



## **Spatial distribution of microbial community composition and activity along a steep slope of the Loess Plateau**

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Spatial heterogeneity of soil microbes introduces great uncertainty to our understanding of microbe-mediated soil carbon cycling, yet was few studied on sloping lands. Along a steep-slope grassland (35°) on the Chinese Loess Plateau, soils of 0–10 cm were sampled in 2016 at three slope positions (upper, middle and bottom) to determine microbial community composition (by Illumina Hiseq sequencing) and activities (enzymes involved in carbon cycling and the in situ soil respiration). The bacterial alpha-diversity were greater at middle- and bottom- than at upper slope position, while fungal alpha-diversity varied little across slope positions. The bacterial phylum Proteobacteria was 9.7% and 19.4% lower but Acidobacteria was 36.5% and 41.3% greater at bottom- than at upper- and middle-slope positions. The fungal community transitioned from being Basidiomycota-dominant (relative abundance of 46.8%) at upper slope position to Zygomycota-dominant (relative abundance of 36.5%) at bottom slope position. The  $\beta$ -D-glucosidase activity generally declined down the slope while  $\beta$ -D-xylosidase and cellobiohydrolase activities hiked at middle slope position. All the enzyme activities were suppressed at bottom slope position. Soil respiration increased by 49.1% ( $P < 0.05$ ) while temperature sensitivity decreased by 13.2% ( $P < 0.05$ ) down the slope. The copiotrophic groups (Acidobacteria and Zygomycota) negatively and oligotrophic groups (Proteobacteria and Basidiomycota) positively correlated with temperature sensitivity of soil respiration. Our findings revealed divergent responses of soil bacterial and fungal communities along the slope and highlighted the importance of microbial information in predicting the spatial variability of soil respiration in hillslope ecosystems.