

Table S1. Recent Microbiology Study of Soil Profiles

Title	Methods	Layers/ Depth (cm)	Land Use	Main Conclusion	Reference
Digging deeper to find unique microbial communities: The strong effect of depth on the structure of bacterial and archaeal communities in soil	16S rRNA	3-180, interval of 10cm for top 30cm, 20cm for deeper	Forest and meadow, USA	microbial biomass and soil carbon decreased exponentially with depth; diversity dropped by 20–40% along the profile; microbial community composition was more variable in the surface horizons	(Eilers <i>et al.</i> , 2012)
Effects of resource availability and quality on the structure of the micro-food web of an arable soil across depth	PLFA, 16S rRNA, ITS, etc.	0-10, 4-50, 60-70	Arable field, Germany	Microbial abundances decreased with depth; litter amendment fostered the microbial abundance but not the diversity; soil profile and crop plant shaped microbial structure	(Scharroba <i>et al.</i> , 2012)
Changes in extracellular enzyme activity and microbial community structure with soil depth at the Luquillo Critical Zone Observatory	PLFA, enzymes assays	10 to 140 cm or bedrock at discrete 10 cm intervals	Sierra palm forest, USA	Microbial biomass, enzyme activities, carbon and nutrients decline exponentially with depth; Subsoils contain metabolically active communities that are structurally distinct from surface communities	(Stone <i>et al.</i> , 2014)
Change in deep soil microbial communities due to long-term fertilization	16S rRNA	0-20, 20-40, 40-60, 60-100, 100-150, 150-200, 200-250, 250-300	Cropped desert, China	Fertilizer applications alter microbial community structure within profile (0–3 m); Community differentiation is greater in subsoil; Subsoil altered by leached substance while topsoil altered by direct fertilization.	(Li <i>et al.</i> , 2014)
Effects of land use on soil microbial biomass, activity and community structure at	PLFA, [14C] leucine incorporation	0-10, 30-40 (grass/crop) or 50-60 (forest),	Grass land, arable field, and mixed forest,	Land use strongly affects soil microbiology, but only in the upper soil horizons; Considerable microbial	(Van Leeuwen <i>et al.</i> ,

different soil depths in the Danube floodplain		55-65 (grass/crop) or 70-80 (forest)	Austria	biomass and activity were found below 30 cm depth.	2017)
Long-term Fertilization Structures Bacterial and Archaeal Communities along Soil Depth Gradient in a Paddy Soil	16S rRNA	0–20, 20–40, 40–60, 60–90	Paddy soil, China	Application of different types of fertilizer (chemical and organic fertilizer) resulted in different microbial structures across the whole soil profile; microbial communities in the topsoil were significantly different from those in subsoils.	(Gu <i>et al.</i> , 2017)
Depth-dependent influence of different land-use systems on bacterial biogeography	16S rRNA	5, 10, 15, 20, 25, 30, 35,40,45	old-growth and mature forests, decommissioned and active agricultural fields, Canada	Bacterial communities were strongly influenced by depth across all sites, but the magnitude of this influence differed by land use	(Seuradge <i>et al.</i> , 2016)
Shifts in the bacterial community composition along deep soil profiles in monospecific and mixed stands of Eucalyptus grandis and Acacia mangium	16S rRNA	0–100,100–300, 300–500, 500–700, 700–800	Cultivated lands, Brazil	A decrease in bacterial abundance found with soil depth; differences in community patterns was observed between monospecific and mixed cultivations	(Pereira <i>et al.</i> , 2017)
Soil physicochemical and microbial characteristics of contrasting land-use types along soil depth gradients	Fumigation (microbial biomass and respiration)	0-10, 10-30, 30-60	farmland, orchard, grassland and abandoned land, China	soil microbial properties were affected by both land-use types and soil depths than nitrogen and physicochemical properties	(Liu <i>et al.</i> , 2018)

Soil microbiomes with distinct assemblies through vertical soil profiles drive the cycling of multiple nutrients in reforested ecosystems	16S rRNA, ITS	0–10, 10–20, 20–40, 40–60, 60–80, 80–100, 100–150, 150–200, 200–250, 250–300.	Farmland, 10-year, 20-year and 30-year forests, China	bacterial and fungal diversity decreased, whereas archaeal diversity increased with increasing soil depth (0–80 cm); the vertical spatial variation in bacterial communities decreased over reforestation time, while that in archaeal and fungal communities increased	(Jiao <i>et al.</i> , 2018)
Effects of different management regimes on microbial biodiversity in vineyard soils	16S rRNA, ITS	5-30, 30-60	Farm land with different management practices, Germany	Fungal community composition differed significantly from organic and biodynamic management, whereas fungal species richness remained unaffected; bacterial species richness was changed by different management	(Hendgen <i>et al.</i> , 2018)
Ecological and Genomic Attributes of Novel Bacterial Taxa That Thrive in Subsurface Soil Horizons	16S rRNA, Shotgun metagenomic	0 to 100 with 10-cm increments	Vegetation covered but land-use type unspecified, USA	bacterial and archaeal diversity generally decreased with depth, as did the degree of similarity of microbial communities to those found in surface horizons; deeper soils harbored distinct microbial communities	(Brewer <i>et al.</i> , 2019)
Soil depth and grassland origin cooperatively shape microbial community co-occurrence and function	16S rRNA, ITS	0–10, 10–30, 30–60, 60–100	Grass land, USA	Microbial diversity decreased with depth, and community composition was distinctly different between shallow and deeper soil depths; grass species influenced bacterial and fungal networks, especial for lower horizons	(Upton <i>et al.</i> , 2020)

Soil acidification modifies soil depth-microbiome relationships in a no-till wheat cropping system	16S rRNA	0, 10, 25, 50,75,100	Farm land, USA	Bacterial communities are highly variable with depth; Nitrification caused depth-specific soil acidification resulted in different dominant taxa in different layers.	(Schlatter <i>et al.</i> , 2020)
Depth-Dependent Patterns of Bacterial Communities and Assembly Processes in a Typical Red Soil Critical Zone	16S rRNA	0-420cm, interval of 10cm for top 100cm, 20cm for deeper	Red Soil Critical Zone Observatory, China	Bacterial richness and diversity decreased with depth in 0–90 cm, but was constant in 90–420 cm; bacterial distribution influenced by soil C and N	(Wu <i>et al.</i> , 2020)
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