

Supplementary materials

Shifts in genes encoding enzymes that degrade plant- and microbial-derived carbon affect soil organic carbon pools in different subtropical forests of China

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Supplementary Tables

Table S1. Summary of metagenomic sequencing data from soils of three forest types. Raw reads: number of raw sequencing reads; Clean reads: number of reads retained after quality control; Contigs: number of assembled contigs; Contig base (bp): total length of assembled contigs; ORFs: number of predicted open reading frames.

Sample	Raw reads	Clean reads	Contigs	Contigs base(bp)	ORFs
Broadleaf _a	76,313,524	74,501,674	343,220	232,570,414	462,655
Broadleaf _b	75,411,618	73,809,940	288,253	196,721,739	390,275
Broadleaf _c	66,344,340	64,828,682	382,213	293,112,539	545,735
Broadleaf _d	92,924,166	90,939,572	586,450	427,674,815	818,371
Broadleaf _e	84,430,218	82,668,038	556,353	390,424,659	749,425
Broadleaf _f	90,068,012	88,074,470	420,444	282,589,488	564,746
Coniferous _a	91,838,986	90,175,022	574,802	396,606,970	784,928
Coniferous _b	66,710,872	65,490,900	291,155	191,704,572	383,568
Coniferous _c	85,004,486	83,368,802	516,445	335,369,600	680,151
Coniferous _d	65,769,538	64,584,870	291,783	174,042,216	370,685
Coniferous _e	78,494,310	77,143,082	390,541	245,357,333	506,171
Coniferous _f	72,756,804	71,421,176	240,569	140,651,827	301,503
Bamboo _a	77,771,748	75,954,572	357,969	222,779,613	462,172
Bamboo _b	71,602,482	70,026,942	277,199	174,194,324	356,548
Bamboo _c	66,908,614	65,687,774	227,005	134,508,083	284,260
Bamboo _d	64,121,100	62,966,246	251,170	152,316,244	318,344
Bamboo _e	78,075,820	76,746,376	458,942	318,786,928	617,899
Bamboo _f	79,560,450	78,053,064	482,674	315,699,016	637,159

Table S2. Functional classification of genes encoding CAZymes that degrade plant- and microbial-derived components.

Compound	CAZyme families	Description
Plant-derived	Hemicellulose	GH2 beta-galactosidase (EC 3.2.1.23); beta-mannosidase (EC 3.2.1.25); beta-glucuronidase (EC 3.2.1.31); alpha-L-arabinofuranosidase (EC 3.2.1.55); mannosylglycoprotein endo-beta-mannosidase (EC 3.2.1.152); exo-beta-glucosaminidase (EC 3.2.1.165); alpha-L-arabinopyranosidase (EC 3.2.1.-); beta-galacturonidase (EC 3.2.1.-); beta-xylosidase (EC 3.2.1.37); beta-D-galactofuranosidase (EC 3.2.1.146); beta-glucosidase (EC 3.2.1.21); beta-galacturonidase RGII specific (EC 3.2.1.-); glycyrrhizin beta-glucuronidase (EC 3.2.1.128)
		GH10 endo-1,4-beta-xylanase (EC 3.2.1.8); endo-1,3-beta-xylanase (EC 3.2.1.32); tomatinase (EC 3.2.1.-); xylan endotransglycosylase (EC 2.4.2.-); endo-beta-1,4-glucanase (EC 3.2.1.4); [retaining] arabinoxylan-specific endo-beta-1,4-xylanase (EC 3.2.1.-); oligosaccharide reducing-end xylanase (EC 3.2.1.156)
		GH11 endo-beta-1,4-xylanase (EC 3.2.1.8); exo-1,4-beta-xylosidase (EC 3.2.1.-)
		GH26 beta-mannanase (EC 3.2.1.78); exo-beta-1,4-mannobiohydrolase (EC 3.2.1.100); beta-1,3-xylanase (EC 3.2.1.32); lichenase / endo-beta-1,3-1,4-glucanase (EC 3.2.1.73); mannobiose-producing exo-beta-mannanase (EC 3.2.1.-)
		GH30 endo-beta-1,4-xylanase (EC 3.2.1.8); beta-glucosidase (3.2.1.21); beta-glucuronidase (EC 3.2.1.31); beta-xylosidase (EC 3.2.1.37); beta-fucosidase (EC 3.2.1.38); glucosylceramidase (EC 3.2.1.45); beta-1,6-glucanase (EC 3.2.1.75); glucuronoarabinoxylan endo-beta-1,4-xylanase (EC 3.2.1.136); endo-beta-1,6-galactanase (EC:3.2.1.164); [reducing end] beta-xylosidase (EC 3.2.1.-)
		GH36 alpha-galactosidase (EC 3.2.1.22); alpha-N-acetylgalactosaminidase (EC 3.2.1.49); stachyose synthase (EC 2.4.1.67); raffinose synthase (EC 2.4.1.82)
		GH39 alpha-L-iduronidase (EC 3.2.1.76); beta-xylosidase (EC 3.2.1.37); alpha-L-arabinofuranosidase (EC 3.2.1.55); beta-glucosidase (EC 3.2.1.21); beta-galactosidase (EC 3.2.1.23); exo-beta-1,4-glucanase / cellodextrinase (EC 3.2.1.74); 3-O-alpha-D-galactosyl-alpha-L-arabinofuranosidase (EC 3.2.1.215)
		GH43 beta-xylosidase (EC 3.2.1.37); alpha-L-arabinofuranosidase (EC 3.2.1.55); xylanase (EC 3.2.1.8); alpha-1,2-L-arabinofuranosidase (EC 3.2.1.-); exo-alpha-1,5-L-arabinofuranosidase (EC 3.2.1.-); [inverting] exo-alpha-1,5-L-arabinanase (EC 3.2.1.-); beta-1,3-xylosidase (EC 3.2.1.72); [inverting] exo-alpha-1,5-L-arabinanase

		(EC 3.2.1.-); [inverting] endo-alpha-1,5-L-arabinanase (EC 3.2.1.99); exo-beta-1,3-galactanase (EC 3.2.1.145); beta-D-galactofuranosidase (EC 3.2.1.146)
	GH44	endoglucanase (EC 3.2.1.4); xyloglucanase (EC 3.2.1.151)
	GH51	endoglucanase (EC 3.2.1.4); endo-beta-1,4-xylanase (EC 3.2.1.8); beta-xylosidase (EC 3.2.1.37); alpha-L-arabinofuranosidase (EC 3.2.1.55); cellobiohydrolase (EC 3.2.1.91)
	GH52	beta-xylosidase (EC 3.2.1.37).
	GH54	alpha-L-arabinofuranosidase (EC 3.2.1.55); beta-xylosidase (EC 3.2.1.37).
	GH62	alpha-L-arabinofuranosidase (EC 3.2.1.55)
	GH67	alpha-glucuronidase (EC 3.2.1.139); xylan alpha-1,2-glucuronidase (EC 3.2.1.131)
	GH74	endoglucanase (EC 3.2.1.4); oligoxyloglucan reducing end-specific cellobiohydrolase (EC 3.2.1.150); xyloglucanase (EC 3.2.1.151)
	GH95	alpha-L-fucosidase (EC 3.2.1.51); alpha-1,2-L-fucosidase (EC 3.2.1.63); alpha-L-galactosidase (EC 3.2.1.-)
	GH115	xylan alpha-1,2-glucuronidase (3.2.1.131); alpha-(4-O-methyl)-glucuronidase (3.2.1.-)
	GH120	beta-xylosidase (EC 3.2.1.37)
	Cellulose	beta-glucosidase (EC 3.2.1.21); beta-galactosidase (EC 3.2.1.23); beta-mannosidase (EC 3.2.1.25); beta-glucuronidase (EC 3.2.1.31); beta-xylosidase (EC 3.2.1.37); beta-D-fucosidase (EC 3.2.1.38); phlorizin hydrolase (EC 3.2.1.62); exo-beta-1,4-glucanase (EC 3.2.1.74); 6-phospho-beta-galactosidase (EC 3.2.1.85); 6-phospho-beta-glucosidase (EC 3.2.1.86); strictosidine beta-glucosidase (EC 3.2.1.105); lactase (EC 3.2.1.108); amygdalin beta-glucosidase (EC 3.2.1.117); prunasin beta-glucosidase (EC 3.2.1.118); vicianin hydrolase (EC 3.2.1.119); raucaffricine beta-glucosidase (EC 3.2.1.125); thioglucosidase (EC 3.2.1.147); beta-primeverosidase (EC 3.2.1.149); isoflavonoid 7-O-beta-apiosyl-beta-glucosidase (EC 3.2.1.161); ABA-specific beta-glucosidase (EC 3.2.1.175); DIMBOA beta-glucosidase (EC 3.2.1.182); hydroxyisourate hydrolase (EC 3.-.-.-); beta-rutinosidase /alpha-L-rhamnose-(1,6)-beta-D-glucosidase (EC 3.2.1.-); protodioscin 26-O-Î²-D-glucosidase (EC 3.2.1.186); alpha-L-arabinopyranosidase (EC 3.2.1.-); isoflavone 7-O-glucosyl beta-glucosidase (EC 3.2.1.-)
	GH3	beta-glucosidase (EC 3.2.1.21); xylan 1,4-beta-xylosidase (EC 3.2.1.37); beta-glucosylceramidase (EC 3.2.1.45); beta-N-acetylhexosaminidase (EC 3.2.1.52); alpha-L-arabinofuranosidase (EC 3.2.1.55); glucan 1,4-beta-glucosidase

		(EC 3.2.1.74); isoprimeverose-producing oligoxyloglucan hydrolase (EC 3.2.1.120); coniferin beta-glucosidase (EC 3.2.1.126); exo-1,3-1,4-glucanase (EC 3.2.1.-); beta-N-acetylglucosaminide phosphorylases (EC 2.4.1.-); beta-1,2-glucosidase (EC 3.2.1.-); beta-1,3-glucosidase (EC 3.2.1.-); xyloglucan-specific exo-beta-1,4-glucanase / exo-xyloglucanase (EC 3.2.1.155); stevioside-beta-1,2-glucosidase (EC 3.2.1.-); lichenase / endo-beta-1,3-1,4-glucanase (EC 3.2.1.73); protodioscin 26-O-beta-D-glucosidase (EC 3.2.1.186); beta-glucuronidase (EC 3.2.1.31); avenacinase (EC 3.2.1.-); tomatinase beta-1,2-glucosidase (EC 3.2.1.-) endo-beta-1,4-glucanase / cellulase (EC 3.2.1.4); endo-beta-1,4-xylanase (EC 3.2.1.8); beta-glucosidase (EC 3.2.1.21); beta-mannosidase (EC 3.2.1.25); beta-glucosylceramidase (EC 3.2.1.45); glucan beta-1,3-glucosidase (EC 3.2.1.58); exo-beta-1,4-glucanase / cellodextrinase (EC 3.2.1.74); glucan endo-1,6-beta-glucosidase (EC 3.2.1.75); mannan endo-beta-1,4-mannosidase (EC 3.2.1.78); cellulose beta-1,4-cellobiosidase (EC 3.2.1.91); steryl beta-glucosidase (EC 3.2.1.104); endoglycoceramidase (EC 3.2.1.123); beta-primeverosidase (EC 3.2.1.149); xyloglucan-specific endo-beta-1,4-glucanase (EC 3.2.1.151); endo-beta-1,6-galactanase (EC 3.2.1.164); beta-1,3-mannanase (EC 3.2.1.-); arabinoxylan-specific endo-beta-1,4-xylanase (EC 3.2.1.-); mannan transglycosylase (EC 2.4.1.-); lichenase / endo-beta-1,3-1,4-glucanase (EC 3.2.1.73); beta-glycosidase (EC 3.2.1.-); endo-beta-1,3-glucanase / laminarinase (EC 3.2.1.39); beta-N-acetylhexosaminidase (EC 3.2.1.52); chitosanase (EC 3.2.1.132); beta-D-galactofuranosidase (EC 3.2.1.146); beta-galactosylceramidase (EC 3.2.1.46); ; beta-rutinosidase /alpha-L-rhamnose-(1,6)-beta-D-glucosidase (EC 3.2.1.-); alpha-L-arabinofuranosidase (EC 3.2.1.55); glucomannan-specific endo-beta-1,4-glucanase (EC 3.2.1.-); hesperidin 6-O-alpha-L-rhamnosyl-beta-glucosidase (EC 3.2.1.168)
	GH5	
	GH6	endoglucanase (EC 3.2.1.4); cellobiohydrolase (EC 3.2.1.91); lichenase / endo-beta-1,3-1,4-glucanase (EC 3.2.1.73); chitosanase (EC 3.2.1.132); cellulase (EC 3.2.1.4); licheninase (EC 3.2.1.73); endo-1,4-beta-xylanase (EC 3.2.1.8);
	GH8	reducing-end-xylose releasing exo-oligoxylanase (EC 3.2.1.156); endo-beta-1,3(4)-glucanase / lichenase-laminarinase (EC 3.2.1.6)
	GH9	endoglucanase (EC 3.2.1.4); endo-beta-1,3(4)-glucanase / lichenase-laminarinase (EC 3.2.1.6); lichenase / endo-beta-1,3-1,4-glucanase (EC 3.2.1.73); exo-beta-1,4-glucanase / cellodextrinase (EC 3.2.1.74); cellobiohydrolase (EC 3.2.1.91); xyloglucan-specific endo-beta-1,4-glucanase / endo-xyloglucanase (EC 3.2.1.151); exo-beta-glucosaminidase (EC 3.2.1.165); endo-beta-1,4-glucanase (xanthanase) (EC 3.2.1.-)

		GH12	endoglucanase (EC 3.2.1.4); xyloglucan hydrolase (EC 3.2.1.151); beta-1,3-1,4-glucanase (EC 3.2.1.73); xyloglucan endotransglycosylase (EC 2.4.1.207)
		GH45	endoglucanase (EC 3.2.1.4); xyloglucan-specific endo-beta-1,4-glucanase / endo-xyloglucanase (EC 3.2.1.151); endo-beta-1,4-mannanase (EC 3.2.1.78)
		GH48	reducing end-acting cellobiohydrolase (EC 3.2.1.176); endo-beta-1,4-glucanase (EC 3.2.1.4); chitinase (EC 3.2.1.14); cellobiohydrolase (EC 3.2.1.91)
		GH116	beta-glucosidase (EC 3.2.1.21); beta-xylosidase (EC 3.2.1.37); acid beta-glucosidase/beta-glucosylceramidase (EC 3.2.1.45); beta-N-acetylglucosaminidase (EC 3.2.1.52)
		AA9	AA9 (formerly GH61) proteins are copper-dependent lytic polysaccharide monooxygenases (LPMOs); cleavage of cellulose chains with oxidation of carbons C1 and/or C4 and C-6); lytic cellulose monooxygenase (C1-hydroxylating) (EC 1.14.99.54); lytic cellulose monooxygenase (C4-dehydrogenating) (EC 1.14.99.56)
		AA10	AA10 (formerly CBM33) proteins are copper-dependent lytic polysaccharide monooxygenases (LPMOs); some proteins have been shown to act on chitin, others on cellulose; lytic cellulose monooxygenase (C1-hydroxylating) (EC 1.14.99.54); lytic cellulose monooxygenase (C4-dehydrogenating) (EC 1.14.99.56); lytic chitin monooxygenase (EC 1.14.99.53); lytic xylan monooxygenase / xylan oxidase (glycosidic bond-cleaving) (EC 1.14.99.-)
	Lignin	AA1	Laccase / p-diphenol:oxygen oxidoreductase / ferroxidase (EC 1.10.3.2); ferroxidase (EC 1.10.3.-); Laccase-like multicopper oxidase (EC 1.10.3.-)
		AA2	manganese peroxidase (EC 1.11.1.13); versatile peroxidase (EC 1.11.1.16); lignin peroxidase (EC 1.11.1.14); peroxidase (EC 1.11.1.-); cytochrome-c peroxidase (EC 1.11.1.5); ascorbate peroxidase (EC 1.11.1.11)
		AA3	cellobiose dehydrogenase (EC 1.1.99.18); glucose 1-oxidase (EC 1.1.3.4); aryl alcohol oxidase (EC 1.1.3.7); alcohol oxidase (EC 1.1.3.13); pyranose oxidase (EC 1.1.3.10); glucose 1-dehydrogenase (FAD, quinone) (EC 1.1.5.9); pyranose dehydrogenase (EC 1.1.99.29); oligosaccharide dehydrogenase (FAD) (EC 1.1.5.-)
		AA4	vanillyl-alcohol oxidase (EC 1.1.3.38)
		AA5	Oxidase with oxygen as acceptor (EC 1.1.3.-); galactose oxidase (EC 1.1.3.9); glyoxal oxidase (EC 1.2.3.15); alcohol oxidase (EC 1.1.3.13); raffinose oxidase (EC 1.1.3.-)
		AA6	1,4-benzoquinone reductase (EC. 1.6.5.6)

Fungal-derived	Chitin	GH16	xyloglucan:xyloglucosyltransferase (EC 2.4.1.207); keratan-sulfate endo-1,4-beta-galactosidase (EC 3.2.1.103); endo-1,3-beta-glucanase / laminarinase (EC 3.2.1.39); endo-1,3(4)-beta-glucanase (EC 3.2.1.6); licheninase (EC 3.2.1.73); beta-agarase (EC 3.2.1.81); kappa;-carrageenase (EC 3.2.1.83); xyloglucanase (EC 3.2.1.151); endo-beta-1,3-galactanase (EC 3.2.1.181); [retaining] beta-porphyrinase (EC 3.2.1.178); hyaluronidase (EC 3.2.1.35); endo-beta-1,4-galactosidase (EC 3.2.1.-); chitin beta-1,6-glucanoyltransferase (EC 2.4.1.-); beta-transglycosidase (EC 2.4.1.-); beta-glycosidase (EC 3.2.1.-); beta-carrageenase (EC 3.2.1.-)
			chitinase (EC 3.2.1.14); lysozyme (EC 3.2.1.17); endo-beta-N-acetylglucosaminidase (EC 3.2.1.96); peptidoglycan hydrolase with endo-beta-N-acetylglucosaminidase specificity (EC 3.2.1.-); Nod factor hydrolase (EC 3.2.1.-); xylanase inhibitor; concanavalin B; narbonin; dIota;-N-acetylchitinase / reducing-end exo-hexosaminidase (EC 3.2.1.-); chitobiosidase (EC 3.2.1.200)
		GH18	chitinase (EC 3.2.1.14); lysozyme (EC 3.2.1.17); [reducing end] chitinase (EC 3.2.1.201)
		GH19	beta-hexosaminidase (EC 3.2.1.52); lacto-N-biosidase (EC 3.2.1.140); beta-1,6-N-acetylglucosaminidase (EC 3.2.1.-); beta-6-SO ₃ -N-acetylglucosaminidase (EC 3.2.1.-)
		GH20	beta-1,3-glucanoyltransglycosylase (EC 2.4.1.-)
	Glucans	GH72	glucan endo-1,3-beta-glucosidase (EC 3.2.1.39); licheninase (EC 3.2.1.73); ABA-specific beta-glucosidase (EC 3.2.1.175); beta-1,3-glucanoyltransglycosylase (EC 2.4.1.-); beta-1,3-glucosidase (EC 3.2.1.-)
		GH17	exo-beta-1,3-glucanase (EC 3.2.1.58); endo-beta-1,3-glucanase (EC 3.2.1.39); laminarin-degrading enzyme (EC 3.2.1.-); hesperidin 6-O-alpha-L-rhamnosyl-beta-glucosidase (EC 3.2.1.168)
		GH55	beta-1,3-glucanase (EC 3.2.1.39)
		GH64	endo-beta-1,3-glucanase (EC 3.2.1.39)
		GH81	beta-1,3-glucanase (EC 3.2.1.39); beta-1,3-glucosidase (EC 3.2.1.-)
		GH128	lysozyme type G (EC 3.2.1.17); peptidoglycan lyase (EC 4.2.2.n1) also known in the literature as peptidoglycan lytic transglycosylase; chitinase (EC 3.2.1.14)
Bacterial-derived	Peptidoglycan	GH23	lysozyme (EC 3.2.1.17)
		GH24	lysozyme (EC 3.2.1.17)
		GH25	lysozyme (EC 3.2.1.17)
		GH73	lysozyme (EC 3.2.1.17); mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase (EC 3.2.1.96); peptidoglycan

		hydrolase with endo-beta-N-acetylglucosaminidase specificity (EC 3.2.1.-)
	GH102	peptidoglycan lytic transglycosylase (EC 3.2.1.-)
	GH103	peptidoglycan lytic transglycosylase (EC 3.2.1.-)
	GH104	peptidoglycan lytic transglycosylase (EC 3.2.1.-)
	GH108	N-acetylmuramidase (EC 3.2.1.17)

Supplementary Figures

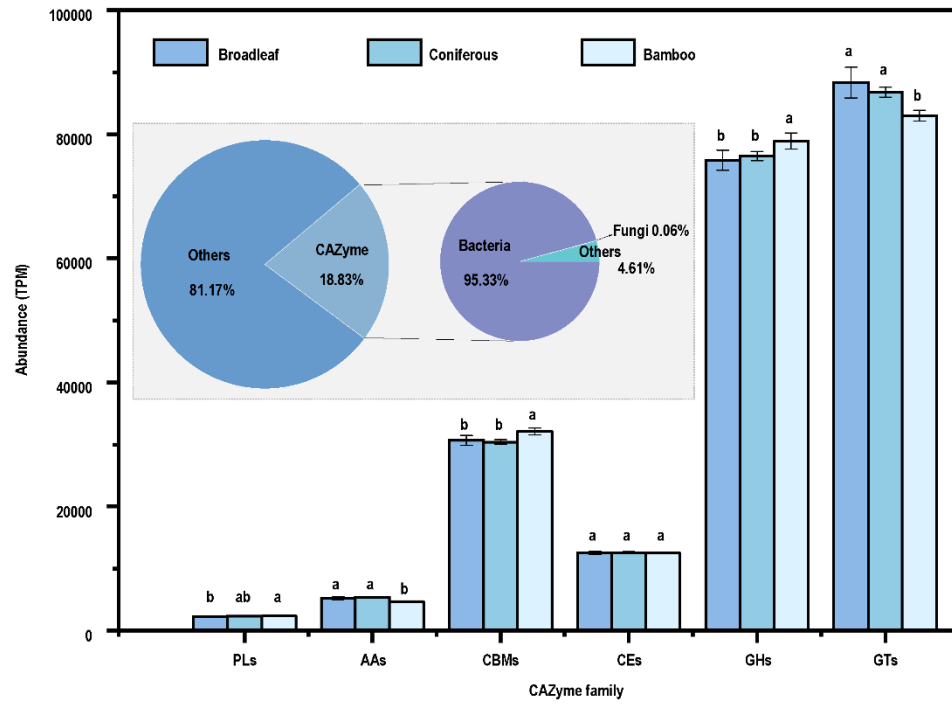


Fig. S1. The abundance of CAZyme families under different forest types. Glycosyl Transferases (GTs), Glycosyl Hydrolases (GHs), Carbohydrate Esterases (CEs), Auxiliary Activities (AAs), Polysaccharide Lyases (PLs), and Carbohydrate-Binding Modules (CBMs). Different lowercase letters represent significant differences at the $p < 0.05$ level.

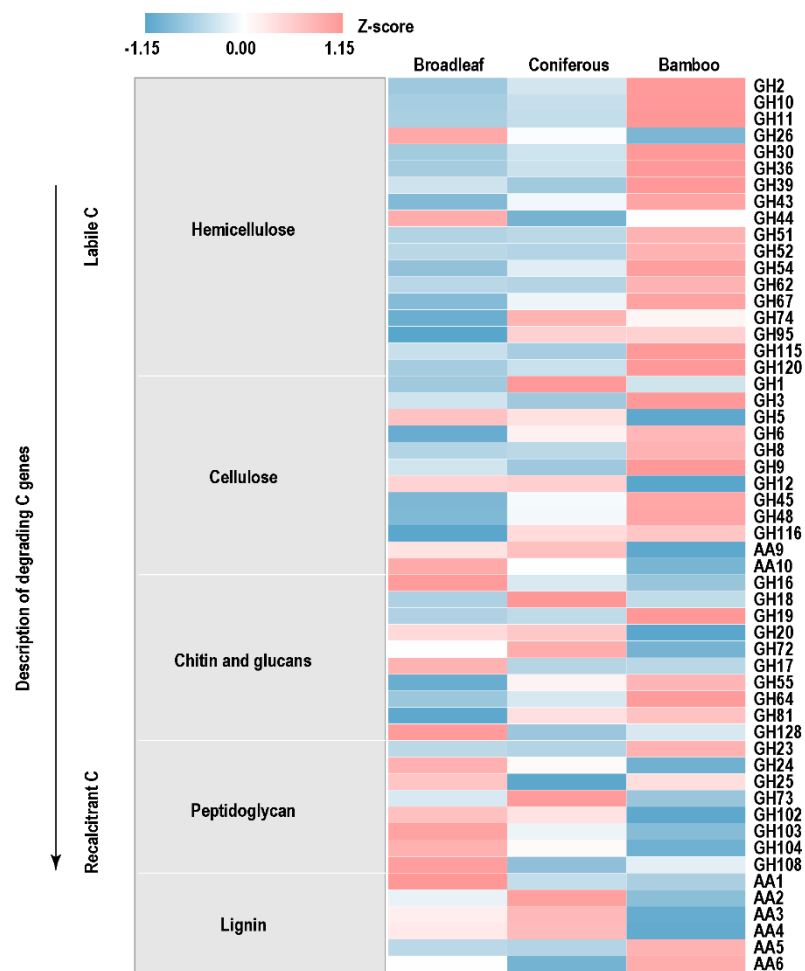


Fig. S2. The relative abundance of specific microbial genes encoding CAZymes that degrade plant- and microbial-derived carbon.



Fig. S3. Comparison of the abundance (Z-score) of specific CAZyme-encoding genes among forest types, based on the Kruskal–Wallis test with Dunn’s post-hoc test (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).

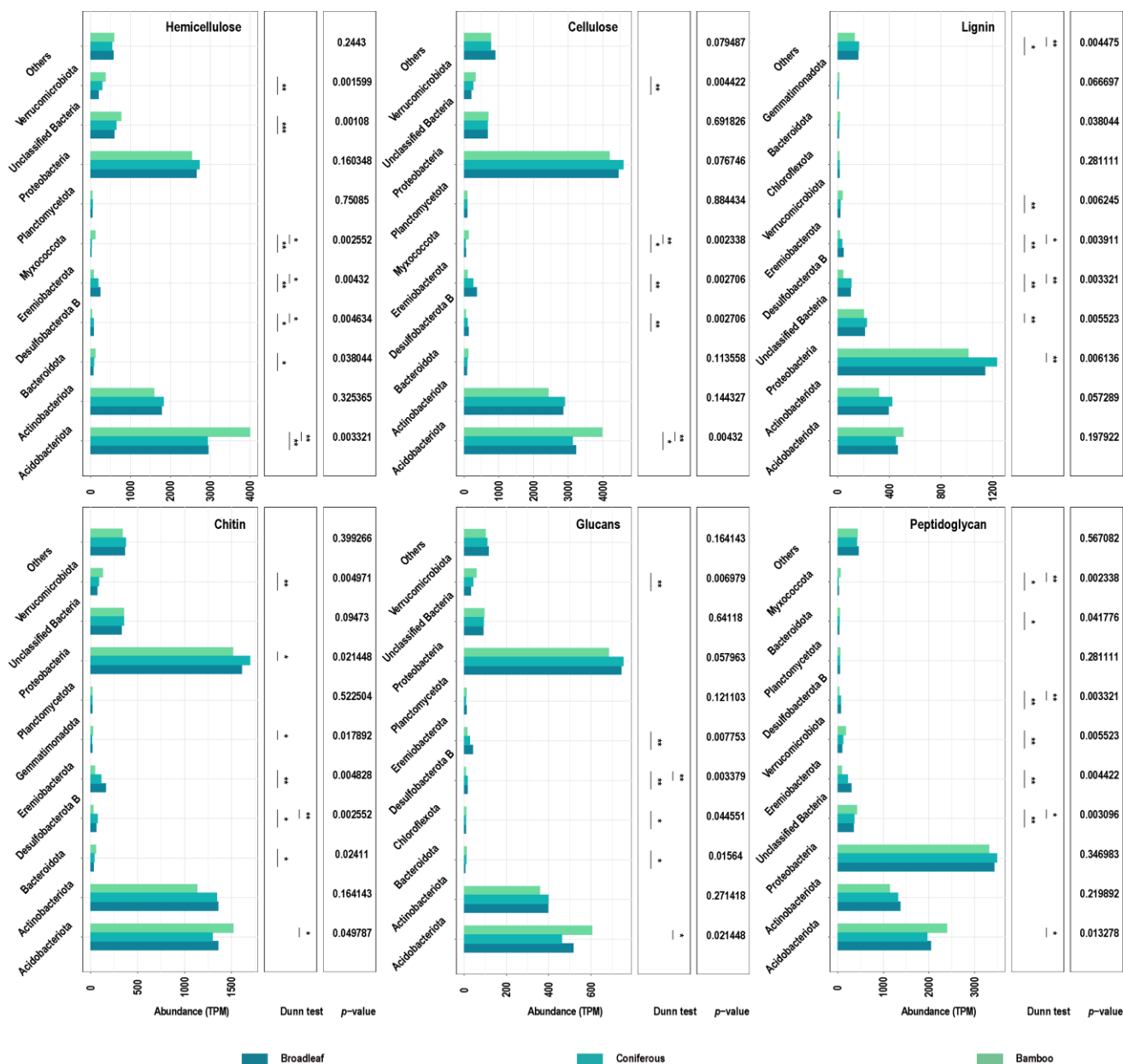


Fig. S4. Abundance of microbial phyla involved in the decomposition of plant-, fungi-, and bacteria-derived components across three forest types, assessed using the Kruskal–Wallis test with Dunn’s post-hoc test ($*p < 0.05$, $**p < 0.01$, $***p < 0.001$).