Out of sight - Profiling soil characteristics, nutrients and microbial communities affected by organic amendments down to one meter in a long-term maize cultivation experiment

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Soil characteristics, nutrients and microbial activity in the deeper soil layers are topics not of-ten covered in agricultural studies since the main interest lies within the most active topsoils and deep soils are more time-consuming to sample. Studies have shown that deep soil does matter, although biogeochemical cycles are not fully understood yet. The main aim of this study is to investigate the soil organic matter dynamics, nutrients and microbial community composition in the first meter of the soil profiles in the long-term maize cropping system ex-periment Tetto Frati, in the vicinity of the Po River in Northern Italy. The trial site lies on a deep, calcareous, free-draining soil with a loamy texture. The following treatments have been applied since 1992: 1) maize for silage with 250 kg mineral N ha-1 (crop residue removal, CRR), 2) maize for grain with 250 kg mineral N ha-1 (crop residue incorporation, CRI), 3) maize for silage with 250 kg bovine slurry N ha-1 (SLU), 4) maize for silage with 250 kg farm yard manure N ha-1 (FYM). Soil characteristics (pH, carbonate content, soil organic carbon (SOC), aggregate stability (WSA)), and nutrients (total nitrogen (Nt), CAL-extractable phos-phorous (P) and potassium (K), potential N mineralisation) were investigated. Bacteri-al community composition was investigated with Ion PGM high-throughput sequencing at the depth of 8000 sequences per sample. Soil pH was moderately alkaline in all soil samples, in-creasing with increasing soil depth, as the carbonate content increased. SOC was significantly higher in the treatments with organic amendments (CRI, SLU and FYM) compared to CRR in 0-25 cm (11.1, 11.6, 14.7 vs. 9.8 g kg-1, respectively), but not in the deeper soil. At 50-75 cm soil depth FYM treatment revealed higher WSA compared to CRR, as well as higher CAL-extractable K (25 and 15 mg kg-1, respectively) and potential N mineralisation (11.30 and 8.78 mg N kg-1 7d-1, respectively). At 75-100 cm soil depth, SLU and FYM had the highest poten-tial N mineralisation. Microbial biomass and bacterial diversity decreased downwards the soil profile. Incorporation of crop residues alone showed no positive impacts on either biomass or diversity, whereas fertilization by FYM instead of mineral fertilizer did. Microbial community composition showed depth-related shifts: Proteobacteria and Actinobacteria dominated the upper layer, whereas Gemmatimonadetes showed the highest relative abundance in the mid-layers and Chloroflexi deeper in the soil profile. The main factor determining soil bacterial community composition in the entire dataset was not the treatments but the layers. Interesting-ly, the surface layers that we expected to be most impacted by the treatments were much more similar to each other, re-gardless of treatment or block, than samples from the deeper layers were to each other. This means that agricultural practices strongly influence the soil bacterial composition and reduce its wide natural heterogeneity. This calls for continuous efforts to study the deeper soil layers in the numerous long-term field experiments, where mostly the topsoils are currently studied in detail.