

Table S1 PKS and NRPS conserved domain structure amongst secondary metabolites gene cluster in *A. ochraceus* fc-1

Scaffold	Cluster	Category	Module	Gene	Domain*	
Scaffold_Scf_10	Cluster 1	NRPS	NRPS	AoFC_11180	A-P-C-A-P-C	
				AoFC_11183	A-P-C-A-NAD	
	Cluster 2	NRPS	NRPS	AoFC_11426	A-P-E-C-A-P-C	
Scaffold_Scf_1	Cluster 3	NRPS	NRPS	AoFC_11716	A-P-E-C-A-A-P-C-A-P-E-C-P-C-P	
	Cluster 5	NRPS-T1pks	PKS-NRPS	AoFC_00015	ER	
				AoFC_00016	KS-AT-DH-cMT-KR-C-A-P-TD	
	Cluster 7	T1pks-Terpene	PKS	AoFC_00120	KS-AT-DH-cMT-ER-KR	
	Cluster 8	T1pks	PKS	AoFC_00237	KS-AT-ACP-TE	
	Cluster 10	T1pks	PKS	AoFC_00328	KS-AT	
	Cluster 11	Terpene-Nrps-T1pks	PKS-NRPS	AoFC_00343	KS-AT-DH-KR-ACP-C-A-P-TD	
	Cluster 12	T1pks	PKS	AoFC_01462	KS-AT	
				AoFC_01463	cMT	
	Cluster 15	T1pks	PKS	AoFC_01791	KS-AT-DH-cMT-ER-KR-NAD	
				AoFC_01795	KS-AT-DH-cMT-ER-KR	
	Cluster 16	T1pks	PKS	AoFC_01818	A-P-KS-AT-KR-ACP-TD	
	Cluster 17	T1pks	PKS	AoFC_01940	KS-AT-DH--KR-ACP	
	Scaffold_Scf_2	Cluster 20	T1pks	PKS	AoFC_02280	KS-AT-ACP-ACP-TE
		Cluster 21	T1pks	PKS	AoFC_02377	KS-AT-DH-cMT-ER-KR
		Cluster 22	T1pks	PKS	AoFC_02401	KS-AT-DH-cMT-KR
		Cluster 24	T1pks	PKS	AoFC_02436	KS-AT-DH-cMT-ER-KR-TD
Cluster 25		T1pks-Nrps	PKS NRPS	AoFC_02449	KS-AT-DH-cMT-ER-KR-ACP	
				AoFC_02451	A-P-C-A-P-C	
Cluster 30		Nrps-T1pks	PKS NRPS	AoFC_02999	KS-AT-DH-cMT-KR-ACP-C-A	
				AoFC_03000	A	
				AoFC_03008	A-P-TD	
Cluster 31		NRPS	NRPS	AoFC_03076	A-P-C-A-P-C-A-P-C-A-P-C	
Cluster 33		Nrps-T1pks	PKS-NRPS	AoFC_03540	oMT	
	AoFC_03541			TE		
	AoFC_03542			KS-AT-DH-KR-C-A-P		
	AoFC_03569			KS-AT-DH-ACP-ACP-TE		
Cluster 34	T1pks	PKS	AoFC_03569	KS-AT-DH-ACP-ACP-TE		
Scaffold_Scf_3	Cluster 38	T1pks	PKS	AoFC_04242	KS-AT-DH-ER-KR	
	Cluster 41	NRPS	NRPS	AoFC_04810	A-P-C-A-P-E-C	
	Cluster 42	NRPS	NRPS	AoFC_04923	A-P-C-A-P-E-C	
Scaffold_Scf_4	Cluster 43	T1pks	PKS	AoFC_05134	KS-AT-ACP-ACP-TE	
	Cluster 44	Nrps-Terpene	NRPS	AoFC_05313	A-C-A-P-C-P	
	Cluster 45	Nrps-T1pks	NRPS	AoFC_05376	C-A	
				AoFC_05377	KS-AT-DH-cMT-ER-KR-ACP	
	Cluster 46	T1pks	PKS	AoFC_05416	KS-AT-DH-cMT-ER-KR-ACP	
	Cluster 48	NRPS	NRPS	AoFC_05882	A	
				AoFC_05883	A-C-A-C-A-C-ACP-C-C	
	Cluster 50	T1pks	PKS	AoFC_06064	KS-AT-DH-cMT-ER-KR	
	Cluster 52	NRPS	NRPS	AoFC_06119	A-P-C-A-P-C	
				AoFC_06120	A-P-C	
Scaffold_Scf_5	Cluster 55	T1pks	PKS	AoFC_06330	KS-AT-DH-ER-KR-ACP	
	Cluster 57	T1pks	PKS	AoFC_06374	KS-AT-DH-ER-KR-ACP	
	Cluster 58	Terpene-Nrps	NRPS	AoFC_06430	C-A-nMT-P-C-A-P-TE	
	Cluster 59	NRPS	NRPS	AoFC_06550	A-P-C-C-A-P-E-C	
	Cluster 60	T1pks	PKS	AoFC_06810	KS-AT-DH-cMT-ER-KR-ACP	
	Cluster 62	NRPS	NRPS	AoFC_07015	C-A-P-E-C-A-P-C-A-P-C	
				AoFC_07020	A-ACP-TE	

Scaffold_Scf_6	Cluster 63	T1pks	PKS	AoFC_07038	KS-AT-DH-cMT-ER-KR-ACP
	Cluster 65	T1pks	PKS	AoFC_07251	KS-AT-DH-cMT-ER-KR
	Cluster 67	T1pks	PKS	AoFC_07482	KR
				AoFC_07483	KS-AT-DH-ER-KR
	Cluster 68	T1pks	PKS	AoFC_07533	KS-AT-DH-cMT-ER-KR
	Cluster 69	T1pks	PKS	AoFC_07597	KS-AT-DH-cMT-ER-KR
Scaffold_Scf_7	Cluster 70	NRPS	NRPS	AoFC_07623	A
				AoFC_07624	P-C-A-P
	Cluster 72	T1pks-Terpene	PKS	AoFC_07667	KS-AT-ACP-cMT-TD
	Cluster 75	NRPS	NRPS	AoFC_08050	A-P-C-A-P-C-A-P-E-C-A-P-C
	Cluster 76	T1pks	PKS	AoFC_08067	KS-AT-DH-cMT-ER-KR-ACP
	Scaffold_Scf_8	Cluster 80	NRPS	NRPS	AoFC_08653
Cluster 81		T1pks	PKS	AoFC_08701	KR-KS-AT-DH-ACP-TE
				AoFC_08706	A-P-TD
Cluster 82		T1pks	PKS	AoFC_08990	KS-AT-DH-cMT-ER-KR
Cluster 84		NRPS	NRPS	AoFC_09529	A-P-C-P-C
Cluster 85		NRPS	NRPS	AoFC_09543	A-P-C-A-P-C-A-P-C-A-P-C
Scaffold_Scf_9	Cluster 86	Nrps-T1pks	PKS-NRPS	AoFC_09572	KS-AT-DH-ER-KR-ACP-C-A-P-TD
				AoFC_09573	KR
	Cluster 88	T1pks-Nrps	PKS NRPS	AoFC_09698	KS-AT-DH-cMT-ER-KR-ACP
				AoFC_09699	A-P-C-A
	Cluster 89	T1pks	PKS	AoFC_09789	KS-AT-DH-cMT-ER-KR-ACP
	Cluster 90	NRPS	NRPS	AoFC_09894	A-P-C-A-TD
Scaffold_Scf_9	Cluster 91	T1pks	PKS	AoFC_10219	KS-AT-DH-cMT-ER-KR-ACP
	Cluster 92	Terpene-Nrps	NRPS	AoFC_10399	A-P-C-A-P-C
	Cluster 96	T1pks	PKS	AoFC_10736	KS-AT-DH-ER-KR
	Cluster 97	T1pks	PKS	AoFC_10776	A
				AoFC_10777	KS-AT-DH-cMT-ER-KR-ACP

*PKS and NRPS proteins were chosen from the secondary metabolic gene clusters after these clusters were predicted by antiSMASH 3.0 and the conserved domains were respectively listed in table. Domain abbreviations: β -ketosynthase (KS); acyl-transferase (AT); dehydratase (DH); C-methyltransferase (cMT); enoylreductase (ER); β -ketoreductase (KR); acyl-carrier protein domain(ACP); adenylation domain (A); condensation domain(C); peptidyl-carrier protein domain (P); NAD: NAD-

Table S2 Genomic properties of OTA-producing fungi, compared to *A. ochraceus*

	<i>A. ochraceus</i> fc-1	<i>A. carbonarius</i> ITEM 5010	<i>A. niger</i> CBS 513.88	<i>A. steynii</i> IBT 23096	<i>A. westerdijkiae</i> CBS 112803	<i>P. nordicum</i> BFE487
Scaffolds						
Total Length (Kb)	37020	36290	33931	37848	36072	30421.3
GC content (%)	48.79	51.72	50.40	49.07	50.38	47.69
N50(Kb)	3843	1827		3921	1603	122
Number of Protein Coding Genes	11740	11624	14165	11437	11744	11075
Mean Gene Length (bp)	1680	1547.93	1573	1797	1687	2190
Percent Coding (%)	53.29	49.58	55.20	54.33	54.93	79.73
Genes with Introns (%)	78.50	77.64	87.00	77.97	80.30	82.95
Exons						
Average size (bp)	475.83	442.40	370	479.31	460.76	418.17
Number	37371	36274	50629	38233	37874	38600
Mean # per Gene	3.18	3.12	3.5	3.34	3.22	3.48
GC Content (%)	54.87	55.04	53.7	55.79	54.99	52.59
Total Length (bp)	17782101	16047660	18733984	18325644	17451059	16141362
Introns						
Average size (bp)	75.92	78.90	97.2	83.49	90.44	102.29
Number	25631	24649	36464	26796	26130	27525
Mean # per Gene	2.18	2.12	2.60	2.34	2.22	2.48
GC Content (%)	46.07	48.57	45.3	47.22	46.19	42.03
Total Length (bp)	1945895	1944796	3544638	2237164	2363125	2815750
RNA						
tRNA number	238	264	269	222	210	183
rRNA number	47	4	59	120	4	30

Fig. S1

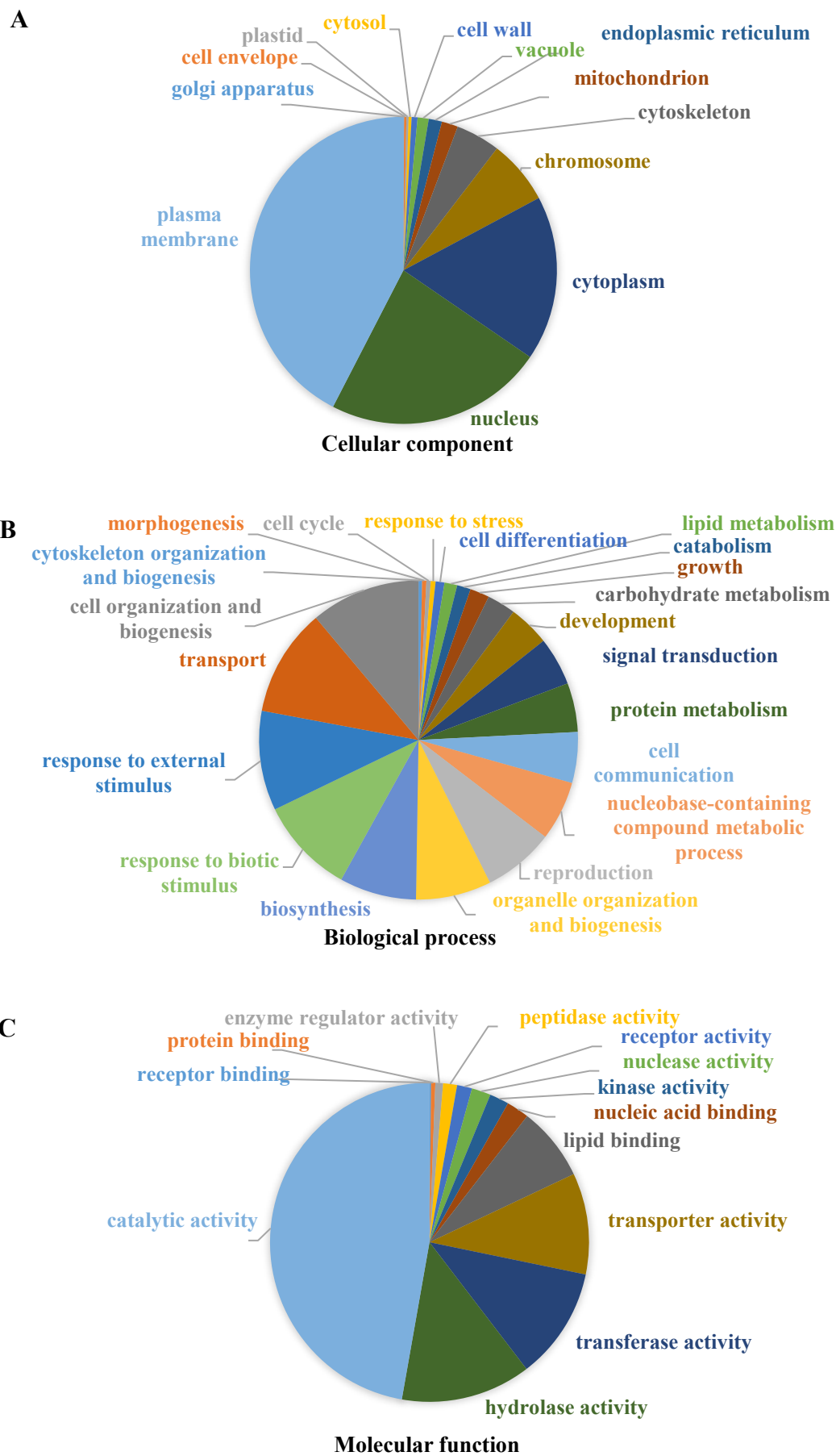


FIG. S1 Gene Ontology (GO) analyse of *A. ochraceus* genome. The functional distribution of the genomic annotation is presented for three principal categories: (A) cellular component, (B) biological process, and (C) molecular function.