

# Applied Microbiology and Biotechnology

## **Complete genome sequence of lovastatin producer *Aspergillus terreus* ATCC 20542 and evaluation of genomic diversity among *A. terreus* strains**

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## Supplementary Tables

**Table S1** Presence of orthologs of catabolic enzymes allowing utilization of carbohydrates based on sequence similarity with proteins of *A. niger* ATCC 1015 (employing threshold of 60% sequence identity across 60% of protein length).

Enzyme	Strain	NIH 2624	45A	M6925	w25	TN-484	IFO 6365	ATCC 20542	ATCC 20542 gene IDs
Glucose oxidase		4	3	4	3	2	2	3	HFD88_005098; HFD88_005956; HFD88_007298
Alpha-glucosidase		4	4	4	4	4	4	4	HFD88_001512; HFD88_003103; HFD88_006204; HFD88_007275
Beta-glucosidase		9	9	9	9	9	9	9	HFD88_000633; HFD88_006243; HFD88_000100; HFD88_002005; HFD88_008328; HFD88_005011; HFD88_010378; HFD88_010359; HFD88_001431
Beta-galactosidase		2	2	2	2	2	2	2	HFD88_000677; HFD88_006315
Galactokinase		1	1	1	1	1	1	1	HFD88_009871
Galactose-1-phosphate uridylyltransferase		1	1	1	1	1	1	1	HFD88_002772
UDP-glucose 4-epimerase		1	1	1	1	1	1	1	HFD88_004936
UDP-glucose pyrophosphorylase		1	1	1	1	1	1	1	HFD88_004565
Phosphoglucomutase		2	2	2	2	2	2	2	HFD88_004565
Invertase		2	1	1	2	2	2	2	HFD88_000821; HFD88_004725
Hexokinase		3	3	3	3	3	3	3	HFD88_010162; HFD88_003424; HFD88_008047
Mannose-6-phosphate isomerase		2	2	2	2	2	2	2	HFD88_006399; HFD88_000452
Oxaloacetate acetylhydrolase		2	2	2	2	2	2	2	HFD88_009453; HFD88_010407
Malate synthase		3	3	3	3	2	3	3	HFD88_003886; HFD88_004697; HFD88_002011
Isocitrate lyase		2	2	2	2	2	2	2	HFD88_003886; HFD88_004697
L-Arabitol dehydrogenase		2	2	2	2	2	2	2	HFD88_000634; HFD88_003751
D-xylose reductase		1	1	1	1	1	1	1	HFD88_008228
L-sylulose reductase		4	4	4	4	4	4	4	HFD88_003695; HFD88_008283; HFD88_001090; HFD88_008006
D-xylulose reductase		4	3	4	3	4	3	3	HFD88_008288; HFD88_009120; HFD88_004639; HFD88_005020

Aldehyde reductase	4	4	4	4	4	4	4	HFD88_001875; HFD88_003199; HFD88_008111; HFD88_000427
D-xylulose kinase	1	1	1	1	1	1	1	HFD88_003734

**Table S2** Presence of orthologs of catabolic enzymes associated with organic acid production based on sequence similarity with proteins of *A. niger* ATCC 1015 (employing threshold of 60% sequence identity across 60% of protein length).

Enzyme	Strain	NIH 2624	45A	M6925	w25	TN-484	IFO 6365	ATCC 20542	ATCC 20542 gene IDs
Pyruvate dehydrogenase E1 component subunit beta		2	2	2	2	2	2	2	HFD88_004098; HFD88_008785
Pyruvate dehydrogenase E1 component subunit alpha		1	1	1	1	1	1	1	HFD88_010188
Pyruvate dehydrogenase E2 component		1	1	1	1	1	1	1	HFD88_010188
Citrate synthase		2	2	2	2	2	2	2	HFD88_002002; HFD88_006968
Aconitate hydratase		2	2	2	2	2	1	2	HFD88_001544; HFD88_001145
Isocitrate dehydrogenase (NAD <sup>+</sup> ) subunit		2	2	2	2	2	2	2	HFD88_004656; HFD88_006462
Isocitrate dehydrogenase [NAD] subunit 2		2	2	2	2	2	2	2	HFD88_006462; HFD88_004656
2-oxoglutarate dehydrogenase		2	2	2	2	2	2	2	HFD88_004285; HFD88_009432
Dihydrolipoyllysine-residue succinyltransferase		1	1	1	1	1	1	1	HFD88_005618
Succinyl-CoA ligase [GDP-forming] subunit alpha		2	2	2	2	2	2	2	HFD88_010271; HFD88_006662
Succinyl-CoA ligase [GDP-forming] subunit beta		1	2	1	1	1	1	1	HFD88_008362
Succinate dehydrogenase [ubiquinone] flavoprotein subunit		1	1	1	1	1	1	1	HFD88_003060
Fumarate hydratase		1	1	1	1	1	1	1	HFD88_002093
Oxaloacetate acetylhydrolase		3	3	3	3	3	3	3	HFD88_010407; HFD88_009453; HFD88_005712
L-lactate dehydrogenase		1	1	1	1	1	1	1	HFD88_007813
Citramalate synthase		1	1	1	1	1	1	1	HFD88_006027
Isopropylmalate isomerase (IPMI)		1	1	1	1	1	1	1	HFD88_002799
Isocitrate lyase		2	2	2	2	2	2	2	HFD88_001243; HFD88_002050

Malate synthase	1	1	1	1	1	1	1	HFD88_002011
Glucose oxidase	3	2	2	3	1	1	2	HFD88_005956; HFD88_005098
Pyruvate carboxylase	1	1	1	1	1	1	1	HFD88_000372
Malate dehydrogenase	2	2	2	2	2	2	2	HFD88_008419; HFD88_003846

**Table S3** Unique genes of *A. terreus* ATCC 20542 with KEGG annotation.

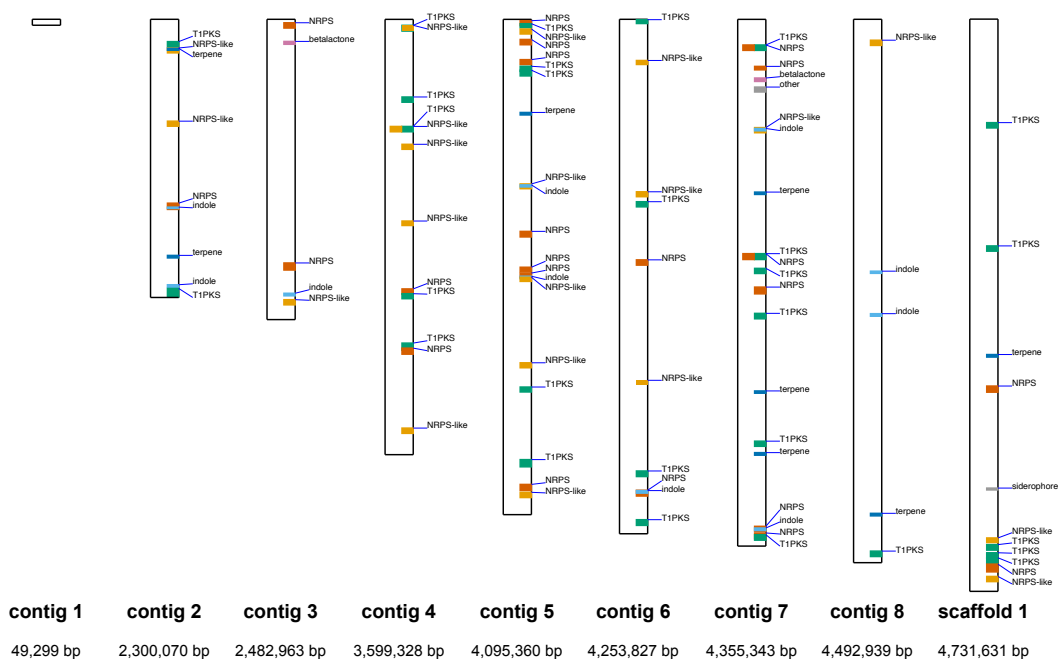
ATCC 20542 gene ID	KEGG ID	Description
HFD88_000052	K23272	Pyranose oxidase [EC:1.1.3.10]
HFD88_000053	K21899	Aldos-2-ulose dehydratase [EC:4.2.1.110]
HFD88_001689	K16219	Protein N-terminal methyltransferase [EC:2.1.1.244]
HFD88_003313	K03781	Catalase [EC:1.11.1.6]
HFD88_003314	K00844	Hexokinase [EC:2.7.1.1]
HFD88_006108	K05665	ATP-binding cassette, subfamily C (CFTR/MRP), member 1 [EC:7.6.2.3]
HFD88_008996	K01426	Amidase [EC:3.5.1.4]
HFD88_009056	K17069	O-acetylhomoserine/O-acetylserine sulfhydrylase [EC:2.5.1.49 2.5.1.47]
HFD88_010689	K00069	15-hydroxyprostaglandin dehydrogenase (NAD) [EC:1.1.1.141]
HFD88_010691	K03380	Phenol 2-monooxygenase (NADPH) [EC:1.14.13.7]

**Table S4** Conservation of genes encoding key virulent factors in *A. terreus* reported by Thakur and Shankar, 2017. Conservation of genes in *A. terreus* genomes is based on proteinortho results.

Gene name	Description	NIH 2624 gene ID	ATCC 20542 gene ID	Conservation in <i>A. terreus</i> genomes
-	Terrelysin	AATEG_03556	HFD88_000914	Conserved in all
<i>hog1</i>	Mitogen-activated protein kinase	AATEG_00489	HFD88_006440	Conserved in all
<i>mpkC</i>	Mitogen-activated protein kinase	AATEG_06557	HFD88_003645	Conserved in all
<i>cgrA</i>	rRNA-processing protein	AATEG_10388	HFD88_000168	Conserved in all
<i>creB</i>	Ubiquitin carboxyl-terminal hydrolase	AATEG_03173	HFD88_001301	Conserved in all
<i>pepP</i>	Xaa-Pro aminopeptidase	AATEG_06859	HFD88_001743	Conserved in all
<i>mep</i>	Metalloproteinase	AATEG_07544	HFD88_004788	Conserved in all
<i>myoA</i>	Myosin-1 OS	AATEG_07759	HFD88_005016	Conserved in all

## Supplementary Figures

### *A. terreus* ATCC 20542 genome



**Fig. S1** Map of *A. terreus* ATCC 20542 genome with marked SM clusters predicted by AntiSMASH

## References

Thakur R, Shankar J (2017) Proteome profile of *Aspergillus terreus* conidia at germinating stage: identification of probable virulent factors and enzymes from mycotoxin pathways. *Mycopathologia* 182:771-784