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Effect of agricultural soil conservation practices on arbuscular mycorrhizal fungal and bacterial communities and crop productivity in two agro-ecological zones in Italy and Zambia

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Agricultural production in regions such as sub-Saharan Africa (SSA) is very low as compared to other regions such as the Mediterranean area (MED). Differences are mainly due to agricultural input use which is generally lower in SSA. Indeed, in both regions, where unsustainable agricultural practices are largely applied although varying in intensification, soil organic carbon degradation and soil biodiversity decline are widespread issues. However, whether changes of soil microbial diversity have consequences on agroecosystem services, like crop productivity, in such agro-ecological zones is still scarcely investigated at field level. This long-term field study aimed to understand how different agricultural practices, such as conservation agriculture (CA)-based systems, affect soil microbiome (i.e., arbuscular mycorrhizal fungi (AMF) and bacteria) and their implications on crop productivity. We selected two contrasting soils and agro-ecological zones, in Italy (Centre of Agro-Environmental Research "Enrico Avanzi" – CiRAA – in Pisa) and in Zambia (Msekera Research Station – MRS – in Chipata), to investigate the responses of AMF and bacterial community to CA practices. The experiment at CiRAA was started in 1993 on a silt loam soil and was set up as a split plot design to test tillage regime as the main plot factor and nitrogen (N) fertilization rate as the sub-plot factor. Tillage regimes were conventional tillage (CT) and minimum tillage (MT), while the N fertilization rates were no fertilization (N0) and fertilized with 200 kg N ha⁻¹ split into three applications (N200). For all treatments, wheat (*Triticum aestivum* L.) was rotated with soybean (*Glycine max* L.) in one-year rotations. The experiment at MRS was started in 2012 on a sandy clay loam soil and tested three treatments: CT and maize (*Zea mays* L.) as sole crop, no-tillage plus mulch (NT+M), and no-tillage plus mulch and rotation (NT+M+R) with maize in rotation with soybean. The climate is cold humid Mediterranean (Csa) at CiRAA and warm temperate with dry winters and hot summers (Cwa) at MRS. DNA was extracted from soil: for AMF PCRs were carried out amplifying part of the SSU, ITS1, 5.8S, ITS2 and part of the LSU of the 18S rRNA region, while for bacteria PCRs were carried out amplifying the V3 and V4 regions of the 16S rRNA region. AMF were characterized by a cloning and Sanger sequencing approach (ca. 1700 bp), whereas bacteria by an Illumina sequencing approach (ca. 630 bp). In both zones, AMF and bacterial composition was similar among CA systems, whereas the long-term implementation of the CA

systems resulted in more diverse microbial communities across the agro-ecological zones. CA systems led to positive interactions between AMF and bacterial communities and more complex soil microbial networks. This ultimately led to an improved crop yield. At MRS, soybean as a rotational crop enriched bacterial diversity and within the AMF communities, members of the family *Gigasporaceae* were more dominant. We finally identified the microbial taxa highly related to crop productivity, providing cause-effect relationships for the involvement of microbes in crop productivity.