

Article

Short-Term Effects of Cover Grass on Soil Microbial Communities in an Apple Orchard on the Loess Plateau

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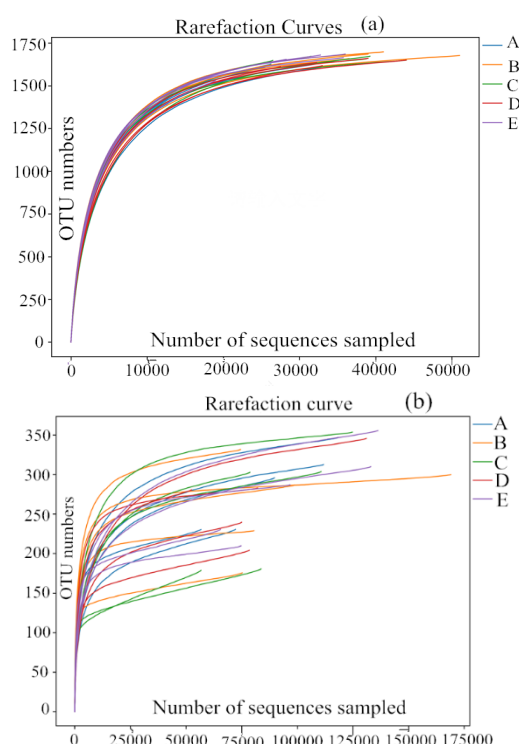


Figure S1. Rarefaction curves of the bacterial(a) and fungal(b).

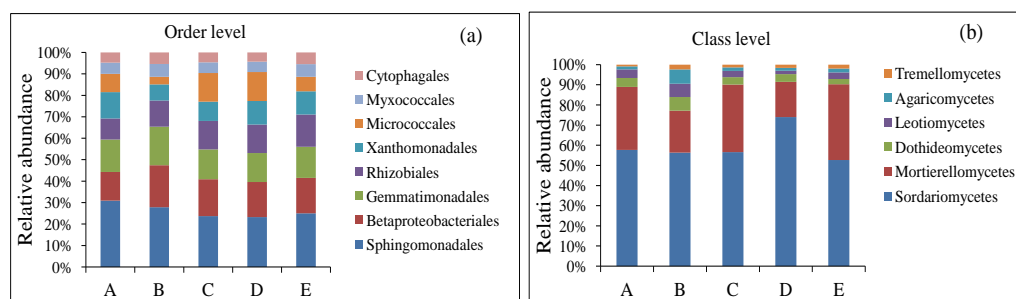


Figure S2 Relative abundance of the dominant groups of the bacterial (a) at the order level and fungal (b) communities at the class level among the different treatments. A indicates 0% (CK), B indicates 20% (LIC), C indicates 40% (MIC1), D indicates 60% (MIC2), and E indicates 80% (HIC).

Table S1. Quality assessment of bacterial sequencing data.

Sample	PE Reads	Raw Tags	Clean Tags	Effective Tags	AvgLen(bp)	GC(%)	Q20(%)	Q30(%)	Effective(%)
A1	80031	75807	67699	62504	417	56.57	95.68	91.64	78.1
A2	60884	57545	51286	47484	418	56.93	95.72	91.69	77.99
A3	69531	65497	58271	54822	417	56.76	95.7	91.67	78.85
A4	67181	63497	56511	51776	418	56.52	95.66	91.62	77.07
A5	55733	52293	46062	44020	419	57.12	95.61	91.49	78.98
B1	68306	64130	56122	55210	419	57.25	95.52	91.31	80.83
B2	83075	78587	69603	66483	419	57.54	95.73	91.66	80.03
B3	109545	104424	94569	89370	417	56.98	96.02	92.2	81.58
B4	79977	76712	70404	66711	417	57.05	96.13	92.43	83.41
B5	87144	83659	76553	72780	418	57.14	96.19	92.51	83.52
C1	60173	57462	52468	48023	418	56.74	96.14	92.44	79.81
C2	67504	64298	58607	58019	419	57.14	96.2	92.53	85.95
C3	59599	56926	51805	51081	419	57.09	96.15	92.45	85.71
C4	76863	73634	67703	62011	417	56.43	96.22	92.58	80.68
C5	77157	73892	67214	61865	419	56.83	96.09	92.34	80.18
D1	68639	65307	59572	57794	418	56.28	96.14	92.45	84.2
D2	79922	73990	61826	56175	418	56.72	94.83	90.13	70.29
D3	71997	66629	56915	53778	417	56.73	95.02	90.45	74.69
D4	79850	73507	60759	57819	418	57.17	94.82	90.1	72.41
D5	79917	73629	60994	59355	419	57.26	94.88	90.21	74.27
E1	80165	73873	61255	59613	418	57.22	94.87	90.19	74.36
E2	80146	73839	61103	57401	418	57.18	94.8	90.05	71.62
E3	79864	73535	60538	57868	418	56.84	94.76	90	72.46
E4	53739	49442	40842	38460	418	56.75	94.84	90.17	71.57
E5	79872	76808	70591	64473	419	56.98	96.2	92.54	80.72

A indicates 0% (NC), B indicates 20% (LIC), C indicates 40% (MIC₁), D indicates 60% (MIC₂), and E indicates 80% (HIC).

Table S2. Quality assessment of fungal sequencing data.

Sample	PE Reads	Raw Tags	Clean Tags	Effective Tags	AvgLen(bp)	GC(%)	Q20(%)	Q30(%)	Effective(%)
A1	132613	122568	121858	121858	253	46.64	99.49	98.67	91.89
A2	97934	92678	92009	92009	236	45.79	99.71	99.05	93.95
A3	79448	74780	74215	74215	229	44.55	99.73	99.11	93.41
A4	129280	121444	120762	120762	240	44.47	99.68	99.01	93.41
A5	64958	60468	59886	59886	243	47.45	99.62	98.88	92.19
B1	85625	78498	77953	77953	263	48.89	99.44	98.55	91.04
B2	85220	78997	78758	78758	252	47.26	99.52	98.71	92.42
B3	89986	84053	83779	83779	247	49.07	99.6	98.84	93.1
B4	188731	176136	175367	175367	252	45.13	99.38	98.5	92.92
B5	109733	102794	102108	102108	254	45.61	99.56	98.78	93.05
C1	138173	128150	127546	127546	240	47.54	99.65	98.91	92.31
C2	92866	86390	85704	85704	240	45.71	99.64	98.91	92.29
C3	63612	59806	59219	59219	243	48.46	99.62	98.86	93.09
C4	119955	113472	112866	112866	231	42.88	99.69	99.03	94.09
C5	87763	82172	81856	81856	242	43.87	99.6	98.84	93.27
D1	60501	55832	55454	55454	235	47.22	99.67	98.96	91.66
D2	142689	134090	133434	133434	236	46.45	99.72	99.07	93.51
D3	82086	77493	76879	76879	236	48.77	99.7	99.02	93.66
D4	91140	85376	84857	84857	240	47.5	99.66	98.94	93.11
D5	86079	81575	81042	81042	239	47.78	99.69	99.01	94.15
E1	72512	68401	67961	67961	242	44.33	99.63	98.92	93.72
E2	143627	136018	135367	135367	235	45.47	99.71	99.05	94.25
E3	81849	76926	76647	76647	240	44.71	99.62	98.89	93.64
E4	104916	98903	98572	98572	234	45.26	99.64	98.95	93.95
E5	147781	139423	138758	138758	239	48.57	99.69	99.01	93.89

A indicates 0% (NC), B indicates 20% (LIC), C indicates 40% (MIC₁), D indicates 60% (MIC₂), and E indicates 80% (HIC).

Table S3. Composition of bacterial community at the phylum level.

Phylum	A	B	C	D	E
<i>Proteobacteria</i>	42.44±3.13a	38.62±3.18b	41.19±1.50ab	41.79±3.89ab	40.18±1.57ab
<i>Acidobacteria</i>	13.27±2.26a	16.06±1.76a	14.42±3.09a	14.08±3.02a	16.40±1.71a
<i>Actinobacteria</i>	11.69±1.09ab	10.03±1.11a	13.84±4.89bc	14.29±1.06b	11.01±1.57ac
<i>Chloroflexi</i>	9.24±0.78ac	12.36±1.39b	9.17±1.21a	9.39±0.85ac	10.54±0.73cd
<i>Gemmatimonadetes</i>	9.12±0.69a	8.83±0.64ab	7.81±1.64ab	7.32±1.54b	7.26±1.14b
<i>Bacteroidetes</i>	5.65±0.79a	4.47±0.29b	4.75±0.39b	4.46±0.72b	4.97±0.71ab
<i>Planctomycetes</i>	1.93±0.32a	2.30±0.41a	1.74±0.57a	1.70±0.58a	2.20±0.33a
<i>Rokubacteria</i>	1.49±0.73a	1.88±0.80a	1.80±0.58a	1.81±0.87a	1.90±0.68a
<i>Nitrospirae</i>	1.12±0.13a	1.46±0.17ab	1.25±0.25a	1.32±0.36a	1.79±0.41b
<i>Verrucomicrobia</i>	1.30±0.16a	1.52±0.24a	1.43±0.33a	1.29±0.12a	1.35±0.19a

The values in the table are mean values (± SD, n =5). Significant differences among different vegetation types are indicated by different letters at the 0.05 level. A indicates 0% (NC), B indicates 20% (LIC), C indicates 40% (MIC₁), D indicates 60% (MIC₂), and E indicates 80% (HIC).

Table S4. Composition of bacterial community at the orders level.

Bacteria orders	A	B	C	D	E
<i>Sphingomonadales</i>	13.89±2.13b	10.26±2.43a	9.96±1.68a	9.46±2.18a	9.77±0.64a
<i>Betaproteobacteriales</i>	5.97±0.88a	7.22±1.18a	7.24±1.19a	6.68±1.07a	6.44±0.74a
<i>Gemmatimonadales</i>	6.79±0.51a	6.64±0.31a	5.83±1.01a	5.49±0.87a	5.66±0.74a
<i>Rhizobiales</i>	4.41±1.13a	4.50±1.18a	5.57±0.28a	5.40±0.59a	5.86±0.81a
<i>Xanthomonadales</i>	5.51±1.36a	2.77±1.25a	3.79±0.74a	4.47±2.73a	4.23±2.72a
<i>Micrococcales</i>	3.8±1.32ac	1.31±0.58a	5.60±0.52bc	5.53±1.50c	2.64±1.24abc
<i>Myxococcales</i>	2.35±0.35a	2.21±0.55a	2.11±0.39a	1.96±0.46a	2.30±0.41a
<i>Cytophagales</i>	2.14±0.43a	1.97±0.19a	1.94±0.20a	1.75±0.59a	2.13±0.57a

The values in the table are mean values (± SD, n =5). Significant differences among different vegetation types are indicated by different letters at the 0.05 level. A indicates 0% (NC), B indicates 20% (LIC), C indicates 40% (MIC₁), D indicates 60% (MIC₂), and E indicates 80% (HIC).

Table S5. Composition of fungi community at the phylum level.

Phylum	A	B	C	D	E
<i>Ascomycota</i>	59.58±10.68ab	58.56±9.96ab	58.80±16.23ab	74.14±6.64a	53.59±13.99b
<i>Mortierellomycota</i>	27.09±5.94abc	17.02±11.37ab	29.83±17.03bc	15.98±8.11ab	34.00±11.80c
<i>Basidiomycota</i>	2.10±1.51a	4.23±3.74a	2.89±2.36a	2.83±1.69a	3.51±1.79a

The values in the table are mean values (± SD, n =5). Significant differences among different vegetation types are indicated by different letters at the 0.05 level. A indicates 0% (NC), B indicates 20% (LIC), C indicates 40% (MIC₁), D indicates 60% (MIC₂), and E indicates 80% (HIC).

Table S6. Compositions of fungi community at the classes level.

Fungi classes	A	B	C	D	E
<i>Sordariomycetes</i>	49.87±10.77a	44.75±8.61a	50.35±15.19a	67.6±7.77a	47.13±16.59a
<i>Mortierellomycetes</i>	27.07±5.98ab	16.53±11.06a	29.83±17.03ab	15.94±8.08a	33.73±11.79bc
<i>Dothideomycetes</i>	3.82±3.27a	5.41±3.51a	3.28±0.98a	3.51±3.11a	2.33±0.68a
<i>Leotiomycetes</i>	3.65±3.25a	5.23±3.08a	2.69±1.00a	1.48±0.63a	2.89±1.81a
<i>Agaricomycetes</i>	1.30±0.56a	5.65±3.22a	1.56±1.18a	1.33±0.59a	1.73±0.89a
<i>Tremellomycetes</i>	0.76±0.34a	1.87±0.91a	1.24±1.08a	1.46±0.88a	1.74±1.27a

The values in the table are mean values (± SD, n =5). Significant differences among different vegetation types are indicated by different letters at the 0.05 level. A indicates 0% (NC), B indicates 20% (LIC), C indicates 40% (MIC₁), D indicates 60% (MIC₂), and E indicates 80% (HIC).