



Depths-dependent response of bacterial community composition and function to subsoil exposure in the loess soil

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Subsoil exposure (terracing, road construction, soil erosion, etc) evidently affects soil water, heat, carbon flux and soil productivity. Little is known about changes in bacterial community composition and function in subsoil after being exposed to surface condition. In 2016, soils at 0–20 cm, 20–60 cm and 60–100 cm from three 100-cm profiles in a spring maize field of the Loess Plateau were incubated under air temperature over the year to simulate subsoil exposure, with soil respiration being consecutively monitored (with Li-Cor 8100). Soils of each depth were sampled in situ as control and in the exposed soil to determine the short-term changes in bacterial community composition (represented by 16S rRNA) and functions (by analyzing enzymes involved in carbon cycling). The result revealed a depth-specific effect of subsoil exposure on the bacterial community composition and carbon-cycling enzymes. Soil exposure exerted no significant effect on the most abundant bacterial communities at 0–20 cm. However, at both 20–60 and 60–100 cm, the copiotrophic phyla Proteobacteria and Actinobacteria increased and the oligotrophic phyla Thermotogae and Nitrospirae decreased in the exposed soil than in the control soil. Both number of species differentiated the two soils and magnitude of the increased abundances increased with depths, due to the increasingly greater effect of soil dissolved organic carbon and soil mineral nitrogen with depths. As a result, the exposed soil had distinct bacterial community structure at 60–100 cm from the control soil. Soil exposure exerted no effect on enzyme activities at 0–20 cm but increased β -D-xylosidase and cellobiohydrolase activities at 20–60 cm and increased β -D-xylosidase and β -D-glucosidase activities at 60–100 cm. In the exposed soil, the lower soil respiration (by 38.5% and 33.9%) and temperature sensitivity (by 21.8% and 24.1%) at 20–60 cm and 60–100 cm than at 0–20 cm were partly a product of bacterial oligotrophic Actinobacteria replacing copiotrophic Proteobacteria, and the suppressed microbial biomass and activities. These results revealed that the exposed subsoil had more copiotrophic microbes than the control soil, but less soil CO₂ emission potential and lower temperature response than the surface soil.