

Supplementary material

Table S1 Site characteristics across a successional gradient in the subalpine forest on eastern Qinghai-Tibet Plateau.

succession stage	Forest type	Coordinate	Altitude (m a.s.l.)	direction (°)	Canopy cover (%)	Soil name	Dominant vegetation	Plot number
S1	Shrubs community	32°55'N, 104°08'E	2483	NE45	75	Fluvisol	<i>H. rhamnoides</i> L.	3
		32°57'N, 104°07'E	2600	SW225	52	Fluvisol	<i>Salix</i> spp.	3
		32°58'N, 104°05'E	2602	S185	68	Fluvisol	<i>Salix</i> spp.	3
		32°58'N, 104°04'E	2643	WS243	48	Fluvisol	<i>U. pumila</i> L.	3
S2	Broad-leaved forest	32°57'N, 104°07'E	2601	SW225	70	Argosols		3
		32°54'N, 104°09'E	2468	ES105	60	Argosols	<i>Betula</i> spp.; <i>Populus</i> spp.	3
		32°57'N, 104°07'E	2536	E90	55	Fluvisol		3
S3	Mixed forest	32°57'N, 104°04'E	2730	WN280	55	Argosols	<i>A. faxoniana</i> Rehd.; <i>P. purpurea</i> Mast; <i>Betula</i> spp.	3
		32°57'N, 104°04'E	2801	ES115	60	Argosols		3
		32°54'N, 104°03'E	2962	ES134	60	Argosols	<i>Salix</i> spp.	3
S4	Mid-coniferous forest	32°59'N, 104°02'E	2798	N359	61	Cambosols	<i>L. gmelinii</i> (Rupr.) Kuzen.	3
		32°52'N, 104°02'E	3075	NE17	52	Cambosols	<i>S. saltuaria</i> Rehd.	3
S5	Mature coniferous forest	33°00'N, 104°01'E	2885	ES128	65	Argosols	<i>A. faxoniana</i> Rehd.	3
		32°53'N, 104°03'E	3027	SW125	62	Argosols		3
S6	primary coniferous forest	32°52'N, 104°02'E	3068	SE150	62	Argosols		3
		32°52'N, 104°02'E	3199	ES75	58	Argosols	<i>P. purpurea</i> Mast	3

S1 to S6 represent successional stages from 1 to 6, respectively; NE: North-East; SW: South-West; S: South; WS: West-South; ES: East-South; E: East; WN: West-North; N: North; SE: South-East.

Table S2 Discrepancy of relative abundance of the dominant phyla of soil bacterial and fungal community composition among different forest succession stages.

Bacterial phyla	H	<i>P</i> value	Fungal phyla	H	<i>P</i> value
Proteobacteria	7.860	0.164	Ascomycota	7.945	0.159
Tenericutes	19.379	0.002**	Basidiomycota	5.248	0.386
Acidobacteria	12.175	0.032*	Mortierellomycota	14.651	0.012*
Firmicutes	21.274	<0.001***	Rozellomycota	17.58	0.004**
Actinobacteria	18.892	0.002**	Chytridiomycota	4.307	0.506
Bacteroidetes	11.790	0.038*	Mucoromycota	3.097	0.685
Verrucomicrobia	10.246	0.069	Zoopagomycota	4.322	0.504
Gemmatimonadetes	19.755	<0.001***	Glomeromycota	7.211	0.205
Rokubacteria	16.124	0.006**	GS01	11.886	0.036*
Chloroflexi	16.942	0.005**	Blastocladiomycota	6.729	0.242

Significant effect: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. Kruskal-Wallis test.

Table S3 The analysis of similarities (ANOSIM) among different forest succession stages based on the distance algorithm of Bray–Curtis.

Group	bacteria		Fungi	
	R-value	<i>P</i> value	R-value	<i>P</i> value
S1-S2	0.01071	0.364	0.04711	0.207
S1-S3	0.3193	0.004**	0.2169	0.002**
S1-S4	0.2051	0.053	0.4465	0.001***
S1-S5	0.3813	0.007**	0.4155	0.008**
S1-S6	0.5269	0.001***	0.566	0.001***
S2-S3	0.32	0.005**	0.3124	0.001***
S2-S4	0.4481	0.005**	0.3493	0.004**
S2-S5	0.5011	0.001***	0.3413	0.005**
S2-S6	0.5897	0.001***	0.528	0.001***
S3-S4	0.1046	0.169	0.2259	0.031*

S3-S5	0.2593	0.04*	0.1285	0.139
S3-S6	0.581	0.001***	0.3188	0.009**
S4-S5	0.3463	0.013*	0.1537	0.1
S4-S6	0.7926	0.002**	0.4352	0.004**
S5-S6	0.4667	0.004**	0.2898	0.002**

S1 to S6 represent successional stages from 1 to 6, respectively; Significant effect: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. **Table S4** The detrended correspondence analysis (DCA) based on based on the OTUs data at 97% sequence identity.

	Bacteria				fungi			
	DCA1	DCA2	DCA3	DCA4	DCA1	DCA2	DCA3	DCA4
Eigenvalues	0.1239	0.02476	0.03420	0.01638	0.2775	0.13428	0.11861	0.13744
Decorana values	0.2180	0.01907	0.01472	0.01104	0.2888	0.09129	0.05638	0.01634
Axis lengths	1.5119	0.74397	0.91304	0.53708	1.6512	1.32027	1.47367	1.44479

Table S5 The detection of collinearity of forest variables by the analysis of Variance Inflation Factor (VIF).

Forest variable	SOC	TN	C:N	T	pH	WD	NWD	Altitude	Canopy
First VIF	46.19128	35.488101	3.765846	1.450231	1.296448	1.931329	1.849688	2.668003	1.496639
Second VIF	2.519368	—	1.947650	1.429947	1.296446	1.922745	1.792969	2.420485	1.370652