

Metagenomics analysis reveals that carbon degradation rather than carbon fixation is dominant during animal carcass decay

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Running title: corpse decay and carbon cycling genes

Fig. S1 - S13

Table S1 - S19

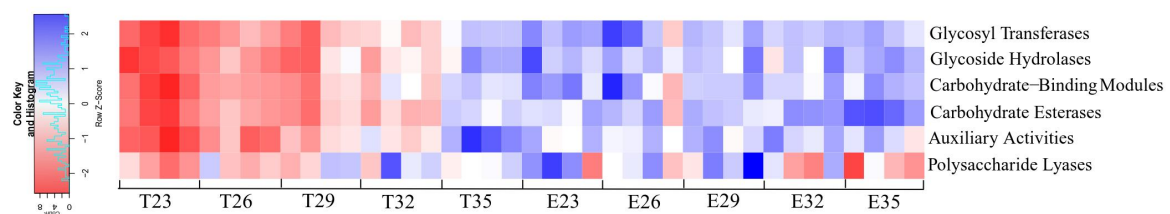


Fig. S1 The heatmap for Level 1 CAZy genes in all samples. Abbreviations: T, control groups; E, experimental groups.

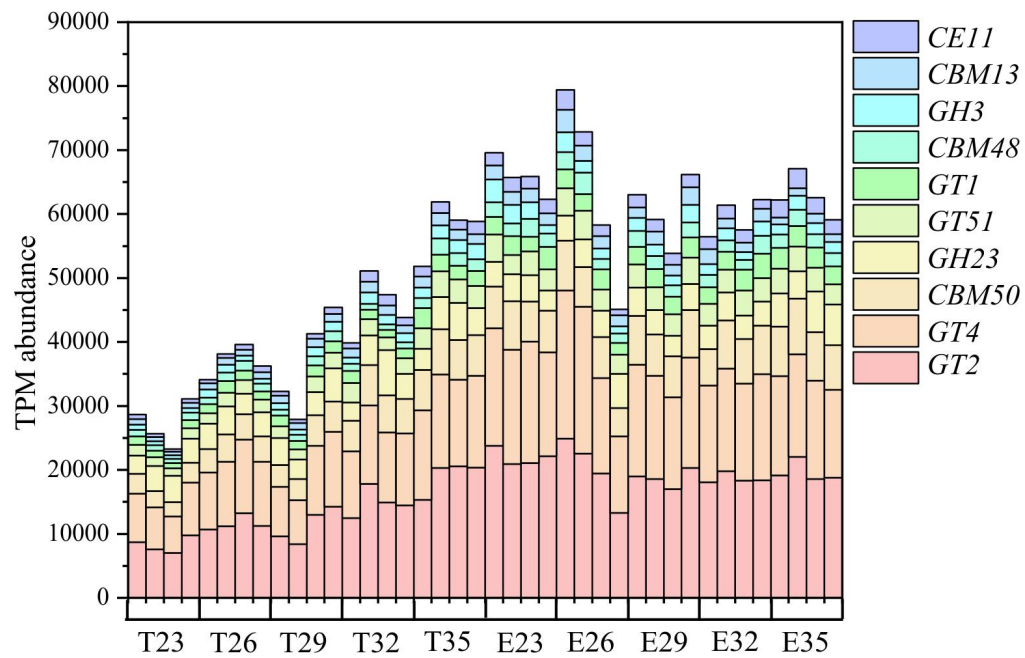


Fig. S2 The transcripts per million (TPM) abundance of Level 2 CAZy genes. Only the top 10 genes with highest relative abundance were shown. Abbreviations: T, control groups; E, experimental groups.

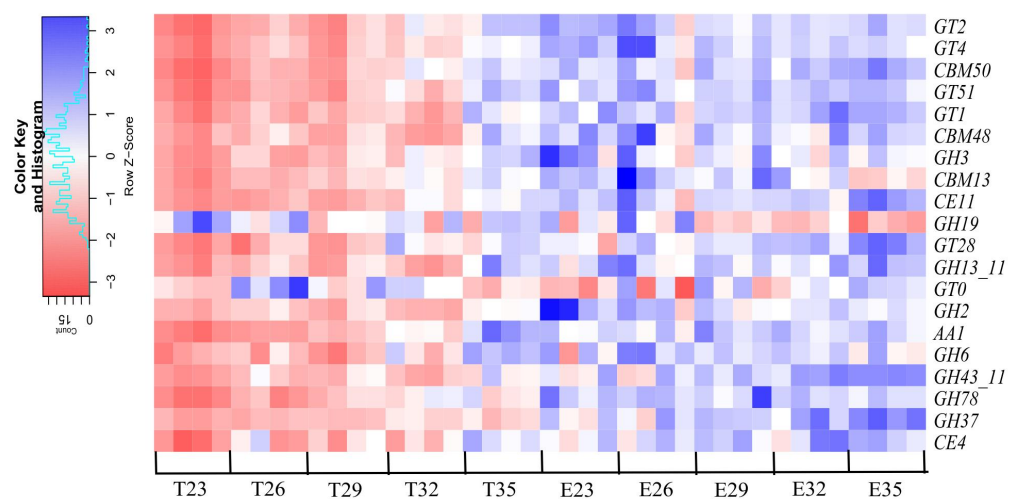


Fig. S3 Heatmap showing the relative abundance of the different CAZy genes between the control and experimental groups in all samples (ANOVA, $P < 0.05$). Abbreviations: T, control groups; E, experimental groups.

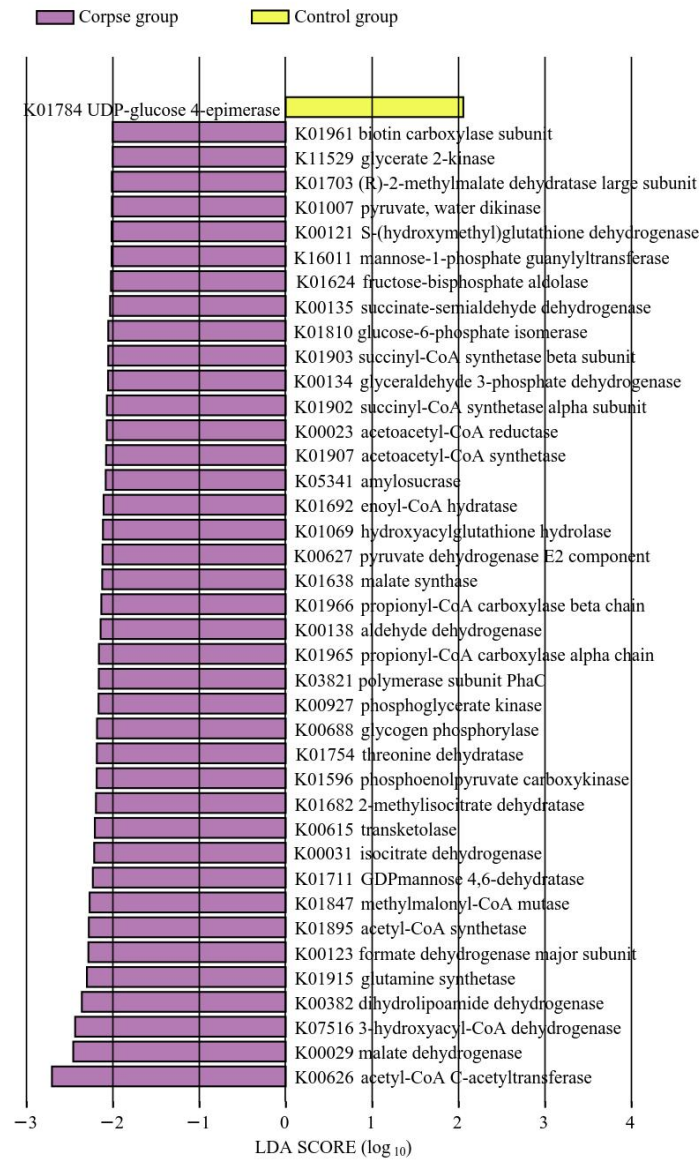


Fig. S4 Lefse analysis showing the carbon cycling KO enriched in control and experimental groups (One-way ANOVA, $P < 0.05$). All carbon cycling KO entry were included.

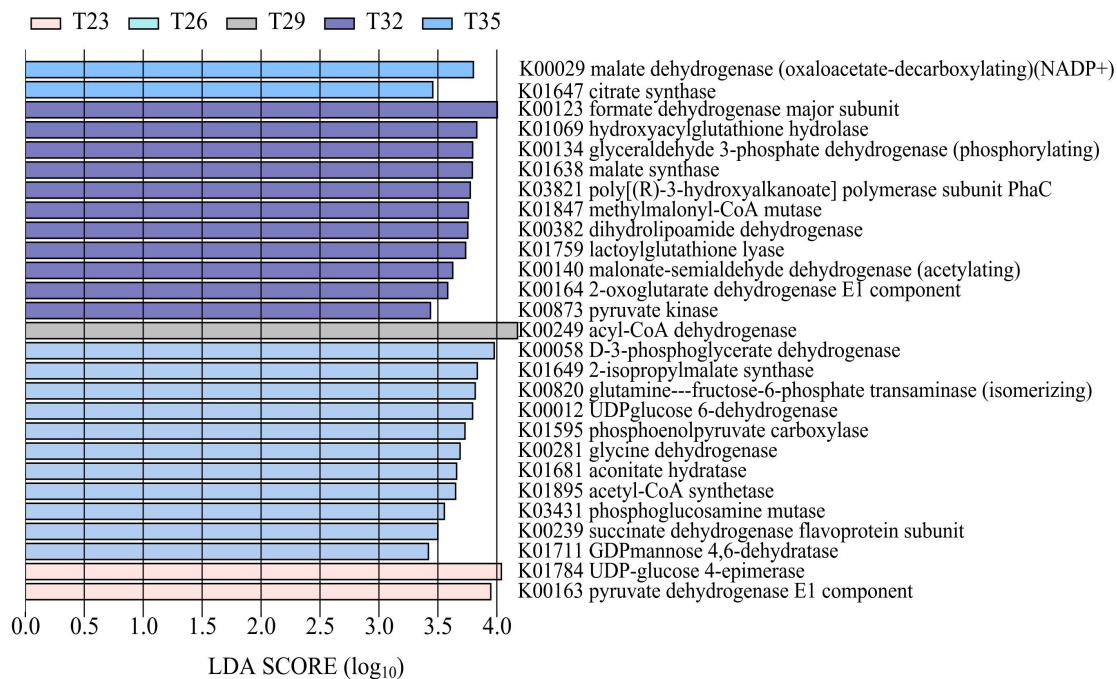


Fig. S5 Lefse analysis showing the carbon cycling KO enriched in control groups at different temperature (One-way ANOVA, $P < 0.05$). Only the carbon cycling KO entry with relative abundance > 0.015 were selected. Abbreviations: T, control groups.

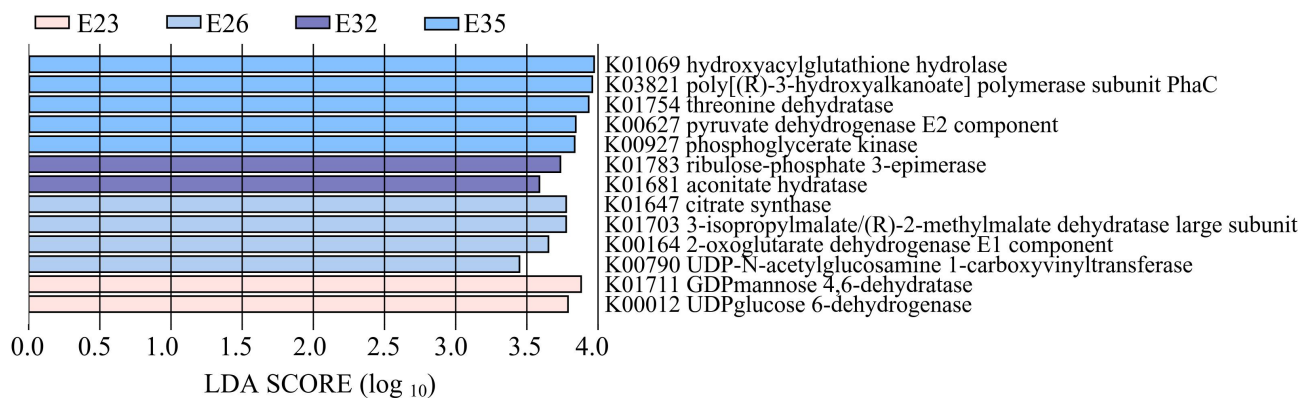


Fig. S6 Lefse analysis showing the carbon cycling KO enriched in experimental groups at different temperature (One-way ANOVA, $P < 0.05$). Only the carbon cycling KO entry with relative abundance > 0.015 were selected. Abbreviations: E, experimental groups.

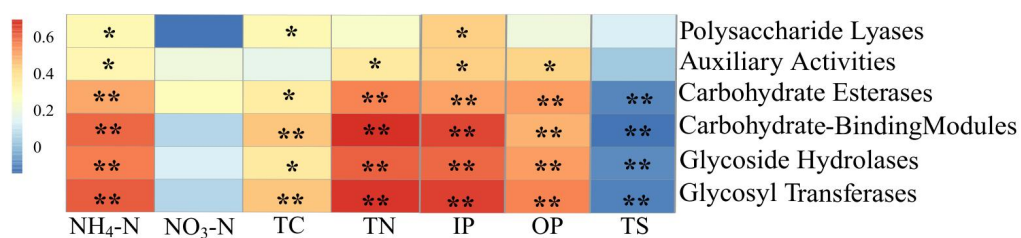


Fig. S7 The heatmap showing the relationship between the relative abundance for Level 1 CAZy genes and physicochemical properties in all samples (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$). Abbreviations: TC, total carbon; TN, total nitrogen; IP, inorganic phosphorus; OP, organic phosphorus; TS, total sulphur.

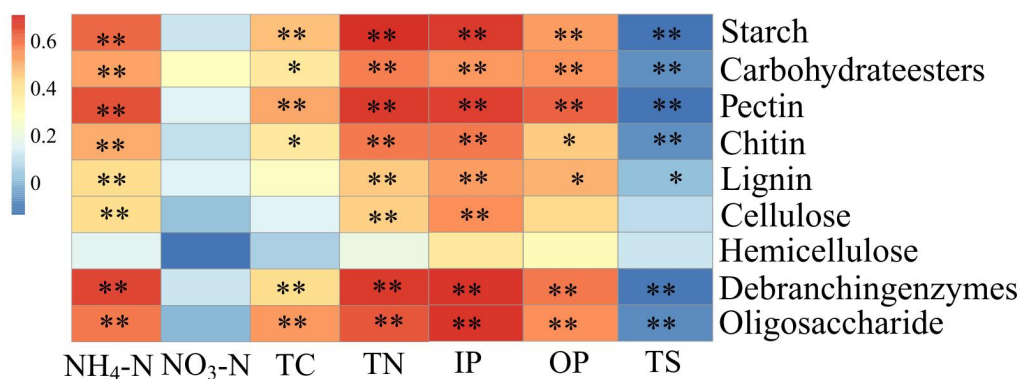


Fig. S8 The heatmap showing the relationship between the relative abundance for Level 2 CAZy genes and physicochemical properties in all samples (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$). Abbreviations: TC, total carbon; TN, total nitrogen; IP, inorganic phosphorus; OP, organic phosphorus; TS, total sulphur.

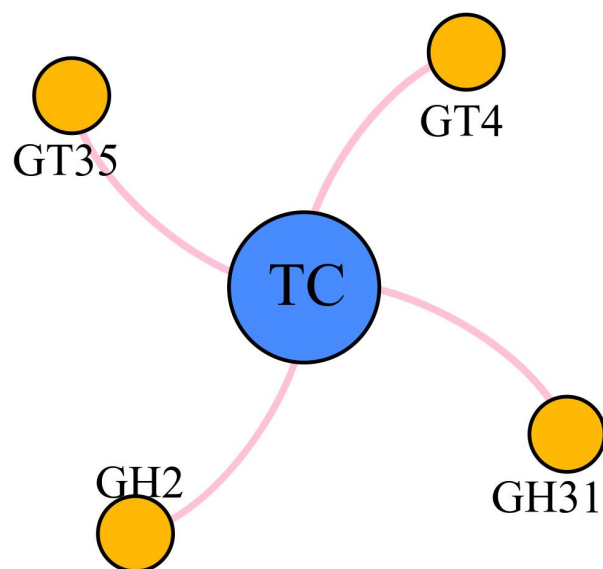


Fig. S9 Network analysis showing the CAZy genes positively related with the concentration of TC ($P < 0.05$, $|r| = 0.5$). The CAZy genes with the top 200 relative abundance were selected. Abbreviations: TC, total carbon.

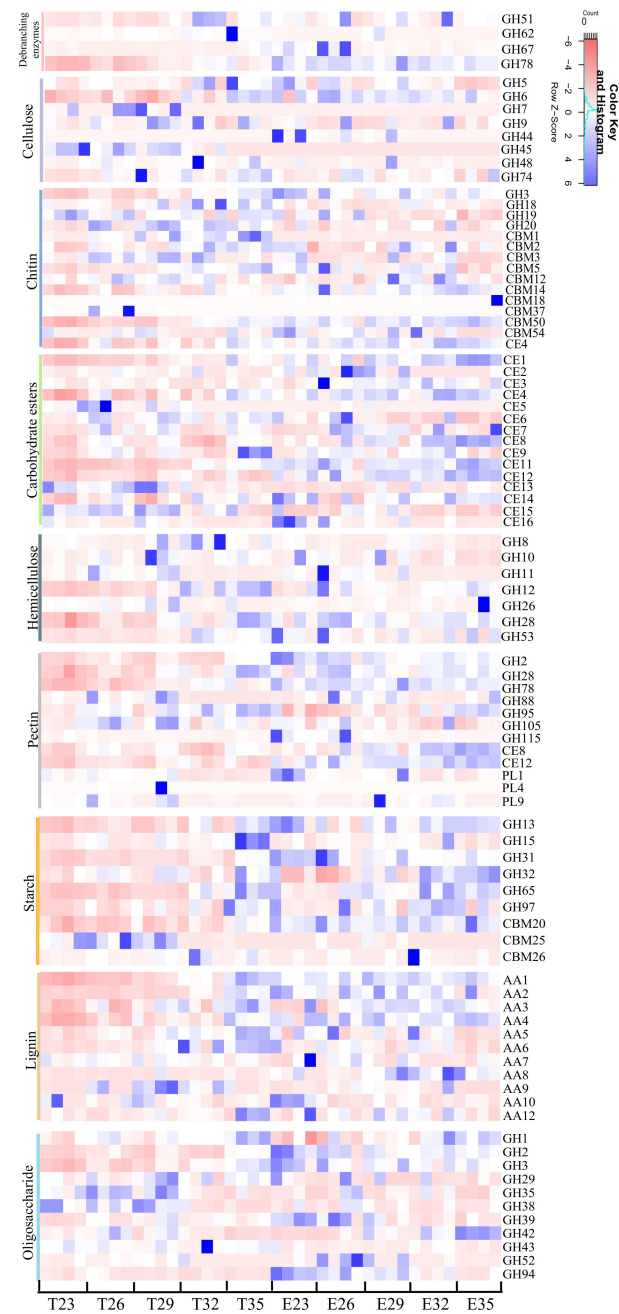


Fig. S10 Heatmap showing the relative abundance of the CAZy genes (including debranching enzymes, cellulose, chitin, carbohydrate esters, hemicellulose, pectin, starch, lignin, oligosaccharide) in all samples. Abbreviations: T, control groups; E, experimental groups.

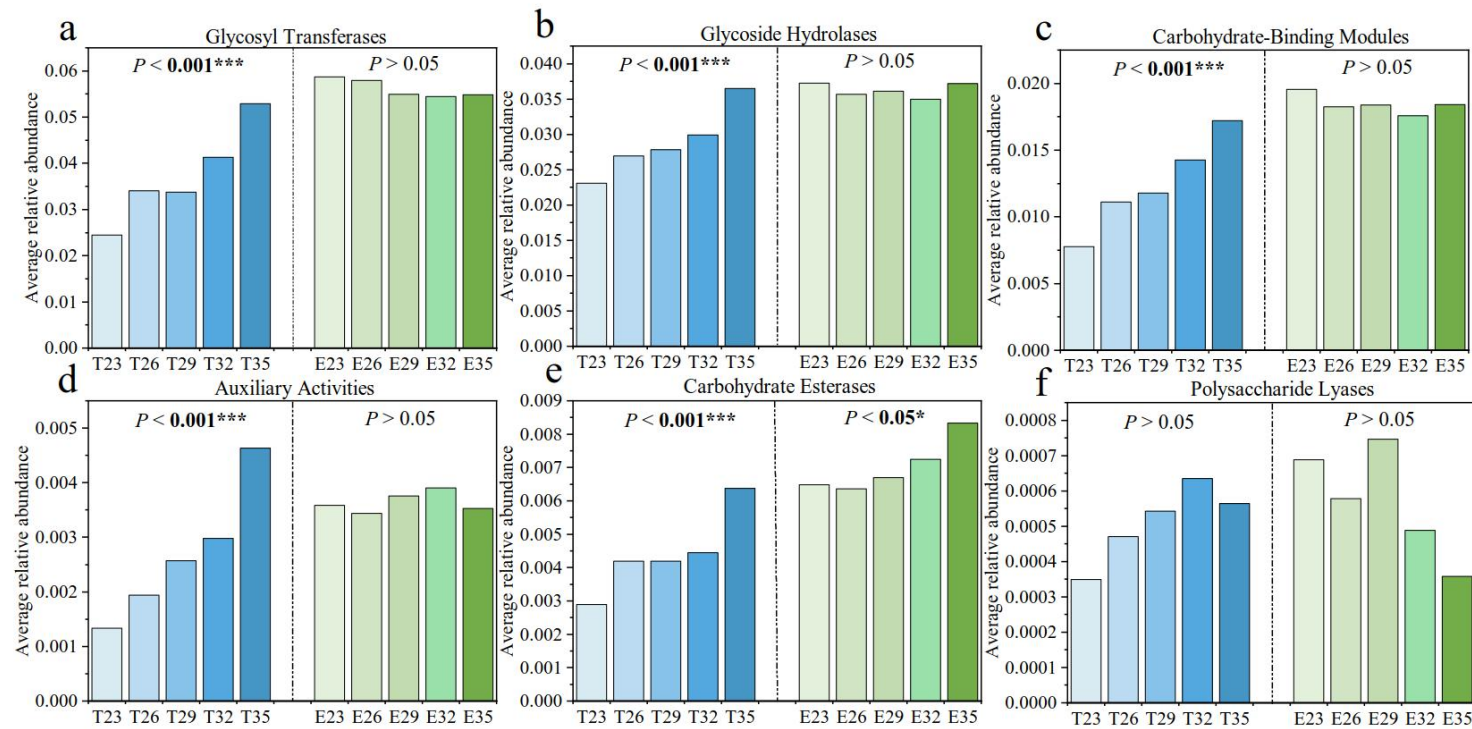


Fig. S11 Bar chart showed the relative abundance of CAZy level 1 (a, glycosyl transferase, GT; b, glycoside hydrolase, GH; c, carbohydrate-binding modules, CBM; d, auxiliary activity redox enzymes, AA; e, carbohydrate esterase, CE; f, polysaccharide lyase, PL) under different temperature. The blue color represented the control groups, and green represented experimental groups. The color from light to dark reflected the temperature rise. Abbreviations: E, experimental groups; T, control groups.

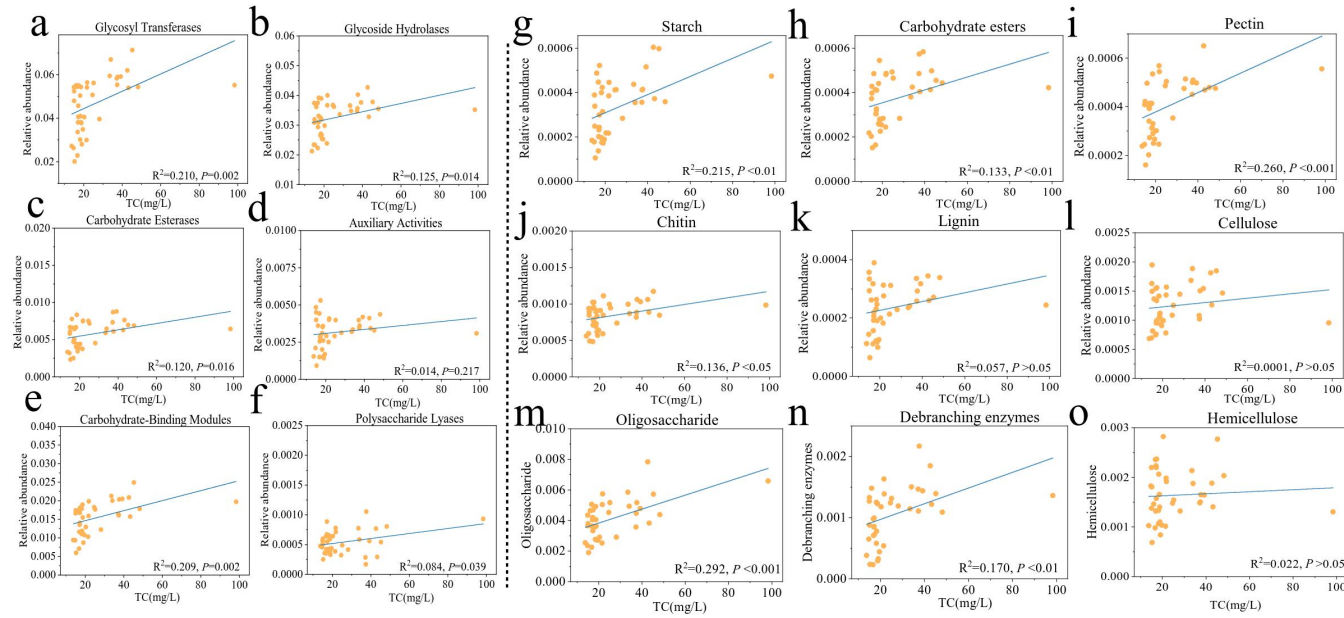


Fig. S12 The linear fitting graphs revealed the interrelationship between relative abundance of nine kinds of carbohydrate decomposition genes (a, starch; b, carbohydrate esters; c, pectin; d, lignin; e, chitin; f, cellulose; g, oligosaccharide; h, debranching enzymes; i, hemicellulose) and the concentration of TC. Abbreviations: TC, total carbon.

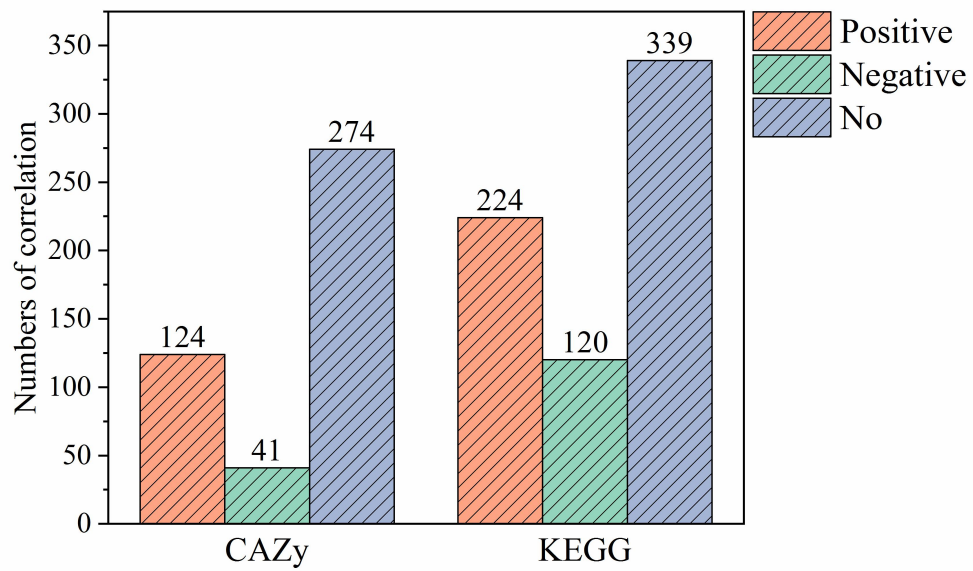


Fig. S13 The bar chart showed the numbers of carbon-cycling genes with positive, negative, and no correlation with temperature.

Table S1. The average value and standard deviation of physicochemical properties. The different lowercase letter after the number represents significant differences (One-way ANOVA, $P < 0.05$). Abbreviations: CON, conductivity; TDS, total dissolved solids; SALT, salinity; ORP, oxidation-reduction potential; DO, dissolved oxygen; TN, total nitrogen; TC, total carbon; AVE, average value; STD, standard deviation.

Group	CON		TDS		SALT		pH		ORP		DO		NH ₄ -N ug/ml		NO ₃ -N ug/ml		TN mg/L		TC mg/L	
	AVE	STD	AVE	STD	AVE	STD	AVE	STD	AVE	STD	AVE	STD	AVE	STD	AVE	STD	AVE	STD	AVE	STD
T23	777.750 ^a	65.061	388.750 ^a	32.066	0.395 ^a	0.030	7.842 ^a	0.259	-23.775 ^a	16.726	0.653 ^a	0.644	14.090 ^a	0.277	0.526 ^a	0.184	31.440 ^a	2.809	52.975 ^a	30.491
T26	775.250 ^a	83.108	387.500 ^a	41.685	0.395 ^a	0.041	7.897 ^a	0.177	-37.575 ^a	10.383	0.603 ^a	0.775	12.115 ^a	1.645	3.220 ^a	3.131	25.578 ^a	11.845	32.358 ^a	10.021
T29	707.250 ^a	70.486	354.250 ^a	35.046	0.3625 ^a	0.035	7.700 ^a	0.176	-38.125 ^a	15.764	0.688 ^a	0.814	10.550 ^a	3.623	6.848 ^b	4.152	20.580 ^a	2.827	32.353 ^a	13.305
T32	642.500 ^a	51.656	321.500 ^a	25.955	0.325 ^b	0.026	7.623 ^a	0.133	-34.125 ^a	16.520	1.140 ^a	0.944	2.570 ^b	2.552	10.230 ^b	3.072	16.115 ^b	7.468	24.080 ^b	13.166
T35	646.750 ^a	31.753	333.750 ^a	31.826	0.330 ^a	0.014	7.882 ^a	0.145	-39.225 ^a	11.426	0.975 ^a	0.682	8.680 ^a	6.549	5.689 ^a	5.050	19.070 ^b	7.435	29.998 ^a	9.966
E23	861.500 ^a	47.431	431.250 ^a	23.056	0.440 ^a	0.022	8.095 ^a	0.109	-64.900 ^b	5.785	5.858 ^b	0.392	0.295 ^b	0.075	3.634 ^a	0.288	2.923 ^b	0.289	16.265 ^b	2.260
E26	821.000 ^a	45.188	410.500 ^a	22.884	0.420 ^a	0.022	8.368 ^b	0.108	-78.550 ^c	4.368	4.298 ^b	0.111	0.293 ^b	0.054	3.284 ^a	0.266	3.115 ^b	0.328	18.438 ^b	1.124
E29	870.500 ^a	59.613	435.500 ^a	30.094	0.445 ^a	0.029	8.115 ^a	0.302	-75.025 ^c	1.982	4.028 ^b	0.163	0.263 ^b	0.033	2.804 ^a	0.717	2.725 ^b	0.691	17.698 ^b	2.805
E32	865.000 ^a	48.436	432.750 ^a	23.936	0.4425 ^a	0.026	8.308 ^b	0.049	-79.650 ^c	1.799	3.103 ^b	0.156	0.225 ^b	0.013	3.671 ^a	0.725	3.303 ^b	0.310	18.730 ^b	1.293
E35	850.750 ^a	61.451	425.750 ^a	29.477	0.440 ^a	0.029	8.320 ^b	0.057	-80.050 ^c	1.863	3.093 ^b	0.322	0.245 ^b	0.019	3.952 ^a	0.326	3.278 ^b	0.189	16.103 ^b	1.203

Table S2. Two-way Analysis of Variance (ANOVA) for the effects of temperature and corpse decay on the relative abundance of the phyla of carbon cycle microbiome. The bold type indicates a significant difference (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

Factors	Temperature		Corpse		Temperature*Corpse	
	F	<i>P</i>	F	<i>P</i>	F	<i>P</i>
Spirochaetes	5.709	0.002**	17.363	<0.001***	3.891	0.012*
Cyanobacteria	4.494	0.006**	6.761	0.014*	6.626	0.001***
Firmicutes	0.384	0.818	54.615	<0.001***	0.517	0.724
Acidobacteria	0.636	0.641	33.144	<0.001***	1.843	0.147
Planctomycetes	1.415	0.253	3.779	0.061	1.043	0.402
Chloroflexi	2.127	0.102	15.137	0.001***	1.145	0.354
Verrucomicrobia	1.534	0.217	14.419	0.001***	1.581	0.205
Bacteroidetes	2.769	0.045*	0.140	0.711	0.565	0.690
Actinobacteria	4.737	0.004**	48.039	<0.001***	7.845	<0.001***
Proteobacteria	0.768	0.554	71.305	<0.001***	17.355	<0.001***

Table S3. Two-way Analysis of Variance (ANOVA) for the effects of temperature and corpse decay on the relative abundance of the genera of carbon cycle microbiome. The bold type indicates a significant difference (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

Factors	Temperature		Corpse		Temperature*Corpse	
	F	<i>P</i>	F	<i>P</i>	F	<i>P</i>
<i>Limnohabitans</i>	1.485	0.232	0.422	0.521	0.648	0.633
Unclassified Bacteria	1.529	0.219	78.280	<0.001***	6.822	<0.001***
Actinobacteria(UG)	19.032	<0.001***	118.113	<0.001***	15.162	<0.001***
<i>Polynucleobacter</i>	3.700	0.015*	16.086	<0.001***	4.051	0.01**
<i>Novosphingobium</i>	1.143	0.355	8.532	0.007**	0.831	0.516
Betaproteobacteria(UG)	3.009	0.034*	29.336	<0.001***	2.628	0.054
<i>Acidovorax</i>	1.069	0.389	10.251	0.003**	0.928	0.461
Alphaproteobacteria(UG)	2.570	0.058	0.033	0.857	8.308	<0.001***
<i>Pseudomonas</i>	1.064	0.391	3.066	0.090	0.964	0.442
Acidimicrobiaceae(UG)	17.749	<0.001***	44.984	<0.001***	12.788	<0.001***
Bacteroidetes(UG)	1.725	0.171	17.500	<0.001***	1.846	0.146
<i>Polaromonas</i>	0.244	0.911	0.003	0.956	1.164	0.346
<i>Mycobacterium</i>	1.743	0.167	0.755	0.392	1.288	0.297
<i>Sphingomonas</i>	0.743	0.570	3.846	0.059	1.675	0.182
<i>Nocardioides</i>	0.838	0.512	5.915	0.021*	0.758	0.561
<i>Sphingobium</i>	4.791	0.004**	2.525	0.123	4.934	0.004**
Acidobacteria(UG)	0.510	0.729	48.446	<0.001***	0.694	0.602
<i>Streptomyces</i>	1.158	0.349	47.702	<0.001***	1.451	0.242
<i>Achromobacter</i>	0.820	0.523	0.191	0.665	0.792	0.540
Others	4.688	0.005**	27.077	<0.001***	0.680	0.611

Table S4. Permutational multivariate analysis of variance (PERMANOVA) showing the effects of temperature and corpse decay on the CAZy genes profile based on Bray-Curtis and Jaccard distance matrix. The bold type indicates a significant difference (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$). Abbreviations: T, control groups; E, experimental groups.

PERMANOVA	Bray-Curtis			Jaccard		
	F	R^2	P	F	R^2	P
T23 vs. T26	2.205	0.269	0.183	8.136	0.576	0.041*
T26 vs. T29	7.498	0.556	0.033*	11.969	0.666	0.024*
T29 vs. T32	9.812	0.621	0.027*	5.316	0.470	0.029*
T32 vs. T35	4.428	0.425	0.029*	3.177	0.346	0.029*
E23 vs. E26	0.359	0.057	0.720	1.280	0.176	0.264
E26 vs. E29	2.923	0.328	0.184	1.997	0.250	0.130
E29 vs. E32	0.540	0.083	0.733	2.638	0.305	0.028*
E32 vs. E35	9.426	0.611	0.042*	3.652	0.378	0.052
T23 vs. E23	11.169	0.651	0.042*	53.825	0.900	0.029*
T26 vs. E26	4.260	0.415	0.039*	51.651	0.896	0.032*
T29 vs. E29	15.353	0.719	0.038*	36.116	0.858	0.037*
T32 vs. E32	7.851	0.567	0.027*	27.340	0.820	0.037*
T35 vs. E35	25.896	0.812	0.030*	18.392	0.754	0.027*

Table S5. Two-way Analysis of Variance (ANOVA) for the effects of temperature and corpse decay on the relative abundance of the genera of Level 1 CAZy genes. The bold type indicates a significant difference (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

Factors	Temperature		Corpse		Temperature*Corpse	
	F	<i>P</i>	F	<i>P</i>	F	<i>P</i>
Glycosyl Transferases	4.747	0.004**	107.928	<0.001***	8.424	<0.001***
Glycoside Hydrolases	5.301	0.002**	61.371	<0.001***	5.084	0.003**
Carbohydrate-Binding Modules	3.189	0.027*	61.182	<0.001***	6.034	0.001***
Carbohydrate Esterases	11.587	<0.001***	114.625	<0.001***	1.808	0.153
Auxiliary Activities	15.911	<0.001***	40.970	<0.001***	12.312	<0.001***
Polysaccharide Lyases	0.954	0.447	1.722	0.199	2.653	0.052

Table S6. The detailed information of specific genes involved in the degradation of starch, carbohydrate esters, chitin, pectin, lignin, cellulose, hemicellulose, debranching enzymes and oligosaccharide.

Soil component	organic	C	Involved enzymes based on CAZy	Reference
Starch			GH13, GH15, GH31, GH32, GH65, GH97, CBM20, CBM25, CBM26	Lopezmondejar et al. 2016; Abdallah et al. 2019; Pold et al. 2016; Noronha et al. 2017
Carbohydrate esters			CE1, CE2, CE3, CE4, CE5, CE6, CE7, CE8, CE9, CE10, CE11, CE12, CE13, CE14, CE15, CE16, CE17, CE18	Yin et al., 2012; Han et al., 2018
Pectin			GH2, GH28, GH78, GH88, GH95, GH105, GH115, CE8, CE12, PL1, PL3, PL4, PL9	Lopezmondejar et al. 2016; Kameshwar and Qin 2018; Prasanth et al. 2022
Chitin			GH3, GH18, GH19, GH20, CBM1, CBM2, CBM3, CBM5, CBM12, CBM14, CBM18, CBM37, CBM50, CBM54, CE4	Lopezmondejar et al. 2016; Abdallah et al. 2019; Pent et al. 2018
Lignin			AA1, AA2, AA3, AA4, AA5, AA6, AA7, AA8, AA9, AA10, AA11, AA12, AA13	Abdallah et al. 2019; Kameshwar and Qin 2018
Cellulose			GH5,GH6,GH7,GH9,GH44,GH45,GH48,GH74	Prasanth et al. 2022; Hakkinen et al. 2018
Hemicellulose			GH8,GH10,GH11,GH12,GH26,GH28,GH53	Prasanth et al. 2022
Debranching enzymes			GH51,GH54,GH62,GH67,GH78	Wilkens et al. 2017; Kuchtova et al. 2016
Oligosaccharide			GH1,GH2,GH3,GH29,GH35,GH38,GH39,GH42,GH43,GH52,GH94	Kelly et al. 2021

Table S7. Permutational multivariate analysis of variance (PERMANOVA) showing the effects of temperature and corpse decay on the carbon cycling KO profile based on Bray-Curtis and Jaccard distance matrix. The bold type indicates a significant difference (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$). Abbreviations: T, control groups; E, experimental groups.

PERMANOVA	Bray-Curtis			Jaccard		
	F	R^2	P	F	R^2	P
T23 vs. T26	2.941	0.329	0.148	8.192	0.577	0.027*
T26 vs. T29	1.109	0.156	0.306	13.502	0.692	0.029*
T29 vs. T32	2.854	0.322	0.167	6.417	0.517	0.029*
T32 vs. T35	10.714	0.641	0.032*	2.750	0.314	0.070
E23 vs. E26	0.204	0.033	1.000	1.277	0.176	0.252
E26 vs. E29	2.980	0.332	0.085	1.891	0.240	0.131
E29 vs. E32	0.523	0.080	0.847	2.337	0.280	0.079
E32 vs. E35	6.866	0.534	0.031*	4.222	0.413	0.033*
T23 vs. E23	29.168	0.829	0.033*	53.287	0.899	0.025*
T26 vs. E26	15.959	0.727	0.031*	59.669	0.909	0.023*
T29 vs. E29	22.777	0.791	0.030*	35.945	0.857	0.024*
T32 vs. E32	16.981	0.739	0.031*	21.304	0.780	0.029*
T35 vs. E35	16.533	0.734	0.029*	16.698	0.736	0.015*

Table S8. The topological characteristics of the CAZy genes network of experimental and control groups. Abbreviations: CG, control groups; EG, experimental groups.

Group	Node	Edge	N/P	Average	Average	Average clustering	Modularity	Diameter	Density
	counts	counts	ratio	degree	path length	coefficient			
CG	105	2592	0.038	49.371	1.586	0.777	0.110	4	0.475
EG	105	894	0.588	17.029	2.206	0.474	0.254	5	0.164

Table S9. Permutational multivariate analysis of variance (PERMANOVA) according to Bray-Curtis distance metrics in comparison of CAZy gene and carbon cycling KO community structure in different factors. The bold type indicates a significant difference (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$). Abbreviations: TN, total nitrogen; TC, total carbon; IP, inorganic phosphorus; OP, organic phosphor; TS, total sulphur.

PERMANOVA	CAZy gene			KO		
	F	R^2	P	F	R^2	P
Temperature	8.707	0.111	0.001***	14.697	0.151	0.001***
Corpse	16.312	0.207	0.001***	4.303	0.044	0.008**
NH ₄ -N	2.429	0.031	0.016**	20.233	0.208	0.001***
NO ₃ -N	1.595	0.020	0.100	9.460	0.097	0.001***
TC	3.186	0.040	0.001***	2.882	0.030	0.021*
TN	2.216	0.028	0.025*	1.905	0.020	0.119
IP	8.488	0.184	0.001***	18.625	0.331	0.001***
OP	0.295	0.006	0.998	0.530	0.009	0.779
TS	1.435	0.031	0.147	1.186	0.021	0.293
Alpha diversity	5.040	0.064	0.001***	4.975	0.051	0.003**
Beta diversity (PCoA1)	3.825	0.049	0.003**	3.149	0.032	0.022*
Beta diversity (PCoA2)	5.451	0.069	0.001***	5.624	0.058	0.002**

Table S10. Multiple regression matrices (MRM) depicting the relative contribution of TC, TN, NO₃-N, NH₄-N, corpse, temperature, alpha diversity and beta diversity on CAZy gene profiles and KO in all 40 samples. The bold type indicates a significant difference (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$). Abbreviations: TN, total nitrogen; TC, total carbon; IP, inorganic phosphorus; OP, organic phosphorus; TS, total sulphur.

MRM	CAZy gene			KO		
	F	R^2	P	F	R^2	P
NH ₄ -N	111.394	0.125	0.001***	454.136	0.369	0.001***
NO ₃ -N	30.780	0.038	0.01**	50.177	0.061	0.002**
TC	67.402	0.080	0.003**	235.889	0.233	0.001***
TN	169.107	0.179	0.001***	510.194	0.396	0.001***
IP	142.021	0.154	0.001***	550.317	0.414	0.001***
OP	22.806	0.028	0.028*	49.142	0.059	0.005**
TS	77.824	0.091	0.001***	106.875	0.121	0.001***
Corpse	186.448	0.193	0.001***	270.570	0.258	0.001***
Temperature	53.078	0.064	0.001***	32.460	0.040	0.002**
Alpha diversity	211.260	0.214	0.001***	0.905	0.001	0.573
Beta diversity (PCoA1)	1007.175	0.564	0.001***	31.772	0.039	0.005**
Beta diversity (PCoA2)	137.268	0.150	0.001***	5.374	0.007	0.123

Table S11. Multiple regression matrices (MRM) depicting the relative contribution of corpse decay, temperature, microbe (alpha diversity and beta diversity) and environmental factors (TC, TN, NO₃-N, NH₄-N, IP, OP, TS) on CAZy gene profiles and carbon cycling KO in all 40 samples. The bold type indicates a significant difference (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

MRM	CAZy gene			KO		
	F	R^2	P	F	R^2	P
Temperature	53.078	0.064	0.001***	32.460	0.040	0.003**
Corpse	186.448	0.193	0.001***	270.570	0.258	0.001***
Microbe	219.354	0.220	0.001***	1.069	0.001	0.554
Environment factor	144.171	0.156	0.001***	517.181	0.399	0.001***

Table S12. The topological characteristics of the carbon cycling KO network of experimental and control groups. Abbreviations: CG, control groups; EG, experimental groups.

Group	Node counts	Edge counts	N/P ratio	Average degree	Average path length	Average clustering coefficient	Modularity	Diameter	Density
CG	205	5145	0.812	50.159	1.984	0.623	0.255	5	0.246
EG	205	2158	0.753	21.054	2.460	0.481	0.404	5	0.103

Table S13. The proportion of microbial domains carrying carbon cycling genes in each group. Abbreviations: T, control groups; E, experimental groups.

Proportion(%)	T23	T26	T29	T32	T35	E23	E26	E29	E32	E35
d__Archaea	0.10	0.18	0.15	0.09	0.04	0.07	0.07	0.05	0.01	0.06
d__Eukaryota	0.20	0.12	0.35	0.04	0.01	0.00	0.00	0.00	0.00	0.00
d__Viruses	0.02	0.02	0.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00
d__unclassified	0.03	0.02	0.04	0.01	0.01	0.01	0.03	0.02	0.02	0.03
d__Bacteria	99.65	99.66	99.41	99.86	99.94	99.92	99.90	99.93	99.96	99.90

Table S14. The genes related to pathway of carbon fixation.

Pathway	Gene cluster	KO	Description	Detected
CBB	<i>rbcLS</i>	K01601	rbcL; ribulose-bisphosphate carboxylase large chain [EC:4.1.1.39]	Yes
		K01602	rbcS; ribulose-bisphosphate carboxylase small chain [EC:4.1.1.39]	Yes
	<i>PRK</i>	K00855	PRK, prkB; phosphoribulokinase [EC:2.7.1.19]	Yes
3HP	<i>mcr</i>	K14468	mcr; malonyl-CoA reductase / 3-hydroxypropionate dehydrogenase (NADP+)[EC:1.2.1.75 1.1.1.298]	Yes
	<i>hpcs</i>		K14469; acrylyl-CoA reductase (NADPH) / 3-hydroxypropionyl-CoA dehydratase / 3-hydroxypropionyl-CoA synthetase [EC:1.3.1.84	
		K14469	4.2.1.116 6.2.1.36]	Yes
3HP4HB	<i>hpcd</i>	K15019	K15019; 3-hydroxypropionyl-coenzyme A dehydratase [EC:4.2.1.116]	Yes
	<i>acr</i>	K15020	K15020; acryloyl-coenzyme A reductase [EC:1.3.1.84]	Yes
DC4HB	<i>4hbl_DC4HB</i>	K14467	4hbl; 4-hydroxybutyrate---CoA ligase (AMP-forming) [EC:6.2.1.40]	Not detected
WL	<i>cooS</i>	K00198	cooS, acsA; anaerobic carbon-monoxide dehydrogenase catalytic subunit [EC:1.2.7.4]	Not detected
	<i>acsB</i>	K14138	acsB; acetyl-CoA synthase [EC:2.3.1.169]	Not detected
rTCA	<i>aclAB</i>	K15230	aclA; ATP-citrate lyase alpha-subunit [EC:2.3.3.8]	Not detected
		K15231	aclB; ATP-citrate lyase beta-subunit [EC:2.3.3.8]	Yes
	<i>ccsA</i>	K15232	ccsA; citryl-CoA synthetase large subunit [EC:6.2.1.18]	Yes
	<i>ccl</i>	K15234	ccl; citryl-CoA lyase [EC:4.1.3.34]	Yes
4HB	<i>4hbl</i>	K14466	K14466; 4-hydroxybutyrate---CoA ligase (AMP-forming)[EC:6.2.1.40]	Not detected
		K14467	4hbl; 4-hydroxybutyrate---CoA ligase (AMP-forming)[EC:6.2.1.40]	Not detected
		K18861	K18861; 4-hydroxybutyrate---CoA ligase (AMP-forming)[EC:6.2.1.40]	Not detected
		K18593	E6.2.1.56; 4-hydroxybutyrate---CoA ligase (ADP-forming) [EC:6.2.1.56]	Not detected

Table S15. The genes related to pathway of aerobic respiration.

Pathway	Gene cluster	Note	KEGG	Description	Detected
Aerobic respiration	<i>COX</i>	cytochrome-c oxidase	K02262	COX3; cytochrome c oxidase subunit 3	Not detected
			K02256	COX1; cytochrome c oxidase subunit I [EC:1.9.3.1]	Not detected
	<i>cox</i>	cytochrome-c oxidase, prokaryotes	K02274	coxA, ctaD; cytochrome c oxidase subunit I [EC:1.9.3.1]	Not detected
			K02275	coxB, ctaC; cytochrome c oxidase subunit II [EC:1.9.3.1]	Not detected
			K02276	coxC, ctaE; cytochrome c oxidase subunit III [EC:1.9.3.1]	Not detected
			K02277	coxD, ctaF; cytochrome c oxidase subunit IV [EC:1.9.3.1]	Not detected
			K15408	coxAC; cytochrome c oxidase subunit I+III [EC:1.9.3.1]	Not detected
	<i>cco</i>	cytochrome-c oxidase cbb3-type	K00404	ccoN; cytochrome c oxidase cbb3-type subunit I [EC:1.9.3.1]	Not detected
			K15862	ccoNO; cytochrome c oxidase cbb3-type subunit I/II [EC:1.9.3.1]	Not detected
	<i>cyo</i>	cytochrome o ubiquinol oxidase	K02297	cyoA; cytochrome o ubiquinol oxidase subunit II [EC:7.1.1.3]	Not detected
			K02298	cyoB; cytochrome o ubiquinol oxidase subunit I [EC:7.1.1.3]	Not detected
	<i>qox</i>	cytochrome aa3-600 menaquinol oxidase	K02827	qoxB; cytochrome aa3-600 menaquinol oxidase subunit I [EC:7.1.1.5]	Not detected
			K02826	qoxA; cytochrome aa3-600 menaquinol oxidase subunit II [EC:7.1.1.5]	Not detected
			K02828	qoxC; cytochrome aa3-600 menaquinol oxidase subunit III [EC:7.1.1.5]	Not detected
			K02829	qoxD; cytochrome aa3-600 menaquinol oxidase subunit IV [EC:7.1.1.5]	Not detected
	<i>cyd</i>	cytochrome bd ubiquinol oxidase	K00425	cydA; cytochrome bd ubiquinol oxidase subunit I [EC:7.1.1.7]	Not detected
			K00426	cydB; cytochrome bd ubiquinol oxidase subunit II [EC:7.1.1.7]	Not detected
			K00424	cydX; cytochrome bd-I ubiquinol oxidase subunit X [EC:7.1.1.7]	Not detected
			K22501	appX; cytochrome bd-II ubiquinol oxidase subunit AppX [EC:7.1.1.7]	Not detected
	<i>sox</i>	cytochrome aa3-type oxidase	K24009	soxB; cytochrome aa3-type oxidase subunit I [EC:7.1.1.4]	Not detected
			K24010	soxA; cytochrome aa3-type oxidase subunit II [EC:7.1.1.4]	Not detected
			K24011	soxA; cytochrome aa3-type oxidase subunit I/III [EC:7.1.1.4]	Not detected

Table S16. The genes related to pathway of fermentation .

Step	Production	KO	Description	Detected
Fermentation	Formate	K00656	E2.3.1.54, pflD; formate C-acetyltransferase [EC:2.3.1.54]	Yes
	Acetate	K18118	aarC, cat1; succinyl-CoA:acetate CoA-transferase [EC:2.8.3.18]	Yes
		K01905	acdA; acetate---CoA ligase (ADP-forming) subunit alpha [EC:6.2.1.13]	Yes
		K24012	acdAB; acetate---CoA ligase (ADP-forming) [EC:6.2.1.13]	Not detected
		K22224	acdB; acetate---CoA ligase (ADP-forming) subunit beta [EC:6.2.1.13]	Yes
		K00925	ackA; acetate kinase [EC:2.7.2.1]	Yes
		K14519	aldH; NADP-dependent aldehyde dehydrogenase[EC:1.2.1.4]	Not detected
		K01067	E3.1.2.1, ACH1; acetyl-CoA hydrolase [EC:3.1.2.1]	Yes
		K01512	acylphosphatase [EC:3.6.1.7]	Yes
	Propionate	K01026	pct; propionate CoA-transferase [EC:2.8.3.1]	Yes
		K00932	tdcD; propionate kinase[EC:2.7.2.15]	Not detected
		K19697	pduW; propionate kinase[EC:2.7.2.15]	Yes
	Lactate	K00016	LDH, ldh; L-lactate dehydrogenase [EC:1.1.1.27]	Yes
		K03778	ldhA; D-lactate dehydrogenase [EC:1.1.1.28]	Yes
	Ethanol	K13951	ADH1_7; alcohol dehydrogenase 1/7 [EC:1.1.1.1]	Not detected
		K13980	ADH4; alcohol dehydrogenase 4 [EC:1.1.1.1]	Not detected
		K00121	frmA, ADH5, adhC; S-(hydroxymethyl)glutathione dehydrogenase / alcohol dehydrogenase [EC:1.1.1.284 1.1.1.1]	Yes
		K13952	ADH6; alcohol dehydrogenase 6 [EC:1.1.1.1]	Not detected
		K04072	adhE; acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]	Yes
		K13953	adhP; alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]	Yes
		K13954	yiaY; alcohol dehydrogenase [EC:1.1.1.1]	Yes
		K18857	ADH1; alcohol dehydrogenase class-P [EC:1.1.1.1]	Not detected

K00001	E1.1.1.1, adh; alcohol dehydrogenase [EC:1.1.1.1]	Not detected
K00002	AKR1A1, adh; alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	Yes
K13979	yahK; alcohol dehydrogenase (NADP+) [EC:1.1.1.2]	Not detected
K12957	ahr; alcohol/geraniol dehydrogenase (NADP+) [EC:1.1.1.2 1.1.1.183]	Not detected

Table S17. The genes related to pathway of CH₄ metabolism.

Step	Gene cluster	KEGG	Description	Detected
Methanogenesis	mcr	K00401	mcrB; methyl-coenzyme M reductase beta subunit [EC:2.8.4.1]	Not detected
		K00399	mcrA; methyl-coenzyme M reductase alpha subunit [EC:2.8.4.1]	Not detected
		K00402	mcrG; methyl-coenzyme M reductase gamma subunit [EC:2.8.4.1]	Not detected
Aerobic CH ₄ oxidation	mmo	K16157	mmoX; methane monooxygenase component A alpha chain [EC:1.14.13.25]	Not detected
		K16158	mmoY; methane monooxygenase component A beta chain [EC:1.14.13.25]	Not detected
		K16159	mmoZ; methane monooxygenase component A gamma chain [EC:1.14.13.25]	Not detected
		K16161	mmoC; methane monooxygenase component C [EC:1.14.13.25]	Yes
	pmo	K10944	pmoA-ammoA; methane/ammonia monooxygenase subunit A [EC:1.14.18.3 1.14.99.39]	Yes
		K10945	pmoB-ammoB; methane/ammonia monooxygenase subunit B	Yes
		K10946	pmoC-ammoC; methane/ammonia monooxygenase subunit C	Yes

Table S18. The genes related to pathway of CO oxidation.

Step	Gene cluster	KEGG	Description	Detected
CO oxidation (K03518+K03519+K03520)/3	coxMLS	K03518	coxS; aerobic carbon-monoxide dehydrogenase small subunit [EC:1.2.5.3]	Not detected
		K03519	coxM, cutM; aerobic carbon-monoxide dehydrogenase medium subunit [EC:1.2.5.3]	Not detected
		K03520	coxL, cutL; aerobic carbon-monoxide dehydrogenase large subunit [EC:1.2.5.3]	Not detected

Table S19. The genes related to pathway of carbon decomposition.

Organic carbon	enzyme	ID	KO	Description	Detected
starch/glycogen	amylase	Sa1	K01176	AMY, amyA, malS; alpha-amylase [EC:3.2.1.1]	Yes
			K07405	E3.2.1.1A; alpha-amylase [EC:3.2.1.1]	Yes
			K05343	treS; maltose alpha-D-glucosyltransferase / alpha-amylase [EC:5.4.99.16 3.2.1.1]	Yes
			K01177	beta-amylase [EC:3.2.1.2]	Not detected
				cd, ma, nplT; cyclomaltodextrinase / maltogenic alpha-amylase / neopullulanase;EC	
			K01208	3.2.1.133	Yes
			K05992	amyM; maltogenic alpha-amylase;EC 3.2.1.133	Not detected
			K01178	SGA1; glucoamylase;EC 3.2.1.3	Yes
			K12047	MGAM; maltase-glucoamylase;EC 3.2.1.3	Not detected
			K21574	susB; glucan 1,4-alpha-glucosidase;EC 3.2.1.3	Yes
	alpha-glucosidase	Sa2	K08254	E3.2.1.59; glucan endo-1,3-alpha-glucosidase [EC:3.2.1.59]	Not detected
			K01215	dexB; glucan 1,6-alpha-glucosidase [EC:3.2.1.70]	Not detected
			K01187	malZ; alpha-glucosidase [EC:3.2.1.20]	Yes
			K12317	GANC; neutral alpha-glucosidase C [EC:3.2.1.20]	Not detected
			K12316	GAA; lysosomal alpha-glucosidase [EC:3.2.1.20]	Not detected
	pullulanase	Sa3	K01200	pulA; pullulanase [EC:3.2.1.41]	Yes
	GDE	Sa4	K01196	AGL; glycogen debranching enzyme [EC:2.4.1.25 3.2.1.33]	Not detected
			K02438	glgX; glycogen debranching enzyme[EC:3.2.1.196]	Yes
	glycogen	Sa5	K00688	PYG, glgP;glycogen phosphorylase [EC:2.4.1.1]	Yes
	phosphorylase		K16153	glycogen phosphorylase/synthase [EC:2.4.1.1 2.4.1.11]	Not detected
trehalose	alpha-trehalase	Tr1	K01194	TREH, treA, treF; alpha,alpha-trehalaseE3.2.1.28	Yes
			K22934	E3.2.1.28; alpha,alpha-trehalase E3.2.1.28	Not detected

PHA	trehalose					
	phosphorylase	Tr2	K05342	alpha,alpha-trehalose phosphorylase E2.4.1.64		Yes
			K05973	phaZ; poly(3-hydroxybutyrate) depolymerase [EC:3.1.1.75]		Yes
	phaZ	Ph1	K22249	phaZ; poly(3-hydroxyoctanoate) depolymerase [EC:3.1.1.76]		Not detected
			K22250	phaZ; poly(3-hydroxyoctanoate) depolymerase [EC:3.1.1.76]		Not detected
			K20844	abf1;non-reducing end alpha-L-arabinofuranosidase [EC:3.2.1.55]		Yes
	arabinofuranosidase	Hd1	K01209	abfA;alpha-N-arabinofuranosidase [EC:3.2.1.55]		Yes
			K15921	xynD;arabinoxylan arabinofuranohydrolase [EC:3.2.1.55]		Yes
			K18205	hypBA1; non-reducing end beta-L-arabinofuranosidase[EC:3.2.1.185]		Not detected
	arabinosidase	Hd2	K06113	abnA;arabinan endo-1,5-alpha-L-arabinosidase [EC:3.2.1.99]		Not detected
			K08257	E3.2.1.101;mannan endo-1,6-alpha-mannosidase [EC:3.2.1.101]		Not detected
			K01192	E3.2.1.25, MANBA, manB;beta-mannosidase [EC:3.2.1.25]		Not detected
			K01230	MAN1;mannosyl-oligosaccharide alpha-1,2-mannosidase [EC:3.2.1.113]		Not detected
			K01191	E3.2.1.24;alpha-mannosidase [EC:3.2.1.24]		Not detected
Hemicellulose	mannanase	Hd3	K01231	MAN2;alpha-mannosidase II [EC:3.2.1.114]		Not detected
			K21065	E3.2.1.197;beta-1,2-mannosidase [EC:3.2.1.197]		Not detected
			K01218	gmuG;mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]		Yes
			K19355	MAN;mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]		Yes
				alpha-mannan endo-1,2-alpha-mannanase / glycoprotein endo-alpha-1,2-mannosidase [EC:3.2.1.198 3.2.1.130]		Not detected
			K21132			Not detected
			K01198	xynB;xylan 1,4-beta-xylosidase [EC:3.2.1.37]		Yes
	beta-xylosidase	Hd4	K15920	XYL4;beta-D-xylosidase 4 [EC:3.2.1.37]		Not detected
			K22268	xylan 1,4-beta-xylosidase [EC:3.2.1.37]		Yes
	xylanase	Hd5	K20845	txyA;endo-1,3-beta-xylanase [EC:3.2.1.32]		Not detected

Cellulose	AXE phosphorylase	CEd1	K13465	EIX;ethylene-1,4-beta-xylanase [EC:3.2.1.8]	Not detected
			K01181	E3.2.1.8, xynA;endo-1,4-beta-xylanase [EC:3.2.1.8]	Not detected
			K05972	AXE1;acetylxytan esterase [EC:3.1.1.72]	Not detected
			K00702	E2.4.1.20;cellobiose phosphorylase [EC:2.4.1.20]	Yes
			K01188	E3.2.1.21;beta-glucosidase [EC:3.2.1.21]	Not detected
			K05349	bglX;beta-glucosidase [EC:3.2.1.21]	Yes
			K05350	bglB;beta-glucosidase [EC:3.2.1.21]	Yes
			K01222	E3.2.1.86A, celF;6-phospho-beta-glucosidase [EC:3.2.1.86]	Yes
			K01223	E3.2.1.86B, bglA;6-phospho-beta-glucosidase [EC:3.2.1.86]	Not detected
			K01210	E3.2.1.58;glucan 1,3-beta-glucosidase [EC:3.2.1.58]	Not detected
	beta-glucosidase	CEd3	K01199	EGLC;glucan endo-1,3-beta-D-glucosidase [EC:3.2.1.39]	Not detected
			K19891	GN1_2_3; glucan endo-1,3-beta-glucosidase 1/2/3 [EC:3.2.1.39]	Not detected
			K19892	GN4;glucan endo-1,3-beta-glucosidase 4 [EC:3.2.1.39]	Not detected
			K19893	GN5_6;glucan endo-1,3-beta-glucosidase 5/6 [EC:3.2.1.39]	Not detected
			K22276	NEG1; glucan endo-1,6-beta-glucosidase [EC:3.2.1.75]	Not detected
			K22277	EXGB; glucan endo-1,6-beta-glucosidase [EC:3.2.1.75]	Not detected
			K01220	E3.2.1.85, lacG;6-phospho-beta-galactosidase [EC:3.2.1.85]	Not detected
	beta-galactosidase	CEd4	K01224	E3.2.1.89;arabinogalactan endo-1,4-beta-galactosidase [EC:3.2.1.89]	Not detected
			K18579	6GAL;galactan endo-1,6-beta-galactosidase [EC:3.2.1.164]	Not detected
			K01190	lacZ;beta-galactosidase [EC:3.2.1.23]	Yes
			K12308	bgaB, lacA;beta-galactosidase [EC:3.2.1.23]	Yes
			K12309	GLB1, ELNR1;beta-galactosidase [EC:3.2.1.23]	Not detected
			K12111	ebgA;evolved beta-galactosidase subunit alpha [EC:3.2.1.23]	Not detected
	endoglucanase	CEd5	K19357	CELB;cellulase [EC:3.2.1.4]	Not detected
			K01179	E3.2.1.4;endoglucanase [EC:3.2.1.4]	Yes
			K20542	bcsZ;endoglucanase [EC:3.2.1.4]	Not detected

Peptidoglycan	exoglucanase	CEd6	K01225	CBH1;cellulose 1,4-beta-cellobiosidase [EC:3.2.1.91]	Not detected	
			K19668	CBH2, cbhA;cellulose 1,4-beta-cellobiosidase [EC:3.2.1.91]	Yes	
			K01185	E3.2.1.17;lysozyme [EC:3.2.1.17]	Not detected	
			K13915	LYZ;lysozyme C [EC:3.2.1.17]	Not detected	
	lysozyme	Pd1	K13381	chiA;bifunctional chitinase/lysozyme [EC:3.2.1.14 3.2.1.17]	Yes	
			K11331	nrsC; cation efflux system protein involved in nickel and cobalt tolerance[EC:3.2.1.17]	Not detected	
			K21509	gp36; peptidoglycan hydrolase [EC:3.2.1.17]	Not detected	
			K11693	femX, fmhB;peptidoglycan pentaglycine glycine transferase (the first glycine) [EC:2.3.2.16]	Not detected	
	glycine transferase	Pd2	K11694	femA; peptidoglycan pentaglycine glycine transferase (the second and third glycine) [EC:2.3.2.17]	Not detected	
			K11695	femB; peptidoglycan pentaglycine glycine transferase (the fourth and fifth glycine) [EC:2.3.2.18]	Not detected	
amidase			Pd3	K01448	E3.5.1.28B, amiA, amiB, amiC;N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]	Not detected
				pdaA	Pd4	K01567
	K22278	pdgA; peptidoglycan-N-acetylglucosamine deacetylase [EC:3.5.1.104]				Not detected
	endo_PG	Pe1		K01184	E3.2.1.15;polygalacturonase [EC:3.2.1.15]	Not detected
Pectin	exo_PG	Pe2	K01213	E3.2.1.67;galacturan 1,4-alpha-galacturonidase [EC:3.2.1.67]	Not detected	
			K01728	pel;pectate lyase [EC:4.2.2.2]	Yes	
	pectinase	Pe3	K22539	PLY; pectate lyase [EC:4.2.2.2]	Not detected	
			K19551	pelC;pectate lyase C [EC:4.2.2.2 4.2.2.10]	Not detected	
			K01731	pelW;pectate disaccharide-lyase [EC:4.2.2.9]	Not detected	
			K01732	E4.2.2.10;pectin lyase [EC:4.2.2.10]	Not detected	
	PME	Pe4	K01051	E3.1.1.11;pectinesterase [EC:3.1.1.11]	Yes	

Chitin	RGAE	Pe5	K15530	RGAE;rhamnogalacturonan acetylsterase [EC:3.1.1.86]	Not detected
			K18195	RGL4, rhiE;rhamnogalacturonan endolyase [EC:4.2.2.23]	Not detected
	RGase	Pe6	K18197	yesW;rhamnogalacturonan endolyase [EC:4.2.2.23]	Not detected
			K18198	yesX;rhamnogalacturonan exolyase [EC:4.2.2.24]	Not detected
	acetylglucosaminidase	CHd1	K01227	E3.2.1.96;mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase [EC:3.2.1.96]	Not detected
			K01205	NAGLU;alpha-N-acetylglucosaminidase [EC:3.2.1.50]	Not detected
			K01207	nagZ;beta-N-acetylhexosaminidase [EC:3.2.1.52]	Yes
	hexosaminidase	CHd2	K20730	FDL; beta-hexosaminidase Fdl [EC:3.2.1.52]	Not detected
			K12373	HEXA_B;hexosaminidase [EC:3.2.1.52]	Yes
			K14459	HEX;hexosaminidase [EC:3.2.1.52]	Not detected
	chbP	CHd3	K18675	chbP; N,N'-diacetylchitobiose phosphorylase [EC:2.4.1.280]	Yes
			K01452	E3.5.1.41;chitin deacetylase [EC:3.5.1.41]	Yes
	chitin deacetylase	CHd4	K03478	chbG;chitin disaccharide deacetylase [EC:3.5.1.105]	Not detected
			K18454	deaA;chitin disaccharide deacetylase [EC:3.5.1.105]	Not detected
			K01183	E3.2.1.14;chitinase [EC:3.2.1.14]	Yes
	chitinase	CHd5	K13381	chiA;bifunctional chitinase/lysozyme [EC:3.2.1.14 3.2.1.17]	Yes
			K20547	CHIB;basic endochitinase B [EC:3.2.1.14]	Yes
Lignin	GAOA	Ld1	K04618	GAOA;galactose oxidase [EC:1.1.3.9]	Yes
	GLX	Ld2	K20929	GLX;glyoxal/methylglyoxal oxidase [EC:1.2.3.15]	Not detected
	mpn	Ld3	K20205	mpn;manganese peroxidase [EC:1.11.1.13]	Not detected
	laccase	Ld4	K05909	E1.10.3.2;laccase [EC:1.10.3.2]	Not detected
	multicopper oxidase	Ld5	K22552	mmcO; multicopper oxidase [EC:1.16.3.1]	Not detected
	phenoloxidase	Ld6	K00422	E1.10.3.1;polyphenol oxidase [EC:1.10.3.1]	Not detected