

Table S1. Pearson correlation (r) between physiological groups and dominant genera of microbial community.

Physiological groups		proteolytics		amylolytics		cellulolytics		ligninolytics		P-solubilizing		N2-fixing		nitrifiers I		nitrifiers II	
		M	T	M	T	M	T	M	T	M	T	M	T	M	T	M	T
	<i>Thermomyces</i>	0.693	0.961	0.544	0.992	0.957	0.946	-0.583	-0.585	-0.139	-0.277	0.984	0.992	-0.558	-0.645	-0.544	-0.289
	<i>Penicillium</i>	-0.024	-0.421	-0.844	-0.256	-0.187	-0.460	-0.667	-0.666	0.464	0.470	-0.319	-0.241	0.798	0.659	-0.139	0.670
	<i>Aspergillus</i>	0.203	0.095	-0.538	0.268	0.273	0.058	-0.999	-0.999	0.190	0.135	0.212	0.289	0.406	0.287	-0.381	0.571
	<i>Byssochlamys</i>	-0.389	-0.246	0.419	-0.412	-0.440	-0.198	1.000	1.000	-0.279	-0.187	-0.353	-0.428	-0.332	-0.186	0.448	-0.454
	<i>Bacillus</i>	-0.796	-0.475	-0.487	-0.376	-0.441	-0.475	-0.104	-0.101	-0.002	0.236	-0.425	-0.357	0.575	0.596	-0.059	0.288
	<i>Aeribacillus</i>	-0.454	-0.144	-0.310	-0.221	-0.309	-0.276	0.865	0.866	-0.230	-0.165	-0.280	-0.231	-0.009	0.271	-0.083	0.594
	<i>Caldibacillus</i>	-0.425	-0.440	-0.400	-0.256	-0.282	-0.334	-0.084	-0.082	0.128	0.433	-0.302	-0.241	0.735	0.338	-0.338	0.055
	<i>Thermobacillus</i>	0.230	0.003	-0.016	-0.001	0.157	-0.086	-0.308	-0.305	0.828	0.859	-0.093	-0.042	0.402	0.091	-0.462	-0.179
	<i>Streptomyces</i>	-0.500	-0.243	0.112	-0.164	-0.279	-0.078	0.992	0.991	-0.362	0.062	-0.171	-0.161	0.210	-0.179	-0.375	-0.283
	<i>Thermobifida</i>	0.375	0.712	0.880	0.646	0.668	0.741	0.399	0.397	0.104	0.257	0.618	0.603	-0.466	-0.875	-0.737	-0.818
proteolytics	M	1															
	T	0.397	1														
amylolytics	M	0.112	0.746	1													
	T	0.421	0.967	0.635	1												
cellulolytics	M	0.559	0.930	0.580	0.974	1											
	T	0.384	0.978	0.785	0.971	0.923	1										
ligninolytics	M	-0.991	-0.399	0.447	-0.564	-0.729	-0.325	1									
	T	-0.991	-0.401	0.445	-0.566	-0.731	-0.327	1.000	1								
P-solubilizing	M	0.407	-0.172	-0.270	-0.093	0.122	-0.221	-0.535	-0.533	1							
	T	0.115	-0.208	-0.109	-0.121	0.044	-0.206	-0.283	-0.281	0.884	1						
N2-fixing	M	0.433	0.964	0.644	0.994	0.962	0.976	-0.524	-0.525	-0.149	-0.196	1					
	T	0.410	0.956	0.605	0.998	0.968	0.963	-0.577	-0.579	-0.110	-0.146	0.996	1				
nitrifiers I	M	-0.111	-0.702	-0.741	-0.532	-0.418	-0.671	-0.314	-0.312	0.638	0.684	-0.575	-0.519	1			
	T	-0.319	-0.780	-0.914	-0.697	-0.632	-0.837	-0.361	-0.359	0.351	0.215	-0.707	-0.669	0.738	1		
nitrifiers II	M	-0.119	-0.551	-0.501	-0.599	-0.583	-0.586	0.408	0.410	-0.126	-0.405	-0.525	-0.569	0.060	0.594	1	
	T	-0.066	-0.476	-0.836	-0.455	-0.472	-0.568	-0.665	-0.663	-0.103	-0.328	-0.454	-0.430	0.282	0.674	0.509	1

Physiological groups include aerobic mesophilic (M) and thermophilic (T) microorganisms during composting.

Table S2. Pearson correlation (r) between community richness and diversity and physicochemical properties.

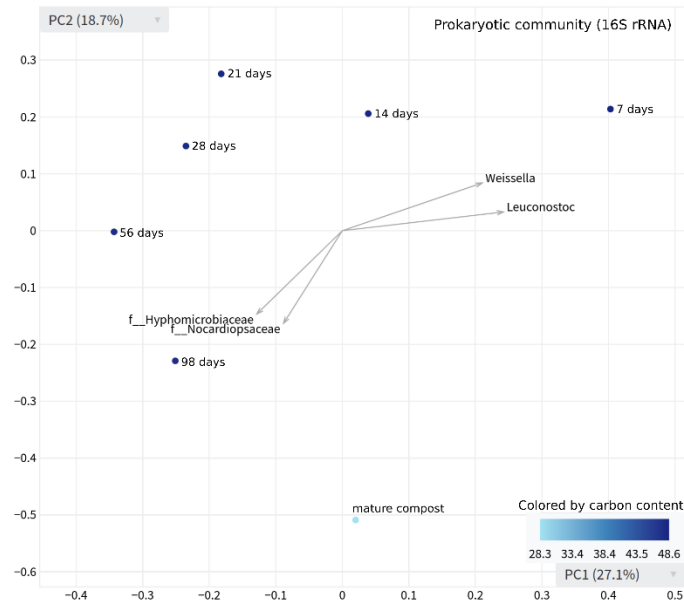
Index	T, °C	w, %	GI, %	NI	C	C/N	pH	EC, μS cm ⁻¹	CO ₂ , vol %	NH ₃ , mg m ⁻³	N-NH ₄ , mg kg ⁻¹	N-NO ₃ , mg kg ⁻¹
Fungi												
Chao1 index	-0.651	-0.758	0.945	-0.369	-0.953	-0.878	0.432	-0.794	-0.311	-0.520	-0.207	-0.030
Shannon index*	-0.313	-0.602	0.703	-0.585	-0.779	-0.640	0.281	-0.782	-0.026	-0.451	0.060	0.126
Simpson index	-0.317	0.158	-0.309	0.625	0.400	0.247	-0.120	0.512	-0.394	0.185	-0.360	-0.359
Bacteria												
Chao1 index	-0.534	-0.923	0.805	-0.278	-0.830	-0.879	0.615	-0.420	-0.267	-0.455	-0.190	0.035
Shannon index*	-0.286	-0.835	0.795	-0.564	-0.646	-0.711	0.663	-0.282	-0.070	-0.066	-0.344	0.120
Simpson index	-0.286	0.645	-0.577	0.863	0.450	0.444	-0.321	-0.006	-0.254	-0.330	0.388	-0.300

Table S3. Pearson correlation (r) between dominant microbial genera and physicochemical properties.

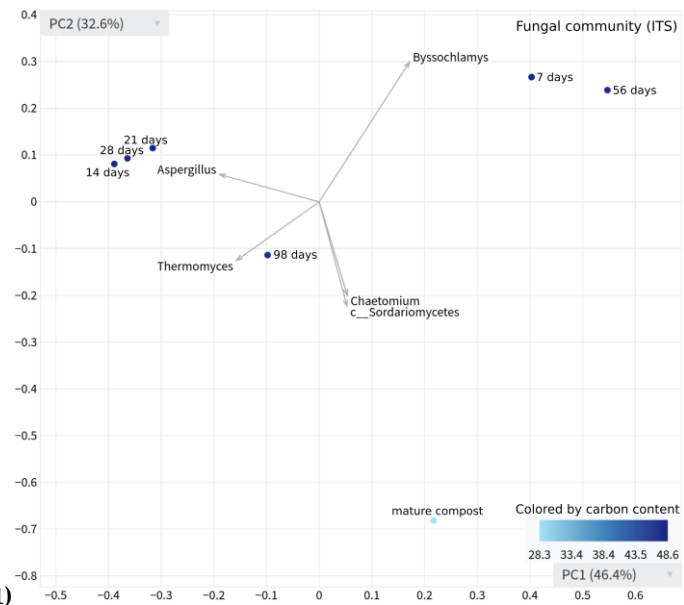
Genus	T, °C	w, %	GI, %	C	C/N	pH	EC, μS cm ⁻¹	CO ₂ , vol %	NH ₃ , mg m ⁻³	N-NH ₄ , mg kg ⁻¹	N-NO ₃ , mg kg ⁻¹
Fungi											
<i>Thermomyces</i>	-0.225	0.333	0.164	0.066	0.239	0.341	-0.388	-0.258	0.236	-0.367	-0.240
<i>Penicillium</i>	0.909	0.167	-0.619	0.464	0.459	-0.191	0.487	0.961	0.277	0.831	0.582
<i>Microascus</i>	-0.615	-0.088	0.629	-0.425	-0.256	0.482	-0.735	-0.515	-0.146	-0.499	-0.261
<i>Aspergillus</i>	0.787	0.395	-0.529	0.513	0.584	-0.088	0.311	0.806	0.446	0.574	0.454
<i>Byssochlamys</i>	-0.213	0.246	-0.240	0.296	0.164	-0.202	0.369	-0.467	0.028	-0.366	-0.338
Bacteria											
<i>Bacillus</i>	0.904	-0.010	-0.273	0.321	0.211	-0.447	0.491	0.870	0.398	0.328	0.703
<i>Aeribacillus</i>	0.568	0.180	-0.237	0.238	0.148	-0.508	0.475	0.517	0.806	-0.077	-0.099
<i>Caldibacillus</i>	0.669	-0.191	-0.213	0.264	0.152	0.143	0.496	0.862	0.032	0.634	0.910
<i>Thermobacillus</i>	0.417	-0.161	-0.270	0.258	0.172	0.138	0.400	0.400	0.304	0.221	0.024
<i>Streptomyces</i>	0.203	-0.216	0.049	0.134	-0.032	0.355	0.459	0.391	0.028	0.191	0.624
<i>Thermobifida</i>	-0.197	0.048	0.045	0.244	0.189	0.589	0.221	-0.254	0.303	-0.379	-0.262

Table S4. Pearson correlation (r) between dominant microbial genera represented during composting.

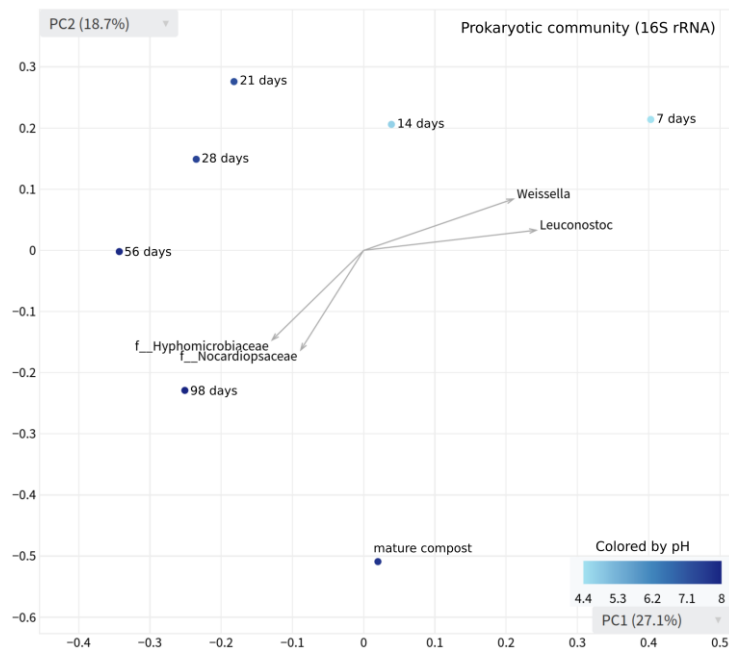
Genus	<i>Thermomyces</i>	<i>Penicillium</i>	<i>Microascus</i>	<i>Aspergillus</i>	<i>Byssoschlamys</i>	<i>Bacillus</i>	<i>Aeribacillus</i>	<i>Caldibacillus</i>	<i>Thermobacillus</i>	<i>Streptomyces</i>	<i>Thermobifida</i>
<i>Thermomyces</i>	1										
<i>Penicillium</i>	-0.137	1									
<i>Microascus</i>	0.862	-0.455	1								
<i>Aspergillus</i>	0.335	0.871	-0.045	1							
<i>Byssoschlamys</i>	-0.424	-0.519	-0.417	-0.654	1						
<i>Bacillus</i>	-0.483	0.784	-0.712	0.590	-0.129	1					
<i>Aeribacillus</i>	-0.158	0.489	-0.392	0.461	-0.196	0.545	1				
<i>Caldibacillus</i>	-0.321	0.711	-0.467	0.556	-0.143	0.779	0.155	1			
<i>Thermobacillus</i>	-0.060	0.505	-0.289	0.319	-0.143	0.153	0.216	0.167	1		
<i>Streptomyces</i>	-0.269	0.105	-0.277	0.058	0.216	0.457	-0.016	0.752	-0.197	1	
<i>Thermobifida</i>	0.546	-0.275	0.385	-0.057	0.222	-0.379	-0.221	-0.153	0.419	0.114	1



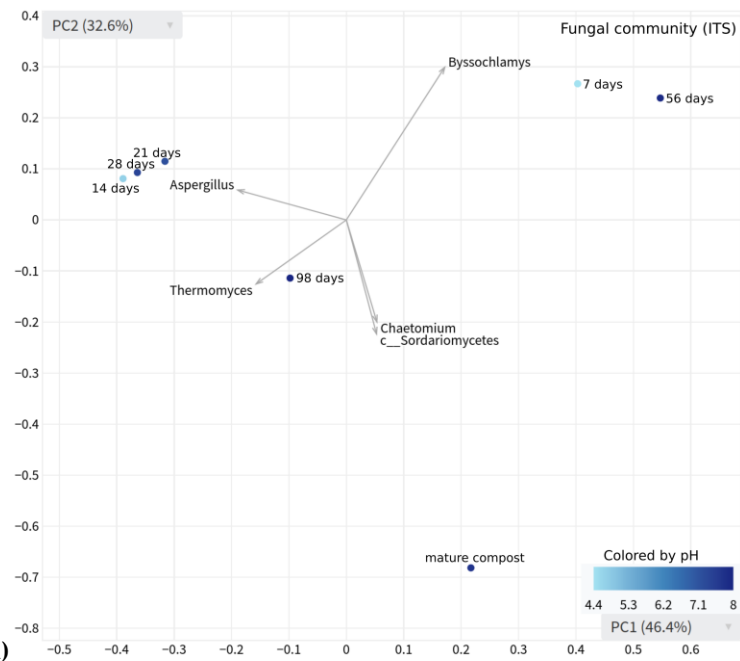
(a1)



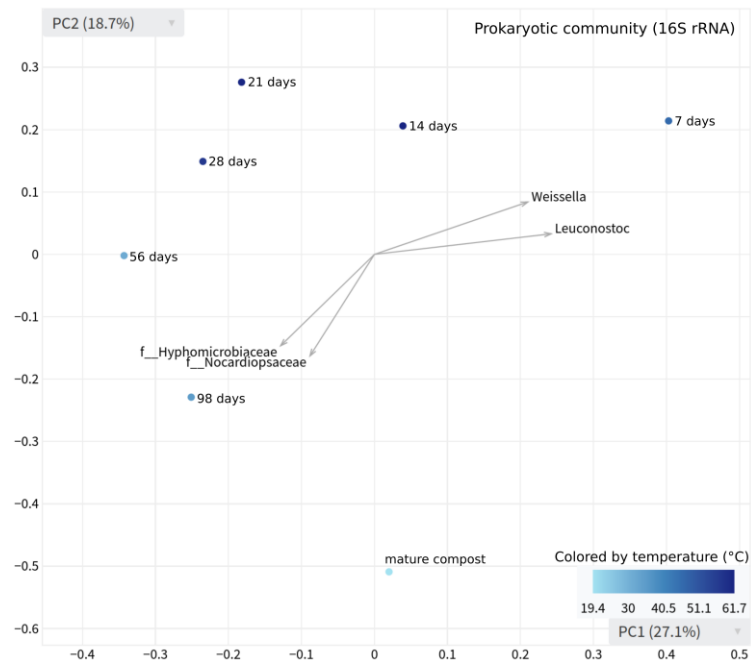
(a2)



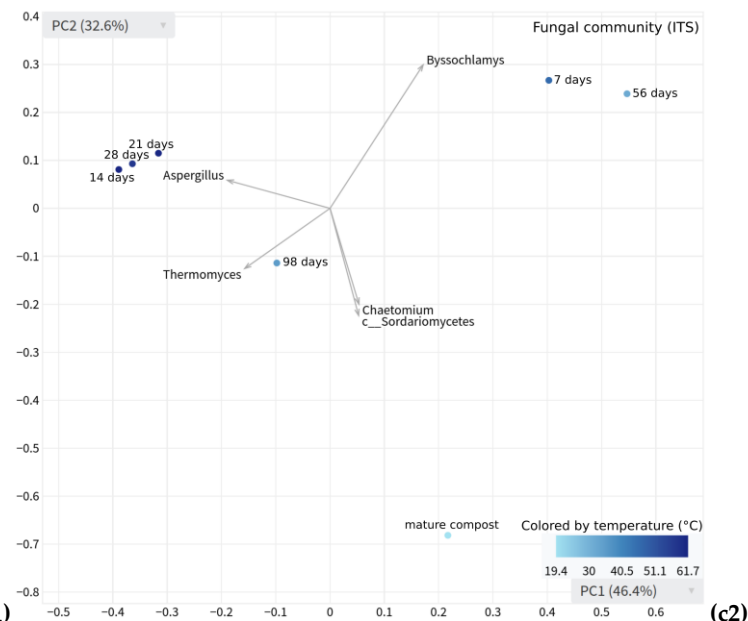
(b1)



(b2)



(c1)



(c2)

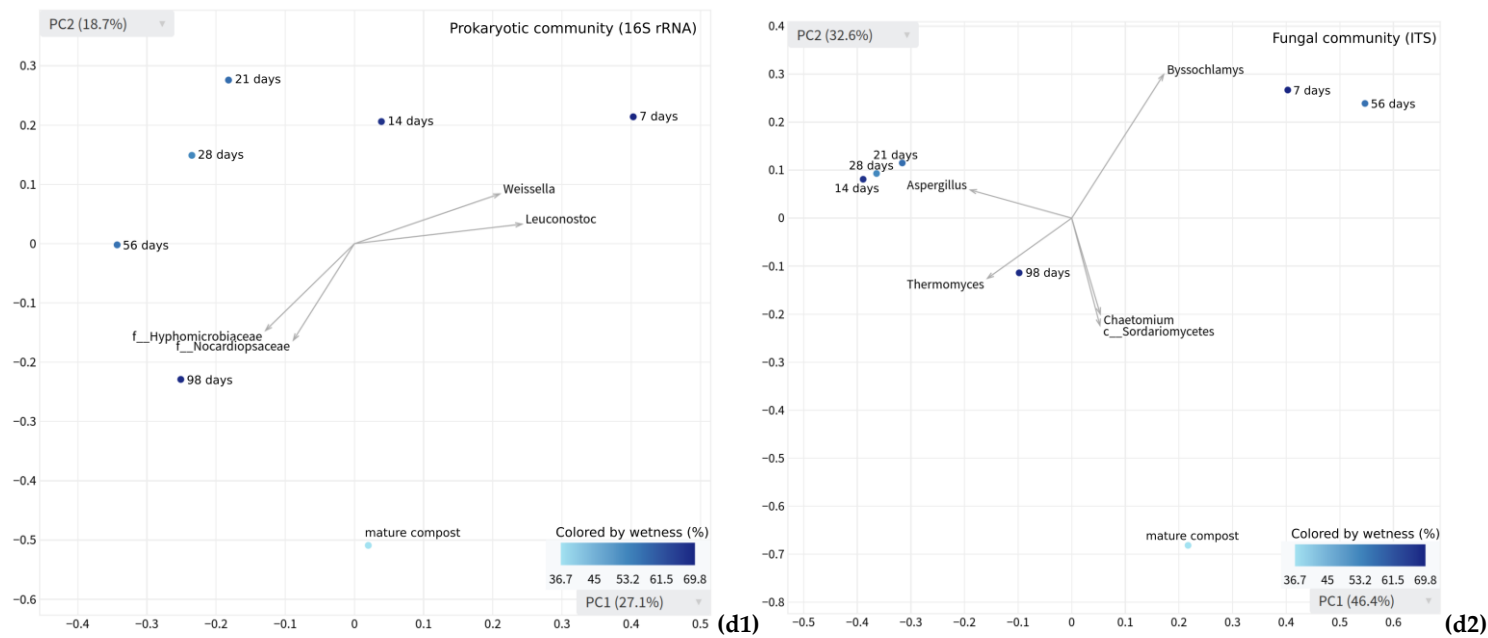


Figure S1. Distribution of the samples by their taxonomic composition in reduced dimensionality with the influence of ambient parameters. (PCoA): relation between carbon content, % (a); pH (b); temperature, °C (c); wetness, w% (d) and the prokaryotic (1) and fungal (2) communities throughout composting. Color of each point refers to a certain value of the parameter. The closer the samples (points) on the plot, the more similar their composition; vectors show the directions in which the levels of the respective major taxa increased.