

Table S1 Responses of microorganisms to land reclamation

Study area	Methods of reclamation	Biodiversity changes	Microbial community structure changes	Main driven factors	Reference
Disturbed sites after opencast mining	Liming and fertilization	Soil from the reconstructed sites showed a significantly lower microbial diversity compared to undisturbed soils	The composition of the microbial community is significantly different from the undisturbed sites	Not given	[8]
Opencast mine	Revegetation	The soil microbial α -diversity index of unreclaimed land being lower than that of vegetation restoration.	The structure of the soil bacterial community did not change significantly, even though the region has undergone nearly 20 years of vegetation restoration.	The bacterial community structure had no significant response to changes in soil biochemical properties, despite 18–20 years of vegetation restoration.	[25]
Coal mine spoils	Backfilling, topsoil handling, application of organic amendments, planting a grass-legume mixture and mulching with crop residues	Bacterial diversity first declined, then increased, and finally approached the predisturbance levels.	Long-term reclamation strongly affected microbial community structure and diversity.	Soil characteristics and vegetation	[29]
Underground mining area	Gangue filling, topsoil cover, vegetation	The diversity and abundance of bacterial communities in reclaimed soils is slightly different from that of natural soils.	After a 15-year reclamation period, the soil bacterial community structure was found to have a high similarity with natural soil.	Not given	[30]
Coal mine spoil	Agronomic treatments and revegetation	Agronomic treatments increased	Agronomic treatments had a positive	Not given	[32]

			functional diversity of soil microbial communities	effect on bacterial community structure	
Opencast coal mining area	Vegetation		Fungal diversity indices significantly changed in response to reclamation vegetation and time, but bacterial and archaeal indices were only slightly influenced by reclamation characteristics	The composition of the microbial community changed in succession.	As major drivers of microbial community diversity and structure, reclamation scenarios, times, and vegetation type have different effects on bacterial, archaeal, and fungal succession. [33]
Opencast coal mining area	Vegetation and supplementary inorganic fertilizer		Bacterial richness and evenness were significantly greater than in nonmined soils.	The bacterial communities on rehabilitated sites became progressively more similar to those of nonmined analogue sites over time.	Bacterial species composition was associated significantly with the plant density and total stem cross-sectional area of woody vegetation. [34]
Open-cut coal mine	Vegetation		The richness but not evenness of fungal communities was significantly greater in rehabilitated than in nonmined soils and increased over time.	Soil fungal community structure would more closely resemble their pre-disturbance states over time.	Fungal community composition was significantly influenced by aboveground vegetation, edaphic variables, and the length of rehabilitation. [42]
Coal mine sites	Fertilizer amendment		Bacterial diversity increased with reclamation duration.	The longer the reclamation duration, the greater the similarity of bacterial	Reclamation duration played a greater role than [44]

			community structure to the undisturbed site.	fertilizer in bacterial community structure.	
An active surface lignite mining operation area	Replacement of overburden and returning of the leased land to the owner in an agriculturally viable manner, typically consisting of pasture or wooded cover.	Reclaimed soil surpasses reference soil in diversity and richness.	Bacterial community structure most likely will not return to its origin.	The primary driver of bacterial community dynamics was vegetative cover, although time also influenced dynamics.	[45]
The abandoned land of former mining waste	Afforestation	Afforestation could increase both fungal and bacterial biomass.	Microbial community structure was altered by different tree species and land use.	Tree species and soil chemical properties made the soil microbial community composition different.	[46]
Coal-mining subsidence land	Organic amendments and vegetation mixed sowing	The reclaimed soil had a higher community diversity of bacteria than subsided soil	There was a significant difference in soil bacterial community structure between the reclaimed and subsided land.	Reclamation practices have a great influence on soil microbial communities, through the effects of soil attributes.	[47]
Coal-mining subsidence area	Fertilizer amendment	Fertilization (organic and chemical fertilizers) and reclamation time improved bacterial diversity.	Soil bacterial community structure in the 7-year reclaimed soils was more similar to those in the undisturbed soils.	Reclamation time is the main driving force for the restoration of soil bacterial communities, and fertilization can shorten the recovery time of the reclaimed soil.	[48]
Opencast Coal Mine dumpsites	Vegetation without irrigation,	Revegetation engineering could increase	Bacterial community composition	Soil microbes are influenced by soil factors	[49]

		fertilization, nor perturbation after planting.	soil microbial diversity.	was significantly different between re-vegetated and non-vegetated soils and among soils re-vegetated by different plant species.	and aboveground plant species.	
surface coal mine site	Vegetation		The higher soil microbial abundance and diversity were from mixed forests compared with that of the control site.	Soil bacterial, archaeal, and fungal T-RFLP profiles differed with reclaimed scenarios.	Reclaimed scenarios were found to determine soil microbial abundance, diversity, and composition.	[50]
Spoil heap in the brown-coal mining district	Revegetation		Not given.	The composition of microbial communities differed among trees and also exhibited seasonal differences	Dominant tree types affect the soil microbial communities.	[58]
