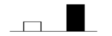
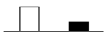
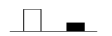
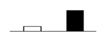
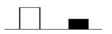
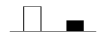
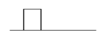
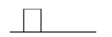
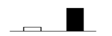
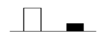
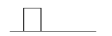
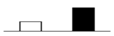
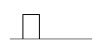
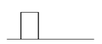
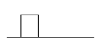
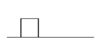
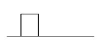
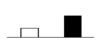
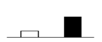
Suppl Data 1 **Table 1** Proteins identified by MS/MS from F1 and F4

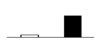
Spot No.[a]	NCBI No.[b]	Function Category Protein name	Fungal species	Exper.[c] *p*I/M*r*	Theor.[d] *p*I/M*r*	MP /TP[e]	SC% (Loc)[f]	MS. S.[g]	Change (F1, F4)[h]
Carbohydrate transport and metabolism (CTM)									
3	475667672	adenosine kinase	*F. oxysporum*	5.47/33.3	5.34/38.1	15/62	59(_)	143	
7	475667960	phospho-kinase	*F. oxysporum*	5.8/48.3	5.77/44.8	18/72	56(_)	90	
9	475673861	fructose-aldolase	*F. oxysporum*	5.74/36.2	5.44/39.8	17/49	51(_)	170	
12	477513214	beta-hexosaminidase	*F. oxysporum*	6.73/35.3	6.25/34.2	11/69	29(*)	83	
13	475667960	Phospho-kinase	*F. oxysporum*	5.92/44.4	5.77/44.8	16/111	48(_)	76	
16	3810873	lactonohydrolase	*F. oxysporum*	5.32/50.2	5.10/43.2	10/60	31(_)	78	
22	475668982	putative enolase	*F. oxysporum*	5.20/48.4	5.06/47.5	22/77	57(*)	129	
31	475667960	Phospho-kinase	*F. oxysporum*	5.80/46.3	5.77/44.8	21/59	57(_)	159	
33	475668458	glucanosyltransferase	*F. oxysporum*	4.72/62.5	4.83/59.2	22/77	44(*)	132	
34	475668458	glucanosyltransferase	*F. oxysporum*	4.80/60.3	4.87/59.1	19/79	42(*)	92	
35	477513214	beta-hexosaminidase	*F. oxysporum*	6.80/37.7	6.25/34.2	(1)	4(*)	(93)	
36	475667960	phospho-kinase	*F. oxysporum*	5.92/47.4	5.77/44.8	20/56	55(_)	162	
41	342888171	carboxy-cyclase	*F. oxysporum*	6.71/46.3	6.67/42.4	14/58	43(S)	88	
42	475672613	Alpha-galactosidase	*F. oxysporum*	4.6/84.32	5.01/83.1	18/65	29(S)	80	
43	475672613	alpha-galactosidase	*F. oxysporum*	4.80/84.3	5.01/83.1	24/79	36(S)	113	
50	475668982	putative enolase	*F. oxysporum*	4.80/47.7	5.06/47.5	17/63	38(*)	80	
51	477507289	acethexosaminidase	*F. oxysporum*	5.5/77.3	5.22/66.1	24/51	48(S)	216	
53	475668458	glucanosyltransferase	*F. oxysporum*	5.12/70.2	4.83/59.2	15/62	29(*)	76	
58	477514377	alpha-galactosidase	*F. oxysporum*	4.7/84.3	5.13/82.9	15/50	27(S)	77	
60	475673339	Chitinase 1	*F. oxysporum*	6.8/62.3	6.31/47.9	16/66	36(S)	93	
64	3810873	lactonohydrolase	*F. oxysporum*	5.3/65.65	5.10/43.2	11/58	31(_)	75	
68	475668458	glucanosyltransferase	*F. oxysporum*	4.9/67.2	4.83/59.2	26/86	52(*)	144	
76	342872804	phospholipase B	*F. oxysporum*	4.67/77.4	4.67/70.5	15/57	25(S)	85	
77	342872804	phospholipase B	*F. oxysporum*	4.75/77.4	4.67/70.5	(4)	8(S)	253	
78	342872804	phospholipase B	*F. oxysporum*	4.50/77.4	4.67/70.5	(2)	2(S)	(80)	
79	475673339	Chitinase 1	*F. oxysporum*	6.9/55.3	6.31/47.9	18/55	39(S)	101	
80	475672613	galactosidase	*F. oxysporum*	5.1/84.3	5.01/83.1	35/67	47(S)	211	
83	475672613	galactosidase	*F. oxysporum*	5.1/84.3	5.01/83.1	27/62	35(S)	150	
98	477513214	hexosaminidase	*F. oxysporum*	6.7/37.65	6.25/34.2	12/64	31(*)	83	
99	475666766	Glucose-epimerase	*F. oxysporum*	4.62/35.4	4.95/33.7	10/60	46(*)	83	
Posttranslational modification, protein turnover, chaperones (PTM)									
10	342888261	peroxiredoxin	*F. oxysporum*	6.17/20.3	5.86/25.4	15/71	71(*)	122	
17	342878892	carboxypeptidase	*F. oxysporum*	6.20/62.3	6.04/59.9	21/70	41(*)	135	
21	475663822	Hsp 70	*F. oxysporum*	5.04/73.2	5.00/70.9	23/70	44(_)	142	
23	342882947	vacuolar protease A	*F. oxysporum*	4.45/44.7	4.66/42.9	(6)	10(S)	218	
24	342882947	vacuolar protease A	*F. oxysporum*	4.38/44.7	4.66/42.9	9/39	21(S)	95	
29	342882947	vacuolar protease A	*F. oxysporum*	4.38/44.7	4.66/42.9	8/49	19(S)	84	
32	475667235	elongation factor 1	*F. oxysporum*	5.90/48.5	5.64/46.2	19/72	51(*)	123	
45	342876003	disulfide isomerase	*F. oxysporum*	6.8/39.4	6.29/42.1	21/81	60(S)	148	

47	170098594	ubiquitin	*L. bicolor*	6.3/9.7	5.71/8.2	7/61	84(_)	81	
54	607818	Hsp 70	*N. crassa*	4.90/48.7	5.03/70.8	(3)	5(_)	(83)	
56	475674506	Peroxiredoxin-1	*F. oxysporum*	4.96/23.5	5.14/23.3	(4)	14(*)	127	
59	475664853	Carboxypeptidase	*F. oxysporum*	7.0/70.3	6.71/57.5	(1)	2(_)	(62)	
70	477507989	Hsp 70	*F. oxysporum*	6.1/83.2	5.00/71.1	25/46	53(_)	217	
71	342889878	Hsp 90	*F. oxysporum*	5.0/70.3	4.85/79.3	26/67	41(_)	174	
73	477507989	Hsp 70	*F. oxysporum*	5.0/70.3	5.00/71.2	21/61	26(_)	117	
74	342889878	Hsp 90	*F. oxysporum*	5.0/78.7	4.85/79.3	19/59	34(_)	110	
85	475670597	Carboxypeptidase	*F. oxysporum*	5.45/68.3	5.94/64.9	14/58	29(S)	78	
94	322700250	Hsp 90	*M. acridum*	4.74/24.2	4.93/80.1	13/52	26(_)	88	

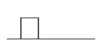
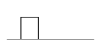
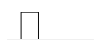
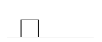
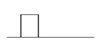
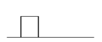
Inorganic ion transport and metabolism (ITM)

5	475672437	Catalase-peroxidase	*F. oxysporum*	6.80/80.2	6.57/85.2	29/71	37(S)	147	
6	477512799	superoxide dismutase	*F. oxysporum*	6.15/16.6	7.07/21.3	11/78	67(S)	95	
15	477512799	superoxide dismutase	*F. oxysporum*	6.7/17.2	7.07/21.3	12/53	51(S)	106	
28	477512799	superoxide dismutase	*F. oxysporum*	6.41/22.3	7.07/21.3	10/59	55(S)	122	
65	475671755	Catalase-peroxidase	*F. oxysporum*	6.5/85.3	5.98/73.3	19/51	39(_)	126	
86	475672437	Catalase-peroxidase	*F. oxysporum*	6.8/78.3	6.57/85.2	33/64	42(S)	216	
87	475672437	Catalase-peroxidase	*F. oxysporum*	6.7/78.3	6.57/85.2	37/84	41(S)	219	
88	475672437	Catalase-peroxidase	*F. oxysporum*	6.9/78.3	6.57/85.2	39/92	49(S)	249	
89	475672437	Catalase-peroxidase	*F. oxysporum*	6.79/78.3	6.57/85.2	39/61	48(S)	314	
90	475672437	Catalase-peroxidase	*F. oxysporum*	6.71/78.3	6.57/85.2	33/61	42(S)	236	
92	475672437	Catalase-peroxidase	*F. oxysporum*	6.69/78.3	6.57/85.2	41/87	49(S)	250	

Amino acid transport and metabolism (ATM)

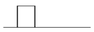
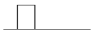
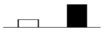
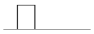
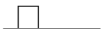
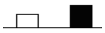
18	475675629	Acetyl-lyase	*F. oxysporum*	6.50/44.4	5.89/47.1	13/52	42(_)	88	
19	477517374	hom-dehydrogenase	*F. oxysporum*	6.14/38.1	6.24/38.6	12/38	50(*)	104	
26	46128717	peptidase	*F. gramiarum*	5.15/22.3	5.53/55.4	(2)	2(_)	(92)	
39	477517233	l-amino acid oxidase	*F. oxysporum*	6.2/73.5	5.69/67.8	17/46	24(S)	90	
63	475675629	Acetyl-lyase	*F. oxysporum*	6.54/58.7	5.89/47.1	15/35	57(_)	134	
82	477517233	l-amino acid oxidase	*F. oxysporum*	6.5/80.7	5.69/67.8	23/83	35(S)	98	
84	477517233	l-amino acid oxidase	*F. oxysporum*	6.2/80.6	5.69/67.8	19/60	25(S)	82	
91	477517233	l-amino acid oxidase	*F. oxysporum*	6.14/80.7	5.69/67.8	19/64	26(S)	86	
93	342871725	l-amino acid oxidase	*F. oxysporum*	6.14/80.7	5.69/67.8	18/69	27(S)	81	

Energy production and conversion (EPC)

20	475671099	glutathione reductase	*F. oxysporum*	6.64/53.4	6.06/51.1	19/76	67(_)	121	
38	475664589	ATP synthase	*F. oxysporum*	6.7/20.3	5.27/55.2	30/68	71(M)	206	
40	475664589	ATP synthase	*F. oxysporum*	4.76/54.3	5.27/55.2	24/84	64(M)	128	
46	475664589	ATP synthase	*F. oxysporum*	4.95/54.3	5.27/55.2	28/71	68(M)	168	
49	475664589	ATP synthase	*F. oxysporum*	4.75/26.5	5.27/55.2	(2)	5(M)	117	
67	354543047	hypothetical protein	*C. parapilosis*	4.7/18.3	10.1/23.1	9/80	38(_)	80	
75	342876053	ATP synthase D chain	*F. oxysporum*	4.55/84.3	6.43/19.4	10/59	60(*)	98	

Coenzyme metabolism (COM)

8	475664008	thionine synthetase	*F. oxysporum*	5.92/45.6	5.77/44.5	16/65	55(*)	90	
11	475664008	thionine synthetase	*F. oxysporum*	6.05/41.3	5.77/44.5	14/49	48(_)	130	
37	342873590	Adenosyl-cysteinase	*F. oxysporum*	5.74/46.2	5.57/49.5	28/85	57(*)	191	

DNA replication, recombination and repair (DRR)									
55	342881318	actin binding protein	*F. oxysporum*	4.9/22.7	4.84/18.8	16/86	69(_)	109	
66	342890194	DEAD box helicase	*F. oxysporum*	5.2/57.5	4.98/44.9	21/68	55(_)	119	
Transcription, translation, ribosomal structure and biogenesis (TRR)									
14	477513214	hexosaminidase	*F. oxysporum*	6.5/26.3	6.25/34.2	10/68	26(_)	80	
81	475668007	amidase	*F. oxysporum*	6.5/64.3	6.86/63.7	18/64	39(S)	112	
Cell motility and secretion (CMS)									
62	283806340	oxidoreductase	*F. oxysporum*	5.5/73.2	5.20/71.4	9/24	27(S)	83	
General function prediction only (Predicted)									
2	342881721	amidotransferase	*F. oxysporum*	5.35/25.3	5.12/24.5	18/35	74(*)	165	
4	342888721	Glycer-dehydrogenase	*F. oxysporum*	6.25/37.5	5.91/37.4	18/43	53(*)	157	
25	342888721	Glycer-dehydrogenase	*F. oxysporum*	6.1/36.5	5.91/37.4	20/75	59(*)	137	
27	342888721	Glycer-dehydrogenase	*F. oxysporum*	6.21/36.5	5.91/37.4	23/47	61(*)	208	
44	342878413	Quin-oxidoreductase	*F. oxysporum*	5.60/18.7	5.54/21.7	(5)	18(_)	163	
52	342879444	Nitropro-dioxygenase	*F. oxysporum*	6.6/50.3	5.78/36.9	18/61	54(*)	136	
NO related COG (NO)									
1	475667056	hypothetical protein	*F. oxysporum*	6.24/51.3	6.62/50.5	16/64	37(S)	96	
30	475667318	actin	*F. oxysporum*	5.45/44.3	6.08/45.2	19/62	53(_)	119	
48	342873137	transport factor 2	*V. dahliae*	4.50/14.4	4.61/13.9	(2)	12(_)	166	
57	340924179	hypothetical protein	*C. therhilum*	5.10/54.4	10.6/17.9	9/66	51(_)	79	
61	171680085	hypothetical protein	*P. anserina*	4.8/77.4	5.61/41.3	10/24	34(*)	81	
69	342872822	Phospho-mutase	*F. oxysporum*	5.3/14.3	5.21/12.4	8/61	70(_)	91	
95	475667056	hypothetical protein	*F. oxysporum*	6.06/50.5	6.62/50.5	17/72	38(S)	110	
96	475671883	Ribonuclease Trv	*F. oxysporum*	5.95/31.3	5.61/29.7	(3)	13(S)	185	
97	477507337	14-3-3 protein	*F. oxysporum*	4.85/34.1	4.87/30.1	13/60	61(_)	92	

Note:

[a] Assigned spot number as indicated in Fig. 2.

[b] NCBI non-redundant database accession numbers.

[c] Experimental [molecular mass (kDa) OR relative molecular mass (M*r*)] and pI of identified proteins.

[d] Theoretical [molecular mass (kDa) OR relative molecular mass (M*r*)] and pI of identified proteins.

[e] Number of matched peptides (MP) with PMF and the total searched peptides (TP). Numbers in parentheses are the MP based on MS/MS.

[f] The amino acid sequence coverage (SC) for the identified proteins and the protein location (Loc) predicted by TargetP. "M" represent the protein located at mitochondria, "S" represent the protein has signal peptidase, "_" represent the protein have multiple location, "*" represent the location of proteins was unkown.

[g] The Mascot searched score (MS) against the NCBI non-redundant database. The numbers in parentheses represent the protein was identified by MS/MS.

[h] The mean relative protein values on 2-DE gels. White, F1; black, F4.