Supplementary information

Table S1. Predictions of cellular location and specificity of action for glucomannan and arabinoxylan degrading enzymes encoded by the genome of *C. pinensis*. This list represents the theoretical potential for degradation of these polysaccharides by the bacterium, and also shows PULs that contain enzymes predicted to deconstruct mannan or xylan polysaccharides. The shaded rows describe predicted activity profiles for complete PULs.

Predicted substrate	**PUL range**	**Locus tag**	**Annotation**	**Signal peptide?[a]**	**Predicted cellular location[b]**	**MW (kDa)[c]**	**Predicted activity[d]**
Glucomannan; GOs; GMOs	-	Cpin_0323	GH3	SpI	Periplasmic	86.9	β-glucosidase.
Arabinoxylan; Arabinan; Arabinogalactan	0353-0356	Cpin_0353	$GH43_{26}$	SpI	Extracellular	39.0	α-L-arabinofuranosidase.
		Cpin_0355	SusD-like	SpII	Lipoprotein	70.7	Sugar binding
		Cpin_0356	SusC-like	TM	Intrinsic membrane	125.5	Sugar transport
XOs	-	Cpin_1751	$GH43_{28}$	No	Unknown	66.1	β-xylosidase.
Arabinoxylan; AXOs	-	Cpin_1805	$GH43_{18}$	SpII	Lipoprotein	34.6	α-L-arabinofuranosidase.
Glucomannan; GOs; GMOs	-	Cpin_1816	GH3	SpI	Periplasmic/Extracellular	83.1	β-glucosidase.
Mannan	-	Cpin_2125	GHnc; CBM13	SpII	Lipoprotein	53.9	Putative β-mannanase.
MOs	-	Cpin_2275	GH2	SpI	Extracellular	98.9	β-mannosidase.
XOs	-	Cpin_2482	$GH43_{33}$	SpI	Periplasmic	43.2	β-xylosidase.
Glucomannan; MOs; GOs; GMOs	2857-2862	Cpin_2857	SusC-like	TM	Intrinsic membrane	128.1	Sugar transport
		Cpin_2858	SusD-like	SpII	Lipoprotein	72.5	Sugar binding

Predicted substrate	**PUL range**	**Locus tag**	**Annotation**	**Signal peptide?[a]**	**Predicted cellular location[b]**	**MW (kDa)[c]**	**Predicted activity[d]**
		Cpin_2861	GH2; CBM32	SpI	Extracellular	110.5	β-mannosidase.
		Cpin_2862	GH3	No	Periplasmic/Cytoplasmic membrane	83.4	β-glucosidase.
Xylan	-	Cpin_2866	$GH43_{34}$; CBM13	SpII	Lipoprotein	53.5	Xylanase.
Mannan; Chitin; Chito-oligos	3123-3129	Cpin_3123	SusC-like	TM	Intrinsic membrane	125.4	Sugar transport
		Cpin_3124	SusD-like	SpII	Lipoprotein	55.4	Sugar binding
		Cpin_3125	GH89	SpI	Extracellular	83.0	α-N-acetylglucosaminidase.
		Cpin_3128	GT2; GH26	TM	Cytoplasmic membrane	140.2	β-mannanase.
		Cpin_3129	GHnc	No	Unknown	50.1	Unknown.
XOs	-	Cpin_3438	$GH43_{19}$	No	Unknown	35.9	β-xylosidase.
Xylan	-	Cpin_4240	GH10	No	Cytoplasmic	37.3	*Endo*-β-1,4-xylanase. *Probable fragment.*
Mannan	-	Cpin_4289[d]	$GH5_{n.c.}$	SpII	Extracellular/ Lipoprotein (T9SS)	78.5	Putative β-mannanase.
Galactomannan; Gal-MOs	-	Cpin_4392	GH110	SpI	Extracellular	65.9	α-galactosidase
Arabinoxylan; AXOs	4501-4504	Cpin_4501	$GH43_{2}$	SpI	Extracellular	36.0	Arabinoxylan arabinofuranosidase.
		Cpin_4503	SusD-like	SpII	Lipoprotein	69.5	Sugar binding
		Cpin_4504	SusC-like	TM	Intrinsic membrane	119.2	Sugar transport

Predicted substrate	PUL range	Locus tag	Annotation	Signal peptide?[a]	Predicted cellular location[b]	MW (kDa)[c]	Predicted activity[d]
Xyloglucan; Xylan; Galactose-oligos	4556-4559	Cpin_4556	GH35; CBM32	SpI	Extracellular	68.9	β-galactosidase.
		Cpin_4557	$GH30_4$	SpI	Extracellular	54.6	Xylanase or β-fucosidase.
		Cpin_4558	SusD-like	SpII	Lipoprotein	62.4	Sugar binding
		Cpin_4559	SusC-like	TM	Intrinsic membrane	112.6	Sugar transport
MOs	-	Cpin_4811	GH2; CBM32	SpI	Extracellular	108.7	β-mannosidase.
Glucuronoxylan; Xyloglucan; Galactose-oligos	4843-4849	Cpin_4843	GH35	TMH	Cytoplasmic membrane	103.5	β-galactosidase.
		Cpin_4845	GH115	SpI	Extracellular	94.1	Xylan α-1,2-glucuronidase.
		Cpin_4846	$GH43_1$	SpI	Extracellular	41.4	β-xylosidase.
		Cpin_4848	SusD-like	SpII	Lipoprotein	57.8	Sugar binding
		Cpin_4849	SusC-like	TM	Intrinsic membrane	114.0	Sugar transport
XOs	-	Cpin_5150	GH39	SpI	Extracellular	63.4	β-xylosidase.
XOs	-	Cpin_5511	$GH43_{10}$	SpI	Periplasmic	59.6	Xylosidase/arabinofuranosidase.
Galactomannan; Maltose	5641-5648	Cpin_5642	$GH13_{16}$	No	Cytoplasmic	63.1	Trehalose synthase.
		Cpin_5645	GH36	SpI	Extracellular	82.9	α-galactosidase.
		Cpin_5646	GH36	SpI	Extracellular	74.9	α-galactosidase.
		Cpin_5647	SusD-like	SpII	Lipoprotein	58.6	Sugar binding
		Cpin_5648	SusC-like	TM	Intrinsic membrane	115.4	Sugar transport
XOs	-	Cpin_6022	$GH43_{31}$	SpI	Extracellular	35.1	β-xylosidase.

Predicted substrate	**PUL range**	**Locus tag**	**Annotation**	**Signal peptide?[a]**	**Predicted cellular location[b]**	**MW (kDa)[c]**	**Predicted activity[d]**
XOs	-	Cpin_6044	$GH43_8$	SpI/II	Non-cytoplasmic/Lipoprotein	55.9	β-xylosidase.
MOs	-	Cpin_7055	GH2	No	Unknown	96.4	β-mannosidase.
XOs	-	Cpin_7193	GH39	TM	Membrane	60.8	β-xylosidase.

[a]Prediction made using SignalP and LipoP. Key to signal peptides: SpI signal peptide, protein is likely secreted; SpII lipoprotein signal peptide, protein is likely membrane-anchored; TM: protein is predicted to contain a trans-membrane domain; No, no signal peptide, protein is likely cytoplasmic. [b]Prediction made using PSORTb and signal peptide prediction. The presence of a C-terminal domain belonging to TIGRFam family TIGR04183 was also used as an indicator of protein secretion. This domain signifies that a protein is secreted via the Type IX Secretion System (T9SS). For more details on this secretion system, we refer the reader to a recent review by Lasica *et al* (2017). [c]Full-length protein, including all domains and any signal peptides. [d]Predicted activity of the GH domain only. Predictions of enzyme activity based on the typical activity of members of that GH family/sub-family or, where possible, BLAST-identified sequence homology with characterised enzymes from other organisms. On the CAZy database, certain families are divided into sub-families for improved classification: if applicable, these are given in subscript.

Table S2. Predictions of cellular location and specificity of action for β-glucan degrading enzymes encoded by the genome of *C. pinensis*. This list represents the theoretical potential for degradation of β-glucans encoded by the genome, and also shows PULs that contain predicted β-glucan degrading enzymes. The shaded rows describe predicted activity profiles for complete PULs In our model of β-glucan metabolism, we have excluded those enzymes and PULs that were shown in our previous proteomic work to specifically be induced only in the presence of β-mannan polysaccharides. We have also excluded those enzymes and PULs that were not detected in cultures grown on glucose.

Predicted substrate	**PUL range**	**Locus tag**	**Annotation**	**Signal peptide?[a]**	**Predicted cellular location[b]**	**MW (kDa)[c]**	**Predicted activity[d]**	**Proteomic evidence[e]**	**Included in model?**
GOs	-	Cpin_0323	GH3	SpI	Periplasmic	86.9	β-glucosidase.	Not detected	No
GOs	-	Cpin_1816	GH3	SpI	Periplasmic/Extracellular	83.1	β-glucosidase.	Not detected	No
β-(1→4)-D-glucans	-	Cpin_2009	$GH5_2$; CBM32	SpI	Extracellular (T9SS)	81.2	*Endo*-β-1,4-glucanase.	Detected	Yes
Chitin; β-(1→3)-D-glucans	2184-2192	Cpin_2184	GH18; GH18; CBM5; CBM5	SpI	Extracellular (T9SS)	144.6	Chitinase.	PUL detected via 2184, 2186, 2187	Yes
		Cpin_2186	GH18; CBM6	SpI	Extracellular (T9SS)	57.2	Chitinase.		
		Cpin_2187	GH16; CBM6	SpI	Extracellular	42.4	*Endo*-β-1,3-glucanase.		
		Cpin_2191	SusC-like	TM	Intrinsic membrane	135.5	Sugar transport		
		Cpin_2192	SusD-like	SpII	Lipoprotein	54.7	Sugar binding		
β-(1→3)-D-glucans	-	Cpin_2796	GH81;CBM32	SpI	Extracellular (T9SS)	124.8	*Endo*-β-1,3-glucanase.	Mannan only	No
GOs; MOs; GMOs	2845-2856	Cpin_2857	SusC-like	TM	Intrinsic membrane	128.1	Sugar transport	Not detected	No
		Cpin_2858	SusD-like	SpII	Lipoprotein	72.5	Sugar binding		
		Cpin_2861	GH2; CBM32	SpI	Extracellular	110.5	β-mannosidase.		

Predicted substrate	PUL range	Locus tag	Annotation	Signal peptide?[a]	Predicted cellular location[b]	MW (kDa)[c]	Predicted activity[d]	Proteomic evidence[e]	Included in model?
		Cpin_2862	GH3	No	Periplasmic/Cytoplasmic membrane	83.4	β-glucosidase.		
β-(1→3)-D-glucans	-	Cpin_3536	GH64; CBM6	SpI	Extracellular (T9SS)	77.8	*Endo*-β-1,3-glucanase.	Detected	Yes
β-(1→6)-D-glucans	3588-3590	Cpin_3588	SusC-like	TM	Intrinsic membrane	108.8	Sugar transport	Not detected	No
		Cpin_3589	SusD-like	SpII	Lipoprotein	54.3	Sugar binding		
		Cpin_3590	$GH30_3$	SpII	Lipoprotein	53.2	*Endo*-β-1,6-glucanase.		
β-(1→6)-D-glucans	-	Cpin_4356	$GH30_3$	SpII	Extracellular/ Lipoprotein	64.6	*Endo*-β-1,6-glucanase.	Mannan only	Yes
β-(1→3)-D-glucans	5109-5117	Cpin_5109	GH16	SpII	Extracellular/ Lipoprotein	44.2	*Endo*-β-1,3-glucanase.	PUL detected via 5109, 5116, 5117	Yes
		Cpin_5113	SusC-like	TM	Intrinsic membrane	120.6	Sugar transport		
		Cpin_5114	SusD-like	SpII	Lipoprotein	53.5	Sugar binding		
		Cpin_5116	GH16; CBM32	SpI	Extracellular (T9SS)	115.5	Licheninase		
		Cpin_5117	CBM6; CBM6	SpI	Extracellular (T9SS)	122.6	Glucan/xylan binding.		
β-(1→3)-D-glucans	-	Cpin_5709	GH55	SpII	Lipoprotein	79.3	*Endo*-β-1,3-glucanase.	Not detected	No
β-(1→4)-D-glucans	-	Cpin_6252	$GH5_{38}$	SpI	Extracellular	42.7	*Endo*-β-1,4-glucanase.	Not detected	No
β-(1→6)-D-glucans;	6730-6742	Cpin_6730	$GH43_{34}$	SpI	Extracellular	36.5	Arabinan arabinofuranosidase.	PUL detected	Yes, except Cpin_6730
		Cpin_6733	SusC-like	TM	Intrinsic membrane	118.8	Sugar transport		

Predicted substrate	PUL range	Locus tag	Annotation	Signal peptide?[a]	Predicted cellular location[b]	MW (kDa)[c]	Predicted activity[d]	Proteomic evidence[e]	Included in model?
β-(1→3)-D-glucans; AXOs; GOs		Cpin_6734	SusD-like	SpII	Lipoprotein	59.9	Sugar binding	via 6739, 6740	
		Cpin_6735	$GH30_1$	SpI	Extracellular	54.6	β-glucosidase.		
		Cpin_6736	$GH30_3$	SpII	Extracellular/ Lipoprotein	52.6	*Endo*-β-1,6-glucanase.		
		Cpin_6737	GH16	SpII	Lipoprotein	32.1	*Endo*-β-1,3-glucanase.		
		Cpin_6739	SusD-like	SpII	Lipoprotein	56.3	Sugar binding		
		Cpin_6740	SusC-like	TM	Intrinsic membrane	121.6	Sugar transport		
β-(1→4)-D-glucans; MOs	6806-6816	Cpin_6806	GH29	SpI	Cytoplasmic	52.4	α-fucosidase.	Not detected	No
		Cpin_6807	SusD-like	SpII	Lipoprotein	46.6	Sugar binding		
		Cpin_6808	SusC-like	TM	Intrinsic membrane	112.8	Sugar transport		
		Cpin_6813	GH9; CE4	SpI	Extracellular	92	*Endo*-β-1,4-glucanase.		
		Cpin_6816	GH92	SpI/II	Extracellular /Lipoprotein	87.2	α-mannosidase.		

[a]Prediction made using SignalP and LipoP. Key to signal peptides: SpI signal peptide, protein is likely secreted; SpII lipoprotein signal peptide, protein is likely membrane-anchored; TM: protein is predicted to contain a trans-membrane domain; No, no signal peptide, protein is likely cytoplasmic. [b]Prediction made using PSORTb and signal peptide prediction. The presence of a C-terminal domain belonging to TIGRFam family TIGR04183 was also used as an indicator of protein secretion. This domain signifies that a protein is secreted via the Type IX Secretion System (T9SS). For more details on this secretion system, we refer the reader to a recent review by Lasica *et al* (2017). [c]Full-length protein, including all domains and any signal peptides. [d]Predicted activity of the GH domain only. Predictions of enzyme activity based on the typical activity of members of that GH family/sub-family or, where possible, BLAST-identified sequence homology with characterised enzymes from other organisms. On the CAZy database, certain families are divided into sub-families for improved classification: if applicable, these are given in subscript. [e]Some proteins or PULs were detected in a previous proteomic analysis of secretomes.

Table S3. Structural analysis of β-glucan polysaccharides extracted from *Agaricus bisporus* fruiting bodies. To quantify monosaccharides, the polysaccharides were subjected to total acid hydrolysis (2 M TFA, 120 °C, 3 h), reduction ($NaBH_4$) and acetylation, prior to analysis by GC-MS. For linkage analysis, polysaccharides were subjected to methylation, total acid hydrolysis, reduction (NaBD4) and acetylation, before again being analysed by GC-MS.

Partially O-methylated alditol acetates	***Ab* glucan**	**Linkage type[a]**
2,3,4,6-Me_4-Glc	1.2	Glc*p*-(1→
2,4,6-Me_3-Glc	-	→3)-Glc*p*-(1→
2,3,4-Me_3-Glc	98.8	→6)-Glc*p*-(1→
2,4-Me_2-Glc	-	→3,6)-Glc*p*-(1→

[a] Based on derived *O*-methylalditol acetates.

Table S4 a-d. Full data from reducing sugar assays performed on secretomes of *C. pinensis* collected after growth on different types of biomass (presented as histograms in Figure 1 in the main manuscript). Activity is expressed in U/mg protein. Errors (one standard deviation; n = 3) are given in brackets. n.a., no activity detected.

Table S4 a: Day 0	**Growth substrate**		
Assay substrate	**Glucose**	**Spruce wood**	**Fungal fruiting body**
Avicel	2.45×10^{-2} (4.2×10^{-3})	8.34×10^{-2} (1.4×10^{-2})	1.02×10^{-2} (1.4×10^{-3})
Carboxymethylcellulose	n.a.	4.51×10^{-2} (8.5×10^{-3})	n.a.
Barley β-glucan (MLG)	9.85×10^{-2} (1.8×10^{-2})	9.91×10^{-2} (2.0×10^{-2})	1.24×10^{-1} (7.1×10^{-3})
A.b extract	9.27×10^{-2} (1.6×10^{-2})	3.14×10^{-1} (4.2×10^{-2})	1.61×10^{-1} (2.1×10^{-2})
Tamarind xyloglucan	1.14×10^{-1} (9.2×10^{-3})	9.23×10^{-2} (2.8×10^{-3})	n.a.
Curdlan	n.a.	n.a.	6.44×10^{-2} (1.4×10^{-2})
Scleroglucan	n.a.	8.48×10^{-2} (6.4×10^{-3})	1.71×10^{-1} (2.8×10^{-2})
Lichenan	4.16×10^{-1} (2.1×10^{-2})	4.59×10^{-1} (6.4×10^{-2})	1.01×10^{-1} (3.5×10^{-2})
Konjac glucomannan	3.11×10^{-1} (1.4×10^{-2})	4.57×10^{-1} (4.2×10^{-2})	4.07×10^{-2} (2.5×10^{-2})
Carob galactomannan	8.06×10^{-2} (4.2×10^{-3})	8.05×10^{-2} (1.2×10^{-2})	4.10×10^{-2} (4.2×10^{-3})
Wheat arabinoxylan	2.43×10^{-1} (3.5×10^{-2})	1.72×10^{-1} (2.8×10^{-2})	n.a.
Birch glucuronoxylan	3.27×10^{-2} (9.9×10^{-3})	8.33×10^{-2} (9.9×10^{-3})	n.a.
Larch arabinogalactan	8.21×10^{-2} (6.4×10^{-3})	1.66×10^{-1} (7.1×10^{-3})	9.27×10^{-2} (5.3×10^{-3})
Sugar beet arabinan	n.a.	4.47×10^{-2} (8.5×10^{-3})	n.a.
Chitin	9.81×10^{-2} (2.8×10^{-3})	2.75×10^{-1} (5.7×10^{-2})	2.79×10^{-1} (4.9×10^{-2})
Chitosan	4.33×10^{-2} (9.9×10^{-3})	1.36×10^{-1} (4.9×10^{-2})	6.22×10^{-2} (3.3×10^{-2})

Table S4 b: Day 3	**Growth substrate**		
Assay substrate	**Glucose**	**Spruce wood**	**Fungal fruiting body**
Avicel	1.11×10^{-3} (7.1×10^{-5})	3.18×10^{-1} (5.7×10^{-2})	1.50×10^{-1} (2.8×10^{-2})
Carboxymethylcellulose	2.24×10^{-3} (5.7×10^{-4})	n.a.	2.14×10^{-1} (5.7×10^{-2})
Barley β-glucan (MLG)	6.33×10^{-3} (8.5×10^{-4})	1.16×10^{-1} (3.5×10^{-2})	1.51×10^{-4} (4.1×10^{-2})
A.b extract	4.42×10^{-3} (1.3×10^{-3})	4.55×10^{-1} (5.7×10^{-2})	3.31×10^{-1} (2.8×10^{-2})
Tamarind xyloglucan	4.12×10^{-4} (2.9×10^{-4})	1.34×10^{-1} (4.9×10^{-2})	1.04×10^{-2} (7.1×10^{-4})
Curdlan	4.58×10^{-4} (1.7×10^{-4})	n.a.	6.09×10^{-2} (1.8×10^{-2})
Scleroglucan	1.37×10^{-4} (8.8×10^{-5})	7.01×10^{-2} (1.8×10^{-2})	3.10×10^{-2} (1.9×10^{-2})
Lichenan	1.84×10^{-3} (2.8×10^{-4})	1.14×10^{-1} (3.5×10^{-2})	4.07×10^{-1} (1.5×10^{-1})
Konjac glucomannan	3.72×10^{-3} (2.8×10^{-4})	2.24×10^{-1} (4.2×10^{-2})	1.08×10^{-1} (1.4×10^{-2})
Carob galactomannan	5.18×10^{-2} (3.3×10^{-2})	n.a.	n.a.
Wheat arabinoxylan	1.11×10^{-4} (7.8×10^{-5})	1.01×10^{-1} (1.4×10^{-2})	1.13×10^{-2} (4.9×10^{-3})
Birch glucuronoxylan	1.53×10^{-4} (1.1×10^{-4})	1.45×10^{-1} (1.4×10^{-2})	8.23×10^{-3} (4.8×10^{-3})
Larch arabinogalactan	8.00×10^{-4} (5.7×10^{-4})	1.75×10^{-1} (1.4×10^{-2})	5.50×10^{-2} (1.6×10^{-2})
Sugar beet arabinan	n.a.	3.24×10^{-2} (1.8×10^{-2})	7.53×10^{-3} (1.1×10^{-3})
Chitin	1.74×10^{-3} (8.5×10^{-4})	4.39×10^{-1} (2.8×10^{-2})	1.71×10^{-1} (1.1×10^{-1})
Chitosan	6.22×10^{-3} (3.1×10^{-3})	9.38×10^{-2} (1.2×10^{-2})	2.86×10^{-2} (2.1×10^{-2})

Table S4 c: Day 5	**Growth substrate**		
Assay substrate	**Glucose**	**Spruce wood**	**Fungal fruiting body**
Avicel	7.05×10^{-4} (5.0×10^{-4})	1.56×10^{-1} (1.4×10^{-2})	1.09×10^{-2} (5.7×10^{-3})
Carboxymethylcellulose	1.81×10^{-3} (2.8×10^{-4})	n.a.	4.31×10^{-2} (1.2×10^{-2})
Barley β-glucan (MLG)	6.42×10^{-3} (4.9×10^{-4})	n.a.	2.61×10^{-1} (3.5×10^{-2})
A.b extract	3.70×10^{-3} (8.5×10^{-4})	3.81×10^{-1} (6.4×10^{-2})	1.28×10^{-1} (4.2×10^{-2})
Tamarind xyloglucan	1.09×10^{-3} (7.1×10^{-5})	1.93×10^{-1} (4.2×10^{-2})	2.51×10^{-3} (1.6×10^{-3})
Curdlan	4.64×10^{-3} (7.8×10^{-4})	n.a.	3.28×10^{-2} (1.1×10^{-2})
Scleroglucan	9.76×10^{-4} (3.4×10^{-4})	2.27×10^{-2} (1.2×10^{-2})	2.71×10^{-2} (4.2×10^{-3})
Lichenan	5.41×10^{-3} (1.3×10^{-3})	3.67×10^{-1} (1.3×10^{-1})	7.59×10^{-2} (1.6×10^{-2})
Konjac glucomannan	3.61×10^{-3} (1.5×10^{-3})	2.13×10^{-1} (7.8×10^{-2})	3.18×10^{-2} (1.6×10^{-2})
Carob galactomannan	5.37×10^{-4} (3.8×10^{-4})	5.12×10^{-2} (2.5×10^{-5})	3.28×10^{-3} (8.5×10^{-4})
Wheat arabinoxylan	2.04×10^{-3} (2.1×10^{-4})	1.52×10^{-1} (4.9×10^{-2})	2.08×10^{-3} (9.9×10^{-4})
Birch glucuronoxylan	1.85×10^{-4} (1.3×10^{-4})	5.02×10^{-2} (2.8×10^{-2})	n.a.
Larch arabinogalactan	1.17×10^{-3} (2.1×10^{-4})	2.05×10^{-1} (7.1×10^{-2})	1.36×10^{-2} (3.5×10^{-3})
Sugar beet arabinan	n.a.	4.88×10^{-3} (2.8×10^{-3})	n.a.
Chitin	1.99×10^{-3} (7.1×10^{-4})	2.06×10^{-1} (8.9×10^{-2})	5.54×10^{-2} (9.2×10^{-3})
Chitosan	n.a.	4.22×10^{-2} (2.3×10^{-2})	1.38×10^{-2} (7.8×10^{-3})

Table S4 d: Day 8	**Growth substrate**		
Assay substrate	**Glucose**	**Spruce wood**	**Fungal fruiting body**
Avicel	8.74×10^{-4} (6.2×10^{-4})	2.26×10^{-2} (3.5×10^{-3})	2.26×10^{-2} (9.1×10^{-3})
Carboxymethylcellulose	1.11×10^{-3} (4.9×10^{-4})	1.31×10^{-1} (4.2×10^{-2})	1.31×10^{-1} (1.4×10^{-2})
Barley β-glucan (MLG)	n.a.	6.35×10^{-1} (1.8×10^{-1})	6.35×10^{-1} (3.5×10^{-2})
A.b extract	2.54×10^{-3} (7.8×10^{-4})	1.45×10^{-1} (1.4×10^{-2})	1.45×10^{-1} (2.1×10^{-2})
Tamarind xyloglucan	n.a.	n.a.	n.a.
Curdlan	4.73×10^{-4} (3.3×10^{-4})	7.41×10^{-2} (1.8×10^{-2})	7.41×10^{-2} (1.1×10^{-2})
Scleroglucan	7.63×10^{-4} (5.4×10^{-4})	2.79×10^{-2} (1.3×10^{-2})	2.79×10^{-2} (9.2×10^{-3})
Lichenan	2.25×10^{-3} (8.5×10^{-4})	1.84×10^{-1} (1.1×10^{-1})	1.84×10^{-1} (2.1×10^{-2})
Konjac glucomannan	n.a.	9.54×10^{-2} (5.3×10^{-3})	9.54×10^{-2} (1.3×10^{-2})
Carob galactomannan	n.a.	n.a.	n.a.
Wheat arabinoxylan	n.a.	n.a.	n.a.
Birch glucuronoxylan	n.a.	1.28×10^{-3} (3.5×10^{-4})	1.28×10^{-3} (2.1×10^{-4})
Larch arabinogalactan	n.a.	1.45×10^{-2} (2.8×10^{-3})	1.45×10^{-2} (4.2×10^{-3})
Sugar beet arabinan	n.a.	3.31×10^{-3} (1.4×10^{-4})	3.31×10^{-3} (2.1×10^{-3})
Chitin	1.64×10^{-3} (8.5×10^{-4})	6.49×10^{-2} (1.3×10^{-2})	6.49×10^{-2} (2.4×10^{-2})
Chitosan	8.18×10^{-4} (5.8×10^{-4})	9.41×10^{-3} (4.2×10^{-4})	9.41×10^{-3} (3.3×10^{-3})

Table S5. Full data from reducing sugar assays performed on secretomes of *C. pinesis* collected after growth on isolated polysaccharides (presented as a histogram in Figure 2 in the main manuscript). Activity is expressed in U/mg protein. Errors (one standard deviation; n = 2) are given in brackets. n.a., no activity detected.

	Growth substrate							
Assay substrate	**Glucose**	**Carboxy-methylcellulose**	**Barley β-glucan**	***A.b* extract**	**Curdlan**	**Scleroglucan**	**Konjac glucomannan**	**Wheat arabinoxylan**
Barley β-glucan	n.a.	0.38 (3.5 X 10^{-2})	0.075 (1.8 X 10^{-2})	0.041 (1.5 X 10^{-3})	0.013 (5.9 X 10^{-3})	0.055 (1.3 X 10^{-2})	0.041 (1.6 X 10^{-2})	0.073 (4.6 X 10^{-3})
Tamarind xyloglucan	n.a.	n.a.	0.023 (8.0 X 10^{-3})	n.a.	n.a.	n.a.	0.012 (3.6 X 10^{-3})	n.a.
Konjac glucomannan	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	0.22 (3.6 X 10^{-2})	0.023 (2.0 X 10^{-3})
Carob galactomannan	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	0.17 (2.5 X 10^{-2})	n.a.
Wheat arabinoxylan	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	0.046 (5.6 X 10^{-3})	0.094 (2.8 X 10^{-3})
Birch glucuronoxylan	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	0.023 (3.2 X 10^{-3})	0.30 (1.8 X 10^{-2})
Larch arabinogalactan	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n-a-
Sugar beet arabinan	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.

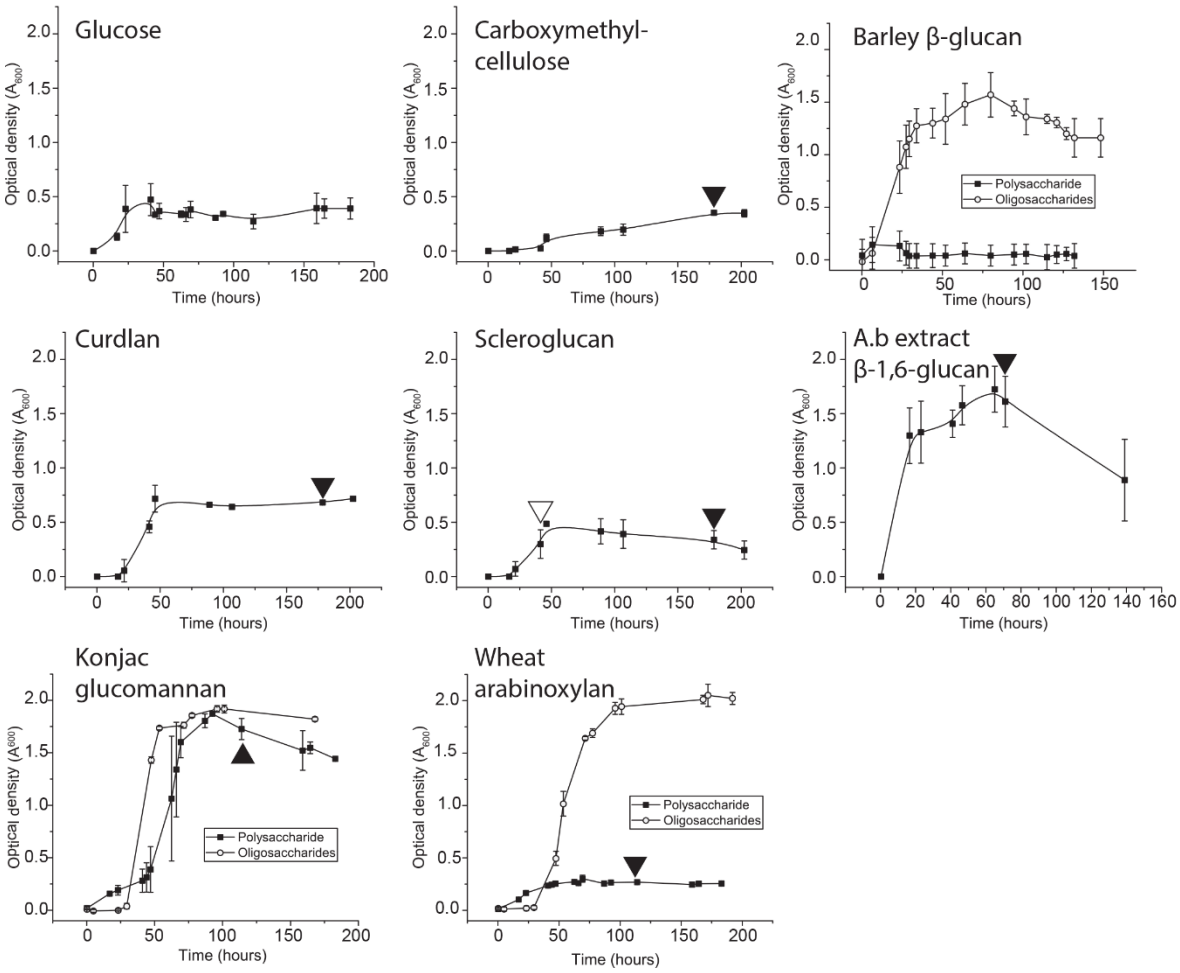

Figure S1. Growth curves for *C. pinensis* incubated with various isolated polysaccharides. Growth substrates are indicated on the graphs. A.b extract is a linear β-1,6-glucan we extracted from fungal fruiting body. Three biological replicate experiments were performed. Curves for growth on glucose, konjac glucomannan polysaccharide, and wheat arabinoxylan polysaccharide were previously published in McKee and Brumer, 2015. Filled arrow heads on the growth curves indicate the point at which oligosaccharide concentration in the medium was quantified. For the scleroglucan cultures, ESI-MS-based sequencing of residual oligosaccharides was performed at both indicated time-points (empty and filled arrow heads).

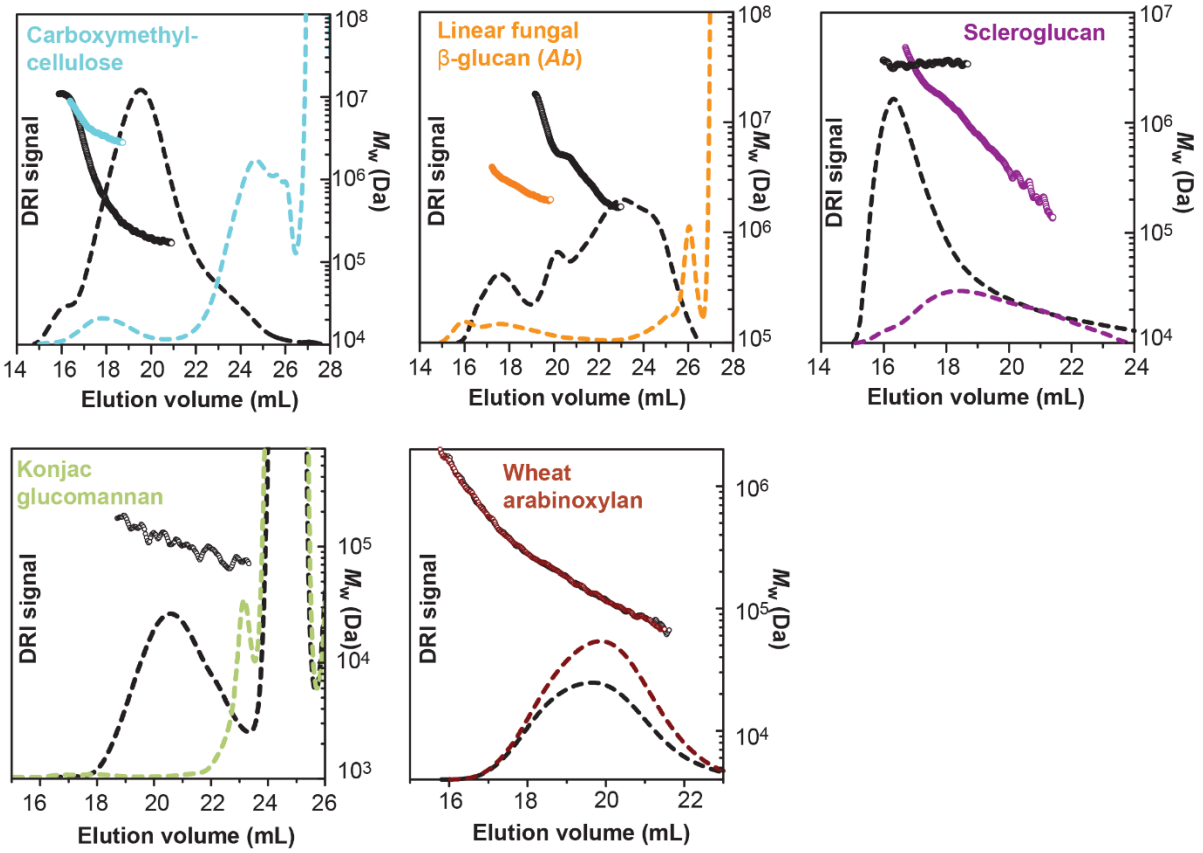

Figure S2. SEC-MALLS analysis of liquid medium in the early (black) and late (coloured) stages of bacterial growth. The differential refractive index (DRI) is a measure of peak homogeneity, and is used in combination with the SEC spectrum to calculate MW, taking polydispersity of MW into account. SEC spectra are shown in dashed lines, while DRI spectra are shown in solid colour.

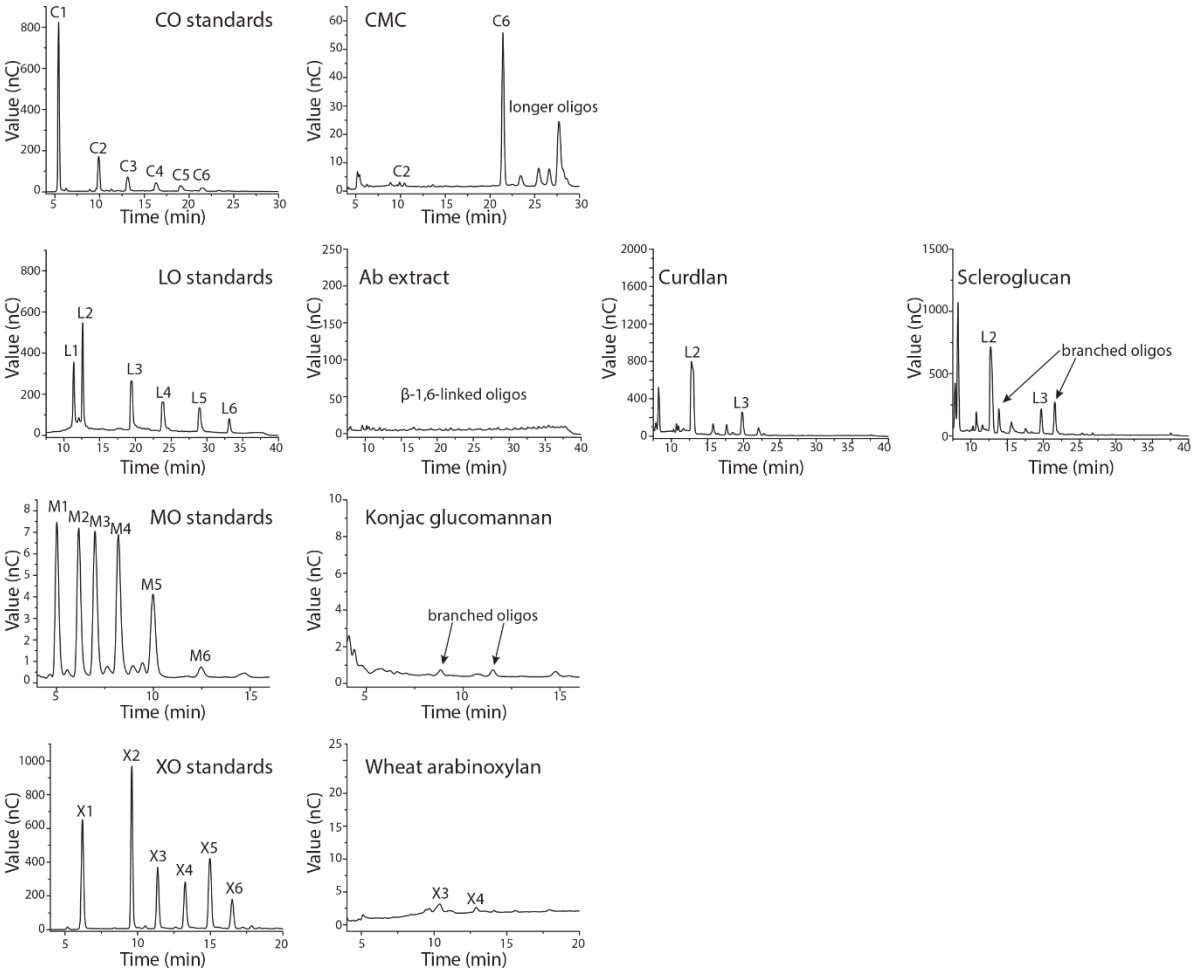

Figure S3. Representative sample chromatograms showing HPAEC-PAD analysis of oligosaccharides residual in growth media after cultivation of *C. pinensis* with the indicated polysaccharides. Oligosaccharides were identified wherever possible by comparing elution times with those of known standards, shown here in separate chromatograms. Oligosaccharides were quantified by comparing peak area to that of the most closely eluting standard of known concentration. CO: cellulose oligosaccharides. LO: laminarin oligosaccharides. MO: mannan oligosaccharides. XO: xylan oligosaccharides.

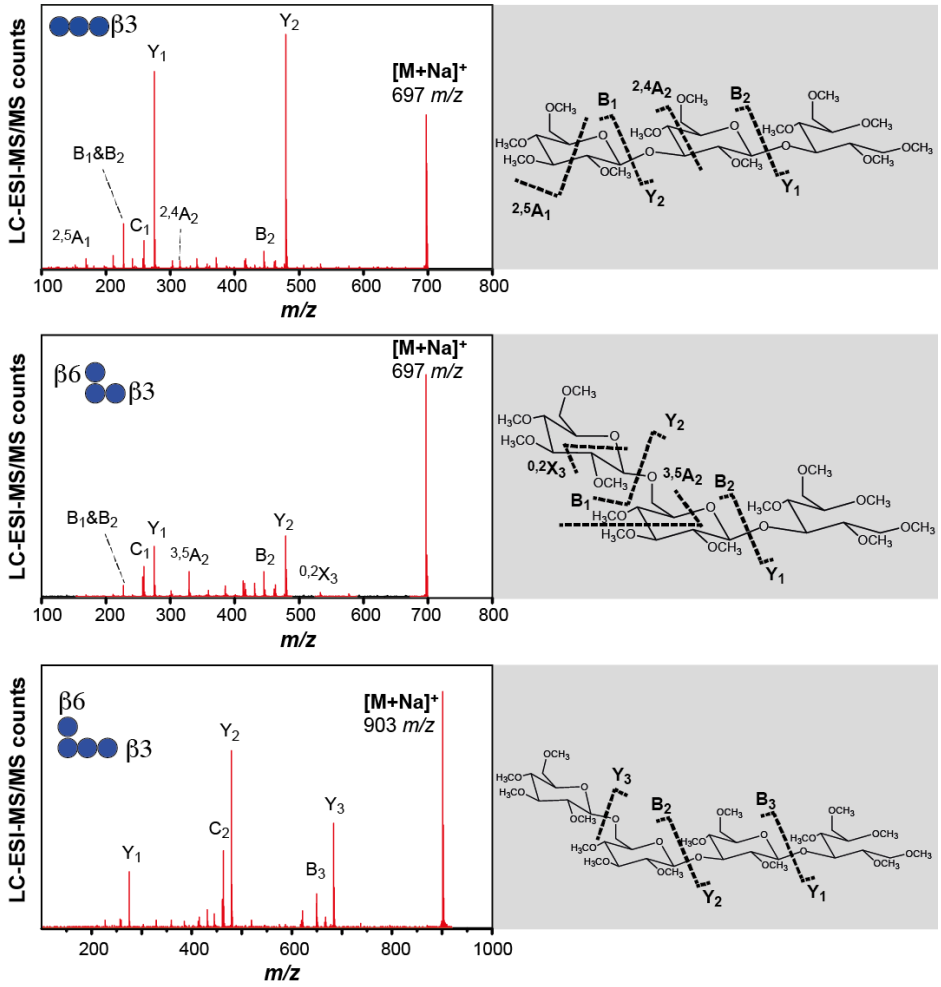

Figure S4. ESI-MS analysis of residual gluco-oligosaccharides (structures represented with blue circles) following deconstruction of scleroglucan in growth medium.

Supplementary references

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