. Overall sM had a higher diversity of prokaryotes and a lower diversity of fungi than mM. Small macroaggregates and mM had distinctive microbial community structures. Prokaryotic taxa, such as Actinobacteria, *Chloroflexi* and *Thermomicrobia*, and fungi, such as *Agaricomycetes*, *Dydimellaceae*, and *Mortierellaceae*, characterized sM, whereas others prokaryotes (*Betaproteobacteria*, *Sphingobacteriia*, *Blastocatellia*) and fungi (*Sordariales*, *Lasiosphaeriaceae* and *Glomeraceae*) characterized mM. Within- and cross-domain network were more complex in mM than sM at surface layer, and the opposite occurred at subsurface. Some prokaryotic and fungal taxa (*Chloroflexi* and *Sordariomycetes*), found abundant in hubs within soil aggregate networks, were consistently positively related to C cycling and soil structuring. We can therefore conclude that soil aggregation should be included in a more complete 'multifunctional' perspective of soil ecology, and that a full understanding of soil processes requires analyses emphasizing feedbacks between soil structure and soil microbiota, rather than a unidirectional approach simply addressing single members in bulk soil. As CA systems and soil structure were strongly connected to soil microbiome and function, the

application of CA practices should be supported for the restoration of disturbed soils, the prevention of soil erosion and the enhancement of SOC storage. Overall, the higher diversity and differentiated soil microbial structures observed in minimum and fertilized tillage systems may offer biological buffering capacity and maintain agriculturally relevant soil functions. This study allows to improve the knowledge on taxa resistant and sensitive to modifications induced by tillage and N fertilization, according to soil aggregation size. We also demonstrate that linking taxonomy to function is a priority for explaining the ecological interactions that promote SOC accumulation in soil aggregates.