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DNA-SIP enabled determination of carbon flow from rice-residue into microbial communities in soils under different fertilization regimes

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Fertilization and plant residue inputs are the primary factors to improve soil fertility, whereas the fate of carbon inputted into the soil was controlled by soil microbes. To better understand how different fertilization regimes affect the flow of C from rice residues into the soil microbial community, ^{13}C-labeled rice-residues were incorporated into the soils with microcosm experiment. DNA stable isotope probing (DNA-SIP) combined with high-throughput sequencing was applied to identify the microbes involved in the turnover of rice residue-derived C. *Proteobacteria* and *Actinobacteria* that occupied approximately 94% of all the ^{13}C-labeled bacteria community were the dominant bacterial phyla involved in rice-residue C flow. And members of *Ascomycota* also act as the predominant role in the degradation and assimilation of rice straw. Different fertilization regimes significantly shifted the community composition of bacteria and fungi involved in the straw assimilation. For the bacteria involved in the rice-residue C assimilation, the relative abundance of *Lysobacter* was increased and *Strepomyces* of bacteria was decreased in soils with inorganic plus organic fertilization (NPKM) compared to soils with inorganic-only fertilization (NPK). Regarding to the fungi involved in the rice-residue C assimilation, the relative abundance of *Syncephalis* was increased by 3-year application of organic manure, but that of *Trichoderma* was decreased. Different fertilization regimes had no influence on the response strategies of dominant bacterial genus, but most of the genus of fungi in soil received organic fertilizer respond faster to the straw addition than the soil received chemical-only fertilizer. The network of microbes involved in the rice-residue C flow was more complex in NPKM treatment than that in NPK treatment. Key microbial species that acted as module hubs and connectors in C-flow networks were taxonomically changed by short-term application of organic fertilizer. Our findings provided fundamental information with respect to the roles of labeled microbes that responsible for residue decomposition and utilization in increasing soil fertility and offered important cue for manipulating the soil microbiome for C turnover in soil.