

Supplementary File 2: Aylward *et al.* Contrasting carbon metabolism in saprotrophic and pathogenic Microascalean fungi from *Protea* trees

Table S2. Proportion of *Knox daviesia capensis*, *K. proteae* and *Ceratocystis albifundus* proteins predicted to belong to each KEGG (Kyoto Encyclopedia of Genes and Genomes) category.

	<i>Knox daviesia capensis</i>		<i>Knox daviesia proteae</i>		<i>Ceratocystis albifundus</i>	
	Number of proteins	Percentage of total proteins	Number of proteins	Percentage of total proteins	Number of proteins	Percentage of total proteins
<i>Query dataset</i>	7940	100%	8174	100%	6967	100%
<i>Total entries annotated</i>	2887	36.40%	2820	34.50%	2893	41.50%
Genetic Information Processing	1631	56.49%	1585	56.21%	1651	57.07%
Cellular Processes	477	16.52%	471	16.70%	481	16.63%
Environmental Information Processing	381	13.20%	376	13.33%	377	13.03%
Human Diseases	366	12.68%	357	12.66%	363	12.55%
Organismal Systems	246	8.52%	245	8.69%	244	8.43%
Amino acid metabolism	242	8.38%	235	8.33%	241	8.33%
Enzyme families	234	8.11%	229	8.12%	237	8.19%
Carbohydrate metabolism	220	7.62%	216	7.66%	229	7.92%
Unclassified	151	5.23%	152	5.39%	140	4.84%
Energy metabolism	149	5.16%	139	4.93%	136	4.70%
Lipid metabolism	123	4.26%	121	4.29%	122	4.22%
Metabolism of cofactors and vitamins	117	4.05%	113	4.01%	115	3.98%
Nucleotide metabolism	101	3.50%	98	3.48%	101	3.49%
Glycan biosynthesis and metabolism	98	3.39%	98	3.48%	90	3.11%
Metabolism of other amino acids	64	2.22%	61	2.16%	62	2.14%
Xenobiotics biodegradation and metabolism	46	1.59%	44	1.56%	37	1.28%
Biosynthesis of other secondary metabolites	36	1.25%	34	1.21%	31	1.07%
Metabolism of terpenoids and polyketides	31	1.07%	30	1.06%	34	1.18%

Taxonomy group: Eukaryotes,Fungi; KEGG database searched: family_eukaryotes.pep.

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Table S3. Carbon-metabolising enzymes (excluding polysaccharide-degrading enzymes) identified only in *Knoxdaviesia* or *Ceratocystis albifundus*, respectively.

<i>Knoxdaviesia</i>		<i>Ceratocystis albifundus</i>	
Enzyme description	EC number	Enzyme description	EC number
3-phytase	3.1.3.8	hprA; glycerate dehydrogenase	1.1.1.29
formamidase	3.5.1.49	katE, CAT, catB, srpA; catalase	1.11.1.6
GAAA; D-galacturonate reductase	1.1.1.-		
GAAB, LGD1; L-galactonate dehydratase	4.2.1.146		
GAAC, LGA1; L-threo-3-deoxy-hexylosonate aldolase	4.1.2.54		
kdUD; 2-deoxy-D-gluconate 3-dehydrogenase	1.1.1.125		
KHK; ketohexokinase	2.7.1.3		
LDH, ldh; L-lactate dehydrogenase	1.1.1.27		
LRA1; L-rhamnose 1-dehydrogenase	1.1.1.173; 1.1.1.377; 1.1.1.378		
LRA3, yfaW; L-rhamnonate dehydratase	4.2.1.90		
UGDH, ugd; UDPglucose 6-dehydrogenase	1.1.1.22		
XR; D-xylose reductase	1.1.1.307		