



Variation in bacterial and fungal community structure and abundance under distinct mulching practices in dryland agricultural region of northeast China

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Information about the effect of plastic film mulching (PFM) on the soil microbial community in soils of dryland agricultural region remains scarce. In the present study, Illumina HiSeq pyrosequencing was employed to compare the bacterial and fungal communities among soils under three treatments: no mulching (NM), spring mulching (SM) and autumn mulching (AM). Our research results demonstrated that different mulching treatments played important roles in shaping bacterial and fungal diversity and composition from the phylum to genus levels, and we found that the magnitude of change was much greater in the fungal communities. The AM treatment soil sample had relatively harboured more taxa related to nitrogen cycling, especially soil denitrification (i.e. bacteria assigned to *Agrobacterium* and *Pseudomonas* and, fungi assigned to *Trichoderma* and *Fusarium*). Moreover, some taxa related to a higher degradation capacity (i.e. bacteria assigned to *Corynebacterium* and *Cellulomonas* and; fungi assigned to *Trichoderma*, *Talaromyces* and *Fusarium*), and some related to antibiotic production (i.e. bacteria assigned to *Streptomyces*) were more abundant in AM. However, it was notable that the pathogenic microorganism of *Cladosporium* was enhanced in AM. Therefore, while vigorously developing technological applications for AM, we must not ignore its potentially high pathogenic risk.