Appendix A. Supplementary tables

Name (with website)	Description	Reference
CAZy (Carbohydrate Active Enzymes database; http://www.cazy.org/)	Database classifying catalytic and functional domains of enzymes degrading, modifying, creating glycosidic bonds	SR[1]
e-Fungi (http://www.cs.man.ac.uk/~cornell/eFungi/database.html)	Database allowing comparative studies of fungal genomes	SR[2]
Fungal Transcription Factor Database (FTFD; http://ftfd.snu.ac.kr/)	Database archiving fungal transcription factors and enabling comparative phylogenetic studies	SR[3]
The Seoul National University Genome Browser (SNUGB; http://genomebrowser.snu.ac.kr/.)	Platform enabling comparative and functional fungal genomics	SR[4]
Comparative Fungal Genomics Platform (CFGP; http://cfgp.snu.ac.kr/)	Comparative genomics platform enabling searches across different species	SR[5, 6]

	simultaneously	
Fungal Secretome Database (http://fsd.snu.ac.kr/intro.php)	Archive of fungal secreted proteins allowing also data analysis	SR[7]
Fungal Growth Database (www.fung-growth.org)	Repository of fungal growth profiles on different C sources derived from plant biomass	-
FungiDB (http://FungiDB.org)	Database for fungal functional genomics	SR[8]
Fungal PCWDE Database (http://pcwde.riceblast.snu.ac.kr/)	Platform archiving fungal wall degrading enzymes enabling also data analysis	SR[9]
MycoCosm (http://jgi.doe.gov/fungi)	Portal entirely dedicated to comparative genomics of fungi and promoting community participation	SR[10]
Fungal peroxidase database (fPoxDB; http://peroxidase.riceblast.snu.ac.kr/)	Database enabling comparative genomics of fungal peroxidases	SR[11]

*myco*CLAP-Characterized Lignocellulose-Active Proteins of Fungal Origin (https://mycoclap.fungalgenomics.ca/mycoCLAP/	Database of fungal lignocellulose-active proteins which have been characterized from the biochemical point of view	SR[12]
1000 Fungal Genomes Project (1KFG; http://1000.fungalgenomes.org/home/)	Project aiming at sequencing more than 1000 fungal genomes	-
Aspergillus Genome Database (AspGD; http://www.aspgd.org/)	Database enabling comparative genomics of *Aspergillii*	-

Supplementary Table 1. Summary of some of the available databases/platforms for fungal cross-comparative studies. Details concerning their description and references are provided. SR, Supplementary Reference.

Organism	Enzyme	k_{cat} (min^{-1})	T$_{opt}$ (°C)	pH$_{opt}$	Salt	Domain/ Kingdom	Ref
Metagenomic library (Himalayan soil)	Endo-cellulase^{P}	1,500 (CMC) (28 °C)	28-30	5.0	N/A	Bacteria	SR [13]
Pseudoalteromonas haloplanktis *Streptomyces* sp.	Xylanase^{P} Xylanase^{M}	31,000 (10 °C) 3,600 (10 °C)	35 50	N/A	N/A		[120]
P. haloplanktis *Erwinia chrysanthemi* (*Dickeya dadantii*)	Endo-cellulase^{P} Endo-cellulase^{T}	11(pNPC) 0.6 (pNPC) (4 °C)	45 55	N/A	N/A		SR [14]
Bacillus subtilis	Endo-cellulase^{PE}	14,760 (CMC)^{WT} 26,220 (CMC)$^{SDM-T}$	60	4.0-6.0	N/A		SR [15, 16]
Bacillus aquimaris	Endo-cellulase^{AL}	N/A	45	11.0	N/A		SR [17]
Thermoascus aurantiacus	Endo-cellulase^{T}	239 (CMC)^{WT} 995 (CMC)^{SDM} (70 °C)	70^{WT} 70^{SDM}	5.0^{WT} 5.0^{SDM}	N/A		[119]
Geobacillus thermoleovorans	Xylanase^{PE}	16,834 (xylan) 80 °C	80 (40–100)	8.5 (6-12)	N/A		SR [18]
Bacillus pumilus	Endo-cellulase^{AL}	N/A	50	10.0	N/A		SR [19]
Dictyoglomus thermophilum	Endo-cellulase^{H,T}	N/A	50-85	5.0	2-4 M		SR [20]
Caldicellulosiruptor bescii	Endo-cellulase, Hemicellulase System^{T}	N/A	75 (Grass, Avicel) 85 (CMC)85 (xylan)	5.0-6.0	N/A		SR [21]
Thermomonospora fusca	Xylanase^{T}	N/A	80	6.0	N/A		SR [22]
Thermoascus aurantiacus SL16W	Xylanase$^{T/ILT}$	N/A	75	4.5	N/A		SR [23]
Zunongwangia profunda	Xylanase$^{PE/ILT}$	2836 (- NaCl) 4820 (+ 3M NaCl)	30	6.5	3-5 M		SR [24]
Gracilibacillus sp.	Xylanase^{PE}	N/A	60 (50-70)	7.5 (5.0-10.0)	0-30 %		SR [25]
Fervidobacterium gondwanense	Endo-cellulase, Xylanase fusion enzyme^{T}	Higher activity than individual enzymes	80 (β-glucan) 70 (xylan)	6.0	N/A		[112]
Halorhabdus utahensis CBH1	Endo-cellulase^{PE}	N/A	80 (5 M NaCl)	9.0-10.0	5M (80 °C)	Archaea	SR [26]
Pyrobaculum-like, *Thermofilum*-like, *Ignisphaera*-like	Endo-cellulase^{PE}	N/A	109 (CMC, Avicel)	6.8	2.5-3.5 M		[80]
Thermotoga maritima	Endo-cellulase^{HT}	47,460 (βlucan)^{WT} 69,300 (β-glucan)^{SDM} (85 °C)	85^{WT} 100^{SDM}	N/A	N/A		[118]
Sulfolobus solfataricus/ Thermotoga maritima	Endo-cellulase^{PE}	30 (hexasaccharide) (80 °C)	80	1.8	N/A		SR [27]
Scopulariopsis sp.	Xylanase^{T}	95,000 (40 °C)	50	N/A	N/A	Fungi	[120]
Trichoderma reesei	β-glucosidase^{T}	3,090 (cellobiose) (50 °C)	65-70	4.6	N/A		SR [28]
Talalaromyces emersonii	β-glucosidase^{PE}	N/A	72	4.0	N/A		SR [29]
Aspergillus	Endo-cellulase,	N/A	70	2.0	N/A		SR

terreus M11	β-glucosidase^{PE}		70	3.0			[30]
Trichoderma viride	Endo-cellulase^{M}	574 (CMC) 108 (Avicel) (50 °C)	60	6.0	N/A		SR [31]
T. emersonii	Exo-cellulase^{T}	31 (Mul) (22 °C)	65	4.0-5.0	N/A		SR [32]
Penicillium citrinum YS40-5	β-glucosidase^{PE}	N/A	70	5.0	N/A		SR [33]
Humicola grisea Var *thermoidea*	Exo-cellulase^{PE}	N/A	60	8.0	N/A		SR [34]
Aspergillus fumigatus	Endo-cellulase, Exo-cellulase Xylanase^{T}	N/A	70 60 60	3.0 5.0 4.0	N/A		SR [35]

Supplementary Table 2: Catalytic properties of mesophilic, extremophilic and genetically-modified plant cell wall degrading enzymes from bacteria, archaea and fungi. Legend: SR, Supplementary Reference; CMC (amorphous) carboxymethylcellulose; Avicel, crystalline cellulose; Mul, 4-methylumbelliferyl-β-D-galactopyranoside; pNPC, p-nitrophenyl-β-D-cellobioside; P, psychrophilic; T, thermophilic; HT, hyperthermophilic; PE, polyextremophilic; M, mesophilic; ILT, ionic liquid-tolerant; AL, alkaliphilic; H, halophilic; WT, wild-type; SDM, site-directed mutant; SDM-T, truncated mutant.

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