

## *Supplementary Material*

### 1 Supplementary Tables

Table S1. Data output from ITS2 amplicon sequencing

Sample	Seq_num	Base_num	Mean_length
CTM13_1	60738	19163437	316
CTM13_2	62080	19920572	321
CTM13_3	59669	18900936	317
CTM9_1	56835	17302582	304
CTM9_2	57994	17754902	306
CTM9_3	57321	17379432	303
CTM5_1	60696	18324559	302
CTM5_2	61899	18821552	304
CTM5_3	55647	16874358	303
CTM3_1	57575	17630805	306
CTM3_2	55556	16798510	302
CTM3_3	59114	17897421	303
CTM1_1	63220	19163739	303
CTM1_2	57200	17342952	303
CTM1_3	62112	18930681	305
	sum(Seq_num)	sum(Base_num)	ave(Mean_length)
	887656	272206438	307

Table S2. Variance Proportion of RDA analysis at OTU level

	Proportion of Variance
RDA1	0.3609
RDA2	0.176
RDA3	0.1285
RDA4	0.0256
RDA5	0.0147
RDA6	0.0039
PC1	0.1252
PC2	0.0835
PC3	0.0526
PC4	0.0151
PC5	0.0067
PC6	0.0037
PC7	0.0024
PC8	0.0011

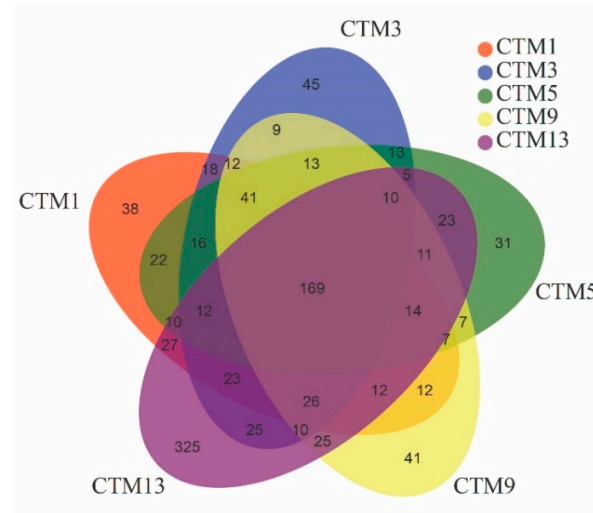
Table S3. Effect of soil chemical properties on soil fungal genera community composition using RDA analysis

	RDA1	RDA2	r <sup>2</sup>	P values
OM	0.9996	0.0266	0.2122	0.233
TN	0.7293	0.6842	0.4712	0.025
TP	-0.4262	0.9046	0.5848	0.004
TK	-0.6914	0.7225	0.2686	0.166
EC	-0.585	0.8111	0.7652	0.001
PH	0.9097	-0.4152	0.7605	0.001

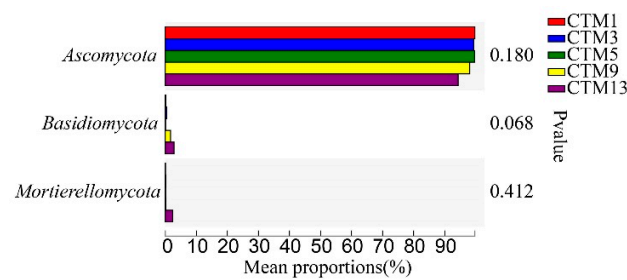
Table S4. Spearman correlation heatmap analysis between soil fungal genera and soil chemical properties

	correlation						p value					
	OM	TN	TP	TK	EC	PH	OM	TN	TP	TK	EC	PH
<i>g__Trichocladium</i>	0.29	0.44	-0.37	-0.06	-0.37	0.70	0.30	0.10	0.18	0.82	0.17	0.00
<i>g__Chaetomium</i>	0.29	0.22	-0.14	0.16	0.00	0.38	0.30	0.44	0.63	0.56	0.99	0.16
<i>g__Lophotrichus</i>	0.23	0.20	-0.06	-0.51	-0.15	-0.03	0.41	0.47	0.82	0.05	0.60	0.90
<i>g__Fusarium</i>	-0.17	0.32	0.59	0.54	0.59	-0.36	0.55	0.25	0.02	0.04	0.02	0.19
<i>g__Acaulium</i>	-0.22	0.14	0.49	0.17	0.53	-0.68	0.43	0.61	0.06	0.54	0.04	0.00
<i>g__Pyrenochaeta</i>	-0.10	-0.17	-0.38	0.01	-0.58	0.02	0.72	0.55	0.17	0.98	0.02	0.94
<i>g__Pseudaleuria</i>	-0.03	0.34	0.77	0.44	0.69	-0.72	0.92	0.22	0.00	0.10	0.00	0.00
<i>g__Heydenia</i>	-0.26	0.25	-0.04	0.07	0.05	-0.14	0.34	0.37	0.90	0.80	0.86	0.61
<i>g__Chrysosporium</i>	0.21	0.21	-0.24	-0.23	-0.45	-0.08	0.45	0.44	0.40	0.40	0.09	0.77
<i>g__Mortierella</i>	-0.47	-0.09	0.33	0.28	0.61	-0.69	0.08	0.75	0.24	0.31	0.02	0.00
<i>g__Cercophora</i>	-0.17	0.10	0.58	0.25	0.76	-0.48	0.54	0.73	0.02	0.36	0.00	0.07
<i>g__Cladosporium</i>	-0.51	-0.01	0.13	0.02	0.30	-0.65	0.05	0.98	0.66	0.95	0.27	0.01
<i>g__Tausonia</i>	-0.46	0.01	0.44	0.26	0.52	-0.50	0.08	0.98	0.11	0.34	0.05	0.06
<i>g__Cheilymenia</i>	0.56	0.38	0.05	0.11	-0.04	0.19	0.03	0.16	0.86	0.70	0.88	0.50
<i>g__Schizothecium</i>	-0.68	-0.31	-0.15	0.07	0.19	-0.42	0.01	0.27	0.59	0.80	0.51	0.12
<i>g__Curvularia</i>	-0.44	-0.20	0.24	0.06	0.36	-0.50	0.10	0.47	0.39	0.82	0.19	0.06

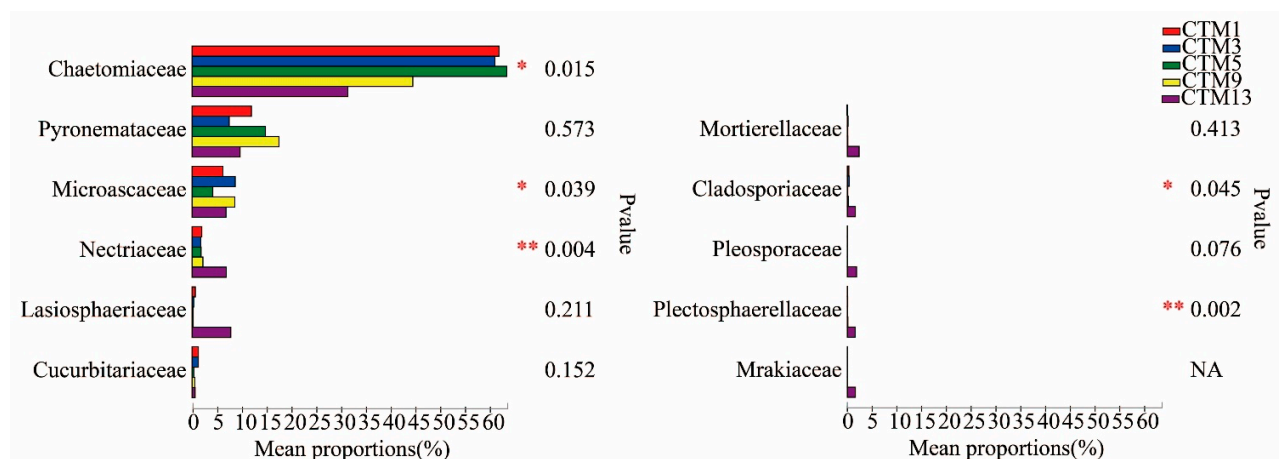
## 2 Supplementary Figures



**Figure S1.** Venn diagram of OTU level among different CTM cycles.



**Figure S2.** Difference analysis of soil fungal phyla among different CTM cycles. Significances between different treatments were compared using One-way ANOVA, with the results indicated by red asterisks.



**Figure S3.** Difference analysis of soil fungal family among different CTM cycles. Significances between different treatments were compared using One-way ANOVA, with the results indicated by red asterisks (\*\* $P < 0.01$ ; \* $P < 0.05$ ).