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The fate of soybean residue-carbon links to changes of bacterial community composition in Mollisols differing in soil organic carbon

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Quantifying residue carbon (C) incorporation into soil organic C (SOC) fractions, and underpinning microbial community in the decomposition process of crop residues are essential for improving SOC management in agricultural systems. However, the fate of residue-C and associated responses of microbial communities remain unclear in Mollisols in north-eastern China, where SOC varies geographically. A 150-day incubation experiment was conducted with ¹³C-labelled soybean residue (4%) amended into two Mollisols differing in SOC (SOC-poor and SOC-rich soils). The ¹³C abundances in SOC fractions and the CO₂-C efflux from soil were determined, and bacterial community composition was analyzed with MiSeq sequencing. The amounts of residue-C incorporated into the coarse particulate organic C (POC), fine POC and mineral-associated C (MOC) fractions were 4.5-, 4.3- and 2.4-fold higher in the SOC-rich soil than in the SOC-poor soil, respectively. The primed CO₂ per unit of native SOC was greater in the SOC-poor soil than in the SOC-rich soil. This indicates that the contributions of residue-C to the POC and MOC fractions were greater in the SOC-rich soil while residue amendment had stronger priming effect in the SOC-poor soil, stimulating the C exchange rate between fresh and native SOC. A principal coordinate's analysis (PCoA) showed that the shift of bacterial community structure in response to residue amendment varied between the two soils. Genera *Verrucosispora*, *Xanthomonadales* and *Steroidobacter* were mainly enriched in the residue-amended SOC-poor soil while *Anaerolineaceae* uncultured was dominant in the SOC-rich soil. The canonical correspondence analysis (CCA) revealed that the relative abundance of the bacterial operational taxonomic unit (OTU) among residue treatments was significantly associated with soil characteristics, especially C content in coarse POC and MOC fractions ($p < 0.01$), implying that the shift of bacterial community composition in response to residue amendment contributes to the sequestration of residue-C in SOC fractions.