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Supplementary material

EXTRACELLULAR DIFFERENTIAL PROTEOME ANALYSIS OF SUBSTRATES OF DIFFERENT LIGNIN MODEL COMPOUNDS DEGRADED BY *ASPERGILLUS FUMIGATUS* G-13

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Table S1. Substrate composition and culture method

Number	Lignin model compound	Cellulose co-substrate	Adding glucose	Culture method	Number	Lignin model compound	Cellulose co-substrate	Adding glucose	Culture method
A	ferulic acid	–	no	static culture	A-6	ferulic acid	–	no	shake-flask culture
B	p-coumaric acid	–	no		B-6	p-coumaric acid	–	no	
C	sinapic acid	–	no		C-6	sinapic acid	–	no	
A-1	ferulic acid	microcrystalline cellulose	no		A-7	ferulic acid	microcrystalline cellulose	no	
B-1	p-coumaric acid	microcrystalline cellulose	no		B-7	p-coumaric acid	microcrystalline cellulose	no	
C-1	sinapic acid	microcrystalline cellulose	no		C-7	sinapic acid	microcrystalline cellulose	no	
A-2	ferulic acid	carboxymethyl cellulose	no		A-8	ferulic acid	carboxymethyl cellulose	no	
B-2	p-coumaric acid	carboxymethyl cellulose	no		B-8	p-coumaric acid	carboxymethyl cellulose	no	
C-2	sinapic acid	carboxymethyl cellulose	no		C-8	sinapic acid	carboxymethyl cellulose	no	
A-3	ferulic acid	–	yes		A-9	ferulic acid	–	yes	
B-3	p-coumaric acid	–	yes		B-9	p-coumaric acid	–	yes	
C-3	sinapic acid	–	yes		C-9	sinapic acid	–	yes	
A-4	ferulic acid	carboxymethyl cellulose	yes		A-10	ferulic acid	microcrystalline cellulose	yes	
B-4	p-coumaric acid	carboxymethyl cellulose	yes		B-10	p-coumaric acid	microcrystalline cellulose	yes	
C-4	sinapic acid	carboxymethyl cellulose	yes		C-10	sinapic acid	microcrystalline cellulose	yes	
A-5	ferulic acid	microcrystalline cellulose	yes		A-11	ferulic acid	carboxymethyl cellulose	yes	
B-5	p-coumaric acid	microcrystalline cellulose	yes		B-11	p-coumaric acid	carboxymethyl cellulose	yes	
C-5	sinapic acid	microcrystalline cellulose	yes		C-11	sinapic acid	carboxymethyl cellulose	yes	

Table S2. Results of protein quantitative

Sample name	Concentration (μg/μL)	Volume (μL)	Total protein (μg)
b-1	2.17	450.00	975.49
b-2	1.75	450.00	789.03
b-3	0.98	450.00	441.98
c-1	3.48	450.00	1564.60
c-2	2.29	450.00	1031.77
c-3	2.94	450.00	1323.90

Note: b: p-coumaric acid was used as a substrate, microcrystalline cellulose was added, and static culture; c: sinapic acid was used as a substrate, carboxymethyl cellulose and glucose were added, shake-flask culture.

Table S3. Protein identification results

Sample name	Total spectrum	Spectrum	Specificity spectrum	Peptide segment	Specific peptide	Protein
A. fumigatus G-13	343789	71032	67171	29138	28015	4963

Table S4. Significantly enriched differential protein GO analysis results

Gene Ontology term	Genes annotated to the term
Proton-transporting two-sector ATPase complex, catalytic domain	EAL88022.1, EAL93227.1, EAL85830.1, EAL91551.1, EAL90395.1, KMK61709.1, EAL86067.1, EAL85296.1, EAL88063.2, EAL90408.1, EAL93428.1
Chaperonin-containing T-complex	EDP50347.1, EAL92792.1, EAL87886.1, EAL88382.2, KMK57547.1, KMK63082.1, EDP52789.1, EAL92280.1
Proton-transporting V-type ATPase complex	AL92245.1, EAL85830.1, EAL90395.1, KMK61709.1, EAL86067.1, EAL90408.1, EAL93428.1, EAL89661.1
Peroxisome	EAL89669.1, EAL86863.1, EAL84885.1, EAL86068.1, EDP49343.1, KMK55653.1, EAL93627.1, EAL91965.1, KEY78456.1, EAL88196.2, AAM08678.1, KMK59799.1, EAL89442.1, BAX07632.1, KEY76623.1, KEY76838.1, EAL85882.1
Proteasome complex	EDP48428.1, EAL88489.1, KMK60224.1, EAL85906.1, KEY77587.1, KMK60215.1, EAL88533.1, EAL88508.1, EAL90920.1, KMK60681.1, EAL84614.1, EAL87584.1, KMK61865.1, EDP50128.1, EAL85561.1, EAL92793.1, EAL90046.2, KMK57144.1, EDP50226.1, EAL87437.1, KMK59357.1, KEY77491.1, EAL88498.1, KMK63573.1
Proton-transporting ATP synthase complex	EAL88022.1, EAL93227.1, KEY75459.1, EDP48768.1, EAL91551.1, EAL90956.1, AFE02835.1, EAL85296.1, EAL87642.1, EAL88063.2, KMK55215.1
Preribosome	AAM08680.1, EDP55866.1, EAL92508.1, KEY83358.1, KMK61743.1, KMK54508.1, EAL90384.1, EAL93433.1, EAL87933.1, KEY83471.1, KMK60525.1, KMK54562.1, KMK60806.1, KMK60024.1, KMK61857.1, EAL90033.1, EAL92621.1, EAL89893.1
Integral to peroxisomal membrane	KEY76623.1, AAM08678.1, EDP49343.1, EAL91965.1
Intrinsic to peroxisomal membran	KEY76623.1, AAM08678.1, EDP49343.1, EAL91965.1
Peroxisomal part	KEY78456.1, KEY76623.1, KMK59799.1, AAM08678.1, EDP49343.1, EAL91965.1, KEY76838.1
Peroxisomal membrane	KEY76623.1, AAM08678.1, EDP49343.1, EAL91965.1, KEY76838.1
Peroxisomal matrix	KEY78456.1, KMK59799.1
Mitochondrial oxoglutarate Dehydrogenase complex	EAL87307.1, EAL93026.1
Oxoglutarate dehydrogenase complex	EAL87307.1, EAL93026.1

Table S5. Pathway enrichments of differential abundance protein species

Pathway	Pathway ID	Proteins
Glycerolipid metabolism	ko00561	EDP47846.1, EAL84793.1, EAL88473.1, EDP50537.1, EAL84915.1, KMK58193.1, EAL85929.1, KMK62869.1, KEY78926.1, EAL92198.1, KEY81558.1, KMK63393.1, EDP55249.1, CAR81082.1, KMK62126.1, KMK59979.1, KEY76145.1, EAL93317.1, EAL93863.1, EAL88208.1, KMK61911.1, KMK62858.1, KMK60355.1, EAL93156.1, EAL89638.1, EAL93146.1, KMK59240.1, KMK55348.1, KMK54865.1, KMK62892.1, EDP50502.1, KMK60164.1, KMK58070.1, EAL87970.1, KMK55971.1, KMK55340.1, KMK58978.1, KMK62748.1, KMK55107.1, EAL91769.1, EAL88074.1, EAL92425.1, KMK63391.1, KMK56053.1, EAL92161.1, KEY82231.1, KEY75564.1, EAL85662.1, EAL90303.1, KMK63448.1, EAL88299.1, KEY82606.1, EAL85055.2, EAL87171.1, KMK58969.1, KMK56813.1, EAL84518.2, EAL90322.1, KMK58116.1, KMK58082.1, KMK62980.1, EAL92087.1
Oxidative phosphorylation	ko00190	EAL90888.1, KMK54443.1, EAL86096.1, EAL90408.1, EAL90200.1, EAL89685.1, KMK59691.1, KMK59608.1, KMK62635.1, EAL85951.1, EAL88372.1, KMK59195.1, KMK57900.1, EAL85830.1, KMK54721.1, EAL93594.1, EAL92245.1, AAK94754.1, AFE02848.1, EDP53575.1, EAL90109.2, EAL91743.1, EDP48768.1, EAL86067.1, EDP53961.1, EAL92195.1, EAL93355.1, EAL88063.2, AFE02833.1, EAL92804.1, AFE02840.1, AFE02889.1, KMK60461.1, EAL84658.1, EAL85005.1, EDP51797.1, EAL86029.1, EAL89119.1, KMK55215.1, EAL93666.2, AFE02837.1, EAL93428.1, KEY75459.1, EAL89661.1, EAL91551.1, EAL88620.1, AFE02836.1, AFE02835.1, AFE02834.1, KMK59815.1, EAL87642.1, AFE02832.1, KMK55134.1, EAL91567.1, EAL90395.1, EAL90559.1, KMK63171.1, AFE02845.1, KMK58066.1, EAL88022.1, EAL93209.1, KMK60798.1, EAL92144.1, AFE02846.1, EDP50213.1, EDP51485.1, EAL93227.1, EAL85296.1, EAL84691.2, EAL92794.1, KMK61709.1, EAL92738.1, EAL90956.1, KMK59304.1
Pentose and glucuronate interconversions	ko00040	EDP47846.1, KMK55960.1, KMK62656.1, EDP50537.1, EAL85687.1, KEY80906.1, KEY84070.1, KEY79513.1, EAL89918.1, KMK55299.1, EAL92808.1, KMK61580.1, EAL88193.1, EDP54959.1, EAL92392.1, KMK61508.1, KMK62005.1, KMK60164.1, sp|B0YAA4.2|PGXB_ASPFC, KMK59530.1, EAL88877.1, KMK55893.1, EAL91618.1, CAF32150.1, EAL91769.1, EAL91052.1, EAL90117.1, EAL92161.1, KEY75564.1, EDP48480.1, EAL90303.1, KMK62531.1, KEY82606.1, EAL88173.1, EDP52870.1, KMK58753.1, KMK55585.1, KEY81513.1, EAL88848.1, KEY82521.1, KMK62263.1
Riboflavin metabolism	ko00740	CAF32050.1, EAL86116.1, EAL87220.2, KEY75945.1, CAD37142.1, KMK55567.1, EAL87673.1, EAL92131.1, EAL88488.1, KMK58105.1, KMK58383.1, KEY78493.1, pdb|1SK8|A, KEY77598.1, KMK62368.1, KMK58661.1, AAL66381.1, KEY83051.1, EAL88335.1, KEY77763.1, EDP48026.1
Peroxisome	ko04146	KMK54413.1, EAL92136.1, KMK55859.1, KMK56644.1,KMK63550.1, KMK59893.1, CAD27312.1, KEY83137.1, EAL86863.1, KEY81384.1, KEY76997.1, EAL87300.1, KEY83455.1, KMK63057.1, EAL93286.1, EAL85874.2, KMK59491.1, EAL85246.1, KMK58631.1, EAL88056.1, KMK62876.1, EAL85767.2, EDP52735.1, KEY76979.1, EDP47638.1, EDP54759.1, KMK56645.1, EAL93430.1, EDP52939.1, KEY82116.1, EAL91849.1, EAL91965.1, EAL88469.1, EAL88189.1, KEY76921.1, KEY76623.1, KEY75672.1, EDP52872.1, KEY80450.1, EAL89669.1, EAL90643.1, EAL93431.1, EDP51376.1, KMK60329.1, KMK55653.1, EAL85878.1, EAL94004.1, EAL85650.1, EDP53650.1, KMK58718.1, EAL88068.1, KEY81350.1, EAL86664.2, KMK57202.1, EAL90276.1, KMK63469.1, EAL90786.1, EAL89695.1, EDP49343.1, EAL90362.2, AAD42060.1, EAL85932.1, EAL88576.1, EAL84195.2, EAL85877.1, KMK56890.1, KMK61241.1, EDP53223.1, KMK60960.1, KMK54433.1, EDP48695.1, KMK54474.1
Glyoxylic acid and dicarboxylic acid metabolism	ko00630	KEY82509.1, CAD29597.1, EAL89485.1, EDP47493.1, KMK62620.1, KMK62164.1, KMK58631.1, EAL85767.2, EDP55716.1, EDP55400.1, KMK62381.1, EAL92649.1, EAL85882.1, EAL89256.1, KMK61118.1, EAL89442.1, EDP50664.1, EAL87307.1, KMK63462.1, EAL85650.1, EDP53650.1, AAP57624.1, KEY80024.1, CBM39612.1, EAL84687.1, KEY76637.1, KMK60634.1, KEY75615.1, EAL90276.1, EAL93079.1, EAL89007.1, EAL89133.1, EAL90162.1, EBA27189.1, EAL85518.1, KMK61241.1, KMK54433.1, KEY80466.1, EAL90537.1, KEY80553.1, KMK58082.1
Carbon metabolism	ko01200	EAL87226.1, EAL89660.1, KEY82509.1, EAL91981.1, KEY83211.1, EDP47620.1, EAL90888.1, EAL85543.1, EDP49442.1, EAL90682.1, EAL90363.1, CAD29597.1, EDP54102.1, EAL89710.1, EAL88658.1, EAL89485.1, EAL88911.1, EDP47493.1, KMK59608.1, EAL92246.1, EAL88727.1, KEY82910.1, KEY82729.1, KMK63057.1,EAL93026.1, KMK62620.1, KMK62164.1, EAL91610.1, EAL91616.1, KMK59196.1, KMK58063.1, EAL88625.1, KMK58631.1, EDP47087.1, EAL91678.1, EAL85767.2, EAL88598.1, KMK60275.1, EDP55716.1, EAL92913.1, KEY78949.1, EDP55400.1, KMK56175.1, EAL89747.1, EAL86696.1, KMK59609.1, KMK62381.1, EAL90016.1, KMK54556.1, EAL92649.1, EAL91574.1, EDP50640.1, EAL85882.1, KMK58284.1, KEY83574.1, EAL89256.1, KMK58078.1, EAL91587.1, CAF31997.1, KMK61508.1, EAL91271.1, EAL92577.1, EAL86900.1, KEY84128.1, EAL89442.1, KMK54601.1, EDP52872.1, EAL92042.1, EAL87307.1, EAL93431.1, EAL85928.1, KMK59300.1, KMK63462.1, KMK62748.1, EAL85650.1, EDP53650.1, AAP57624.1, EAL84600.1, EAL93425.1, KEY80024.1, EAL92817.1, CBM39612.1, EAL84687.1, EAL87900.1, KMK61210.1, KMK58983.1, KEY76637.1, KEY76450.1, EAL92414.1, KMK57069.1, CAQ53727.1, KEY75615.1, EAL90276.1, EAL85790.1, EAL86013.1, EAL93079.1, EAL89133.1, KMK55943.1, EAL91567.1, EAL93397.1, KEY81004.1, EAL85816.1, KMK63105.1, EAL93274.1, KEY77889.1, EAL85518.1, EAL85877.1, KMK61934.1, KMK61241.1, KMK58698.1, KMK54433.1, EAL87202.1, EDP54369.1, KEY80466.1, EAL92794.1, KEY84002.1, KEY78537.1, KEY80553.1, KMK58082.1, EDP54494.1, KMK62966.1, EBA27329.1, EAL87682.1, EAL88532.1, EAL86200.1

End of Table S5

Pathway	Pathway ID	Proteins
Glycine, serine and threonine metabolism	ko00260	EAL87226.1, EAL93059.1, EAL90594.1, KEY84119.1, EAL85543.1, CAD29597.1, EDP54102.1, EAL89485.1, EDP51374.1, EAL87300.1, KMK62620.1, KMK62164.1, KMK58063.1, EAL91672.1, EAL93863.1, KMK62876.1, EDP49302.1, EDP52885.1, EDP52735.1, EDP55716.1, EAL91487.1, EAL92913.1, EDP47638.1, EDP55400.1, KMK56175.1, EAL86614.1, KMK54556.1, EAL84357.1, EAL92649.1, KEY81920.1, KMK57557.1, KMK58793.1, KMK60190.1, EAL92577.1, EDP47329.1, EAL92012.2, EAL92042.1, EAL87307.1, EAL85928.1, KEY78899.1, KMK61534.1, KEY80024.1, CBM39612.1, EAL84687.1, CAE47972.1, KMK59748.1, KEY76637.1, KEY78573.1, EDP53643.1, KMK56018.1, EAL90276.1, EAL86535.1, EAL93079.1, KMK55943.1, EAL90162.1, KMK60441.1, KMK60527.1, KEY83039.1, EAL89282.1, EDP50929.1, EAL91860.1, KMK58698.1, KEY80466.1, EAL90537.1, KEY80553.1, KMK58082.1, EDP48695.1, KEY75599.1, EDP49115.1

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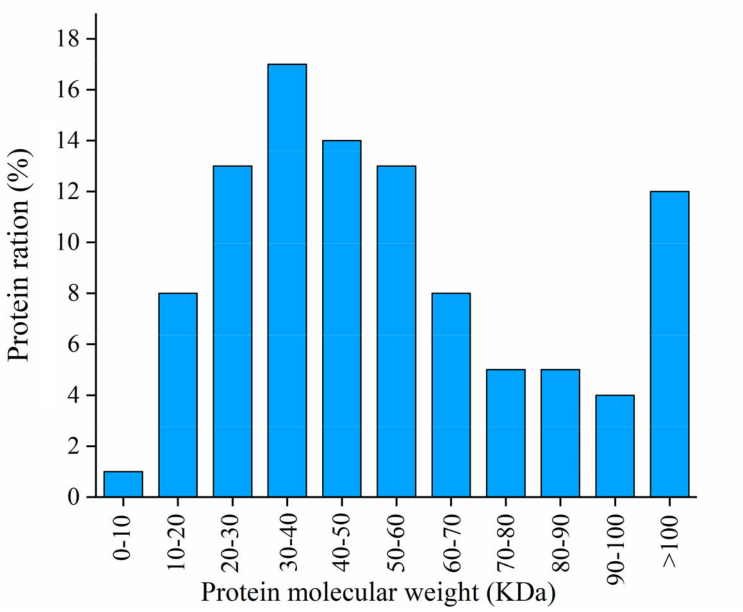

Figure S1. Protein molecular weight distribution map

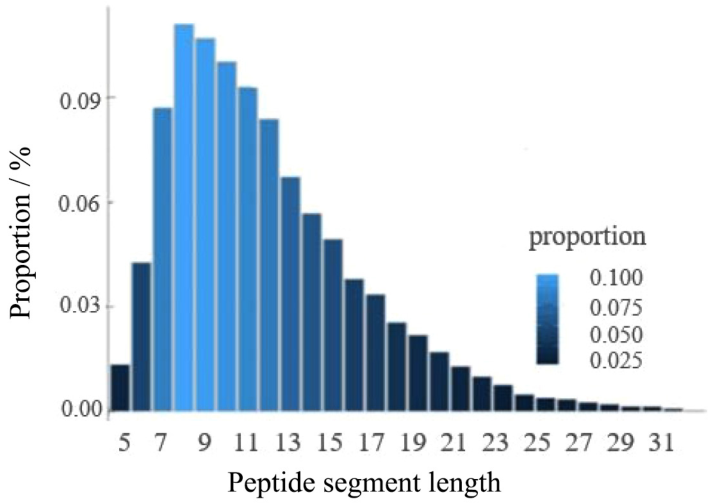

Figure S2. The length distribution of peptide segments

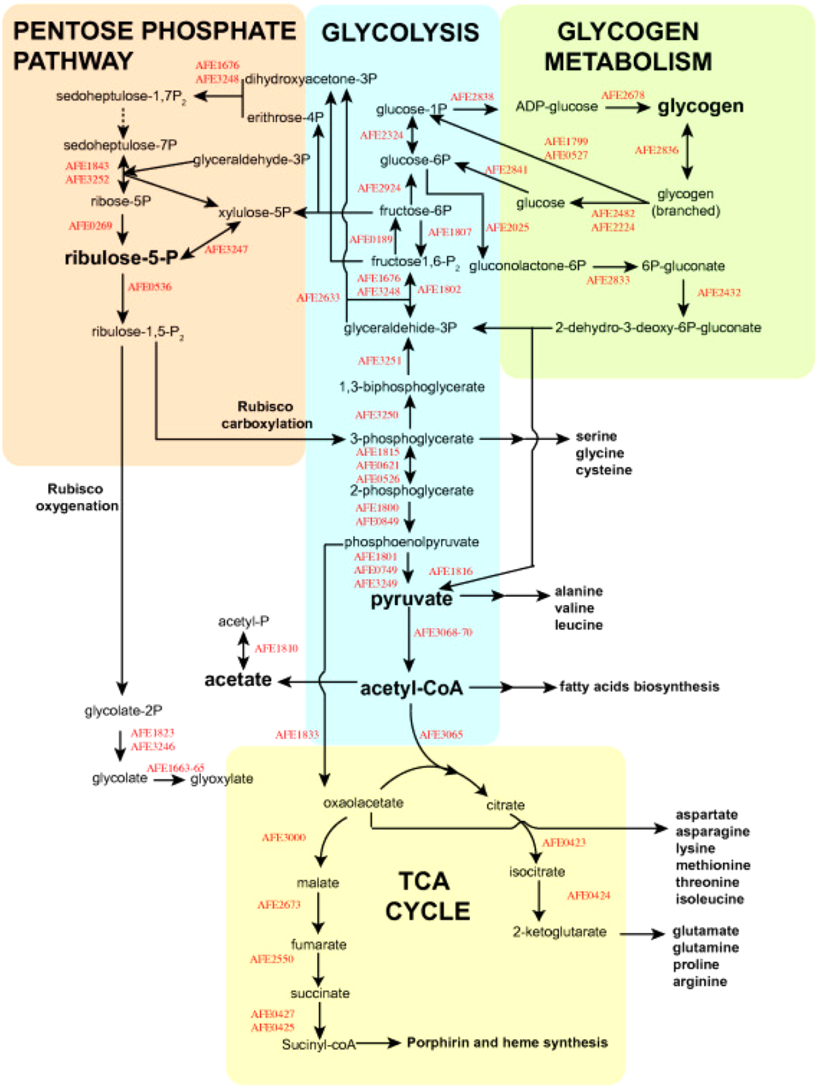

Figure S3. Central carbon metabolism