

Electronic Supplementary Material

Response of soil microbial community composition and diversity at different gradients of grassland degradation in the central Mongolia

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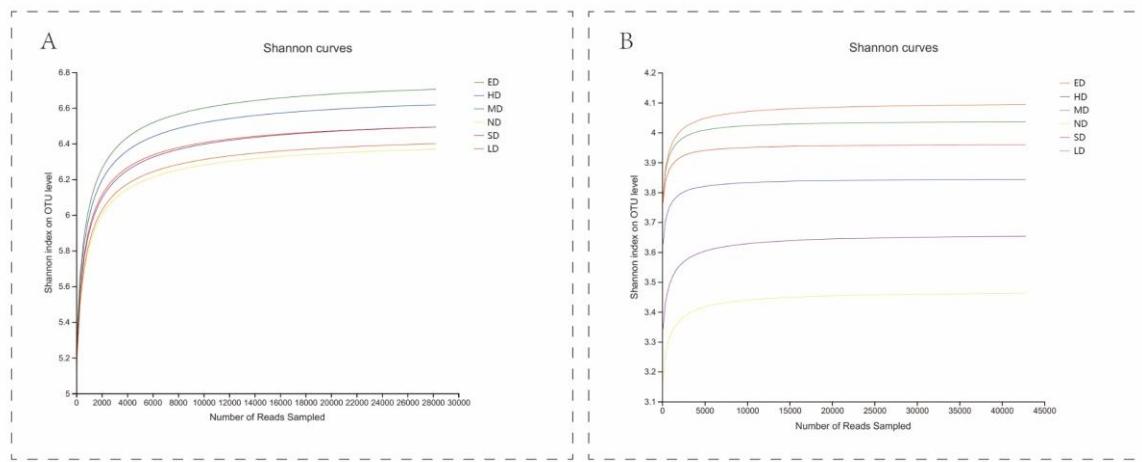


Figure S1. The rarefaction curve analysis of the bacterial (A) and fungal (B) sequences. The curves were drawn with the number of reads as the X-axis and the Shannon index values on OTU level as the Y-axis.

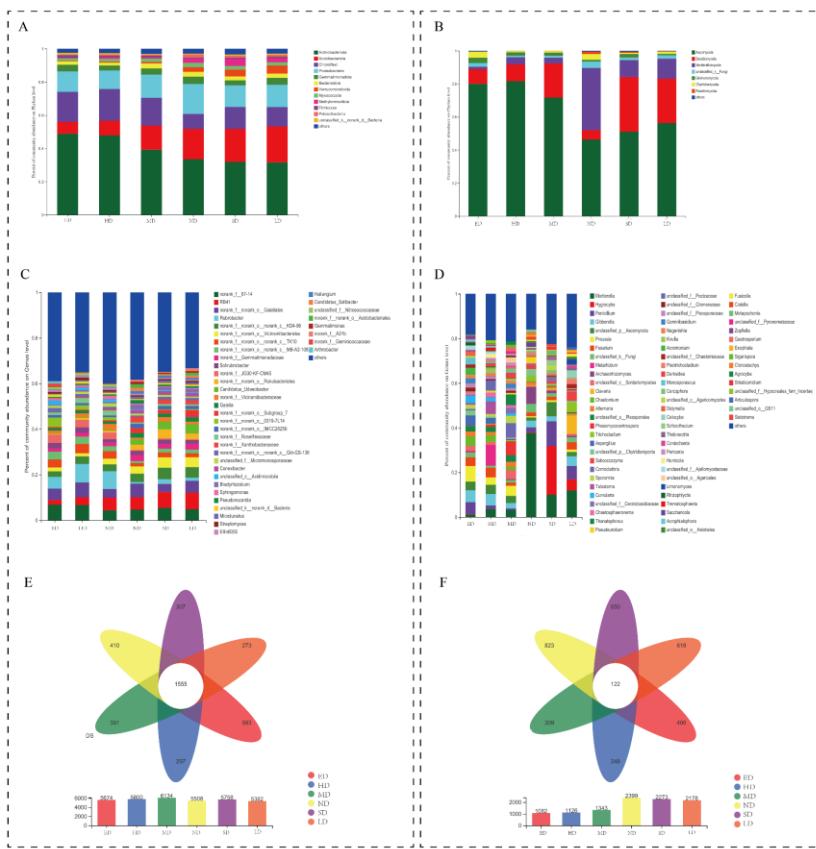


Figure S2. soil microbial community barplot analysis and Venn diagrams.

A: bacterial community composition at the phylum level. B: fungal community composition at the phylum level. C: bacterial community composition at the genus level. D: fungal community composition at the genus level; the X-axis were the sampling plots, and the Y-axis were the percent of community abundance. E: bacterial Venn diagram at the OTUs level. F: fungal Venn diagram at the OTUs level; the six petals correspond to the numbers of OTUs unique to each sample, and the petal center was the number of OTUs common to all samples. In addition, the column chart shown the total number of OTUs for each sample.

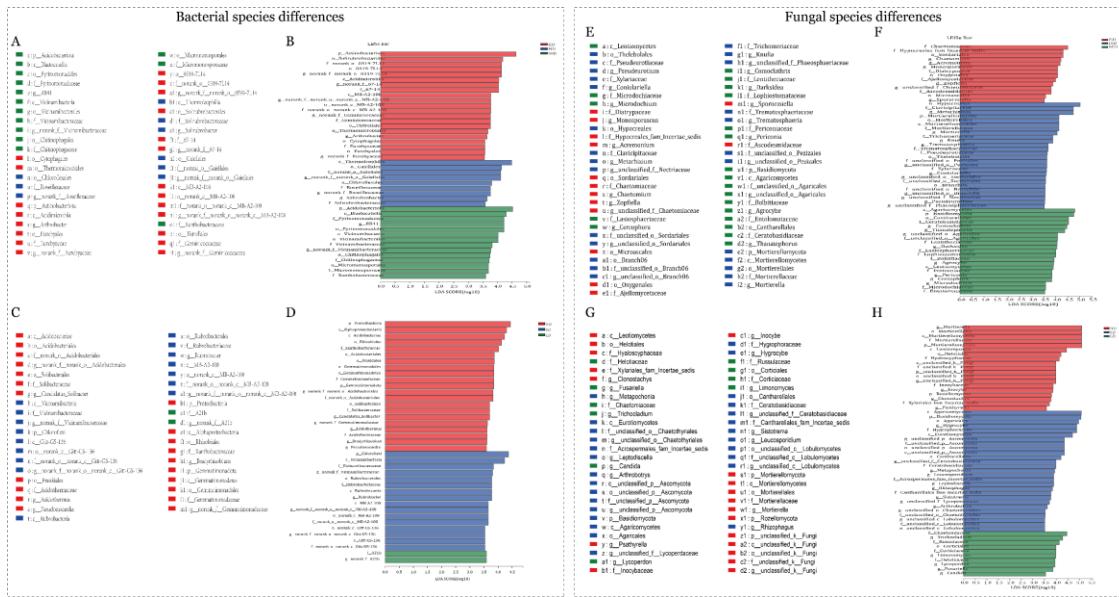


Figure S3. Microbial groups with significant differences at different grassland degradation gradients screened by Linear discriminant analysis effect size (LEfSe). Significantly different groups of the bacterial (A, B) and fungal (E, F) communities between ED, HD and MD site and that of the bacterial (C, D) and fungal (G, H) communities between ND, SD and LD. Microbial groups marked with different colors in A, C, E and G corresponds to different color nodes of Fig. 3 B, D, F and H. The LDA score obtained by Linear discriminant analysis in LEfSe bar (B, D, F and H).

Table S1. The coordinates of sampling sites, vegetation types, coverage, dominant species and sampling time

sampling site	coordinate	altitude	degrees of grassland degradation	coverage (%)	dominant species	sampling time
ED1	100°39'19.80" E 45°24'14.76" N	1399.3 m	extremely	5	<i>Caragana microphylla</i> Lam.; <i>Stipa klemenzii</i> Rooshev.	2019.7.01
ED2	100°42'10.44" E 45°24'56.88" N	1426.3 m	extremely	5	<i>Caragana microphylla</i> Lam.; <i>Stipa klemenzii</i> Rooshev.	2019.7.01
ED3	100°36'29.16" E 45°23'32.64" N	1390.5 m	extremely	10	<i>Achnatherum splendens</i> (Trin.) Nevski.; <i>Leymus chinensis</i> (Trin.) Tzvel.; <i>Peganum harmala</i> L.	2019.7.01
HD1	100°34'54.84" E 45°39'57.60" N	1615.1 m	heavily	10	<i>Caragana microphylla</i> Lam.; <i>Stipa klemenzii</i> Rooshev.; <i>Salsola collina</i> Pall.	2019.7.01
HD2	100°35'09.60" E 45°39'47.88" N	1620.0 m	heavily	10	<i>Caragana korshinskii</i> Kom.; <i>Stipa klemenzii</i> Rooshev.; <i>Salsola collina</i> Pall.	2019.7.01
HD3	100°35'08.16" E 45°40'07.68" N	1613.6 m	heavily	15	<i>Stipa klemenzii</i> Rooshev.; <i>Poa annua</i> L.; <i>Artemisia frigida</i> Willd.	2019.7.02
MD1	100°35'17.52" E 45°40'30.72" N	1635.3 m	moderately	15	<i>Agropyron cristatum</i> (Linn.) Gaertn.; <i>Haplophyllum dauricum</i> (L.) G. Don. <i>Achnatherum splendens</i> (Trin.) Nevski.	2019.7.02
MD2	100°36'16.56" E 45°42'10.44" N	1691.6 m	moderately	15	<i>Poa annua</i> L.; <i>Cleistogenes squarrosa</i> (Trin.) Keng.	2019.7.02
MD3	100°36'48.60" E 45°44'14.28" N	1752.9 m	moderately	15	<i>Stipa klemenzii</i> Rooshev.; <i>Poa annua</i> L.; <i>Cleistogenes squarrosa</i> (Trin.) Keng.	2019.7.02
ND1	101°07'07.32" E 47°18'17.28" N	1993.5 m	Non-degraded	90	<i>Festuca arundinacea</i> Schreb.; <i>Geranium wilfordii</i> Maxim.; <i>Carex pediformis</i> C.A.Mey.	2019.7.05
ND2	101°23'16.44" E 47°31'23.16" N	1713.0 m	Non-degraded	85	<i>Festuca lenensis</i> Drob.; <i>Filifolium sibiricum</i> (Linn.) Kitam.; <i>Carex pediformis</i> C.A.Mey.	2019.7.06
ND3	101°16'21.36" E 47°32'33.36" N	1748.7 m	Non-degraded	90	<i>Festuca lenensis</i> Drob.; <i>Cleistogenes squarrosa</i> (Trin.) Keng.; <i>Carex pediformis</i> C.A.Mey.	2019.7.07
SD1	101°07'14.88" E 47°18'33.84" N	1950.6 m	slightly	80	<i>Artemisia frigida</i> Willd.; <i>Cleistogenes squarrosa</i> (Trin.) Keng.; <i>Koeleria altaica</i> (Domin) Krylov.	2019.7.05
SD2	101°23'16.80" E 47°31'26.04" N	1710.5 m	slightly	80	<i>Festuca lenensis</i> Drob.; <i>Leymus chinensis</i> (Trin.) Tzvel.; <i>Carex pediformis</i> C.A.Mey.	2019.7.06

SD3	101°16'26.76" E 47°32'36.60" N	1740.1 m	slightly	75	<i>Leymus chinensis</i> (Trin.) Tzvel.; <i>Stipa krylovii</i> Roshev.; <i>Carex duriuscula</i> C.A.Mey.	2019.7.07
LD1	101°07'35.04" E 47°18'50.40" N	1902.4 m	lightly	75	<i>Leymus chinensis</i> (Trin.) Tzvel.; <i>Artemisia frigida</i> Willd.; <i>Cleistogenes squarrosa</i> (Trin.) Keng.	2019.7.05
LD2	101°23'18.60" E 47°31'27.12" N	1705.4 m	lightly	75	<i>Leymus chinensis</i> (Trin.) Tzvel.; <i>Carex duriuscula</i> C.A.Mey.; <i>Cleistogenes squarrosa</i> (Trin.) Keng.	2019.7.06
LD3	101°16'47.64" E 47°33'08.28" N	1668.1 m	lightly	70	<i>Stipa krylovii</i> Roshev.; <i>Carex duriuscula</i> C.A.Mey.; <i>Cleistogenes squarrosa</i> (Trin.) Keng.	2019.7.07

Table S2. Alpha-diversity indices of the soil microbial community in sampling sites

Sampling		Bacteria				Fungi			
plot		chao1	ACE	shannon	pd	chao1	ACE	shannon	pd
ED		3075.243 ±	3078.124 ±	6.493 ±	243.562 ±	298.412 ±	322.946 ±	3.959 ±	68.431 ±
		275.516c	276.821b	0.169bc	14.462d	63.342b	73.599b	0.429	17.910b
HD		3637.985 ±	3647.419 ±	6.617 ±	273.976 ±	343.768 ±	347.339 ±	3.843 ±	78.069 ±
		193.756ab	198.127a	0.069ab	6.766abc	130.677b	122.151b	0.560	27.979b
MD		3788.175 ±	3838.903 ±	6.704 ±	285.697 ±	400.697 ±	395.249 ±	4.036 ±	91.485 ±
		139.393a	148.009a	0.094a	11.857a	139.366b	128.705b	0.549	25.487b
ND		3375.114 ±	3499.203 ±	6.369 ±	260.418 ±	712.727 ±	696.451 ±	3.462 ±	174.750 ±
		296.434bc	479.018a	0.082c	7.537bc	194.875a	189.645a	0.839	37.893a
SD		3634.339 ±	3691.934 ±	6.493 ±	275.823 ±	799.809 ±	788.184 ±	3.754 ±	169.825 ±
		309.563ab	320.014a	0.103bc	14.499ab	276.467a	257.950a	0.979	53.062a
LD		3413.343 ±	3674.155 ±	6.400 ±	257.899 ±	712.513 ±	706.705 ±	4.093 ±	160.800 ±
		260.613b	304.462a	0.225c	18.398cd	182.265a	175.155a	0.544	21.449a

The values were presented as mean ± standard error of mean (S.E.M). Different lowercase letters indicate significant differences at different types' samples ($p < 0.05$). Abbreviation: ACE: abundance-based coverage estimator; pd: phylogenetic diversity.