Comparative analysis of CAZymes from *Trichoderma longibrachiatum* LMBC 172 cultured with three different carbon sources: sugarcane bagasse, tamarind seeds, and hemicellulose simulation

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Table S1. Comprehensive LC-MS/MS secretome analysis for 18 proteins found using the simulation of hemicellulose and sugarcane bagasse classified according to which biomass they degrade.

Degraded biomass	iBAQ (a) Hemicellulose simulation	iBAQ (a) Sugarcane bagasse	Protein IDs (b)	Family	MS/MS View: Identified Proteins	Molecular Weight (kDa) (c)
cellulose	2.78×10^7	1.50×10^8	A0A2T3YZK3	CBM24	carbohydrate-binding module	50
chitin	6.19×10^6	6.81×10^5	G9MM35	GH18	chitinase	37
chitosan	3.75×10^6	7.49×10^7	A0A6V8R358	GH75	*endo*-chitosanase	52
hemicellulose	7.16×10^9	2.32×10^7	KAH6607018.1	GH3	glycoside hydrolase	77
hemicellulose	3.04×10^9	1.26×10^6	A0A0W7W2I7	GH11	*endo*-1,4-β-xylanase	78
hemicellulose	9.24×10^8	3.54×10^6	A0A6V8R6T7	GH16	glycoside hydrolase	45
hemicellulose	2.72×10^8	2.66×10^6	A0A2N1LZN6	CE5	acetylxylan esterase	17
hemicellulose	1.47×10^8	1.37×10^7	A0A6V8QLB7	GH16	glycoside hydrolase	49
hemicellulose	9.67×10^7	1.47×10^7	A0A6V8QQ21	GH55	glucan *endo*-1,3-β-glucosidase	64
hemicellulose	8.33×10^7	8.33×10^6	A0A6V8R8V9	GH71	mutanase	88
hemicellulose	6.35×10^7	1.86×10^6	A0A395NFT7	CE5	acetylxylan esterase	56
hemicellulose	3.61×10^7	3.87×10^5	A0A2T4BLF2	GH3	xylan 1,4-β-xylosidase	93
hemicellulose	1.98×10^7	1.94×10^7	A0A2T3YXG1	GH5	mannan *endo*-	28

					1,4-α-mannosidase	
hemicellulose	1.81 x 10^7	7.89 x 10^5	A0A6V8QV85	GH79	β-glucuronidase	39
hemicellulose	7.32 x 10^6	3.17 x 10^6	A0A2T3YRE8	GH5	glycoside hydrolase	41
pectin	4.36 x 10^7	2.64 x 10^6	G9MN58	GH28	glycoside hydrolase	47
peptidoglycan	5.01 x 10^8	7.90 x 10^7	A0A6V8QPT2	GH25	lysozyme	57
trehalose	1.18 x 10^8	1.49 x 10^7	A0A6V8QL82	CBM32	α-trehalase	26

(a) The iBAQ corresponds to the sum of all the peptides intensities divided by the number of observable peptides of a protein.

(b) Accession number with protein information and family information were obtained from UniProt/Swiss-Prot database or NCBI database.

(c) Hypothetical molecular weight of the proteins.

Table S2. Comprehensive LC-MS/MS secretome analysis for 11 proteins found using the simulation of hemicellulose and tamarind seeds classified according to which biomass they degrade.

Degraded biomass	iBAQ (a) Hemicellulose simulation	iBAQ (a) Tamarind seeds	Protein IDs (b)	Family	MS/MS View: Identified Proteins	Molecular Weight (kDa) (c)
cellulose	1.02×10^9	5.53×10^5	A0A6V8R0L8	GH7	endoglucanase 1	96
cellulose	1.31×10^6	3.80×10^6	A0A0W7VA76	GH7	exoglucanase	82
hemicellulose	2.00×10^{10}	1.33×10^8	A0A2T3YS04	GH11	*endo*-1,4-β-xylanase	85
hemicellulose	6.49×10^7	2.87×10^5	A0A8G0LD67	GH54	α-L-arabinofuranosidase	38
hemicellulose	5.69×10^7	4.98×10^6	A0A2T4BFA3	GH76	mannan *endo*-1,6-α-mannosidase	31
hemicellulose	3.35×10^7	7.89×10^5	A0A6V8QKA4	GH17	glucan *endo*-1,3-β-glucosidase	94
hemicellulose	1.56×10^7	1.93×10^6	G9NYH4	GH54	α-L-arabinofuranosidase	57
hemicellulose	1.06×10^7	7.51×10^6	G9NNW8	GH54	α-L-arabinofuranosidase	86
hemicellulose	7.07×10^6	7.70×10^5	G9NE77	GH11	*endo*-1,4-β-xylanase	53
hemicellulose	7.03×10^6	3.23×10^6	A0A2T3ZA57	GH64	glycoside hydrolase	90
hemicellulose	5.79×10^6	5.96×10^6	A0A2P4ZLU3	GH30	glycoside hydrolase	41

(a) The iBAQ corresponds to the sum of all the peptides intensities divided by the number of observable peptides of a protein.

(b) Accession number with protein information and family information were obtained from UniProt/Swiss-Prot database or NCBI database.

(c) Hypothetical molecular weight of the proteins.

Table S3. Comprehensive LC-MS/MS secretome analysis for 15 proteins found using sugarcane bagasse and tamarind seeds classified according to which biomass they degrade.

Degraded biomass	iBAQ (a) Sugarcane bagasse	iBAQ (a) Tamarind seeds	Protein IDs (b)	Family	MS/MS View: Identified Proteins	Molecular Weight (kDa) (c)
carboxylic ester	1.58×10^8	1.36×10^6	A0A2T3ZAT8	CE1	carboxylic ester hydrolase	83
cellulose	3.57×10^8	2.49×10^8	A0A6V8R8Q4	AA9	lytic polysaccharide monooxygenase	43
cellulose	3.87×10^7	8.62×10^5	G9P6W2	GH3	β-glucosidase	47
chitin	7.76×10^7	3.49×10^5	A0A2T3YV63	GH18	glycoside hydrolase	40
chitin	2.03×10^7	2.76×10^5	A0A6V8QK33	GH18	chitinase	45
fucose	4.76×10^7	1.13×10^8	A0A6V8R1E0	GH95	α-L-fucosidase 2	43
hemicellulose	2.83×10^9	1.43×10^8	G0RA32	GH10	*endo*-1,4-β-xylanase 3	85
hemicellulose	1.40×10^9	5.88×10^7	A0A2T3YQI3	CE1	feruloyl esterase C	48
hemicellulose	3.84×10^8	2.93×10^6	A0A6V8QK39	GH47	mannosyl-oligosaccharide α-1,2-mannosidase	51
hemicellulose	4.37×10^7	1.37×10^6	KAH6607020.1	GH3	glycoside hydrolase	87
hemicellulose	2.37×10^8	1.36×10^6	A0A2T3ZLU6	GH3	glycoside hydrolase	182
hemicellulose	6.53×10^8	6.52×10^5	A0A2T3YRW0	GH93	glycoside hydrolase	25
hemicellulose	1.10×10^7	5.21×10^5	A0A6V8R6A9	GH30	*endo*-1,6-β-D-glucanase	99

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hemicellulose	1.53×10^6	5.01×10^5	A0A2T3YRF3	GH3	glycoside hydrolase	51
hemicellulose	3.72×10^8	9.70×10^4	A0A2T3YRE9	GH39	glycoside hydrolase	95

(a) The iBAQ corresponds to the sum of all the peptides intensities divided by the number of observable peptides of a protein.

(b) Accession number with protein information and family information were obtained from UniProt/Swiss-Prot database or NCBI database.

(c) Hypothetical molecular weight of the proteins.