

Supplementary Tables

Table S1. Genome sequence statistics

		PFGE	Sequencing
Genome assembly size		-	37,047,050 b
Largest contig		-	4,427,704 b
Largest scaffold		-	6,340,603 b
Chromosome size	1	7.0 Mb (I)	6.4 Mb
	2		6.2 Mb
	3	5.2 Mb (II)	5.0 Mb
	4	5.0 Mb (III)	4.8 Mb
	5	4.5 Mb (IV)	4.4 Mb
	6	4.0 Mb (V)	4.1 Mb
	7	3.7 Mb ¹ (VI)	3.4 Mb ¹
	8	2.8 Mb (VII) + 2.8 Mb (VIII)	3.3 Mb
Total genome size		35.0 Mb ¹	37.6 Mb ¹
Mitochondrion		-	29,202 b

The chromosome numbers in parentheses are those previously assigned by PFGE. The nucleotide lengths include a complete rDNA repeat (7,795 b) and two telomeric repeats for each chromosomal end except the right end of chromosome 8, where the sequence adjacent to the telomeric repeats is not known.

¹ The values include rDNA repeats estimated to have 0.6 Mb in length.

Table S2. Comparison of gene numbers for each COG

		<i>A. oryzae</i>	<i>A. fumigatus</i>	<i>A. nidulans</i>	<i>N. crassa</i>	<i>S. cerevisiae</i>
Information storage & processing						
J	Translation, ribosomal structure and biogenesis	264	262	252	256	329
A	RNA processing and modification	173	170	168	170	175
K	Transcription	147	145	138	153	181
L	Replication, recombination and repair	140	145	136	140	137
B	Chromatin structure and dynamics	34	33	29	36	43
Cellular processes and signaling						
D	Cell cycle control, cell division, chromosome partitioning	74	72	70	72	88
Y	Nuclear structure	5	3	4	5	3
V	Defense mechanisms	47	32	28	22	26
T	Signal transduction mechanisms	232	201	197	184	179
M	Cell wall/membrane/envelope biogenesis	89	70	55	38	24
N	Cell motility	2	2	2	2	0
Z	Cytoskeleton	76	69	77	72	57
W	Extracellular structures	3	1	4	4	5
U	Intracellular trafficking, secretion, and vesicular transport	197	206	186	184	230
O	Posttranslational modification, protein turnover, chaperones	356	345	325	325	327
Metabolism						
C	Energy production and conversion	299	239	267	202	163
G	Carbohydrate transport and metabolism	477	356	389	237	171
E	Amino acid transport and metabolism	417	293	313	200	180
F	Nucleotide transport and metabolism	97	79	78	62	74
H	Coenzyme transport and metabolism	103	79	74	69	66
I	Lipid transport and metabolism	275	217	240	169	117
P	Inorganic ion transport and metabolism	189	144	155	127	95
Q	Secondary metabolites biosynthesis, transport and catabolism	413	231	296	132	56
Poorly characterized						
R/S ¹	General function prediction only/ Function unknown	1,415	1,098	1,192	868	870
X ²	Gene of unknown function	7,124	4,967	5,223	5,642	3,085
COG hit		4,950	4,040	4,170	3,383	3,133
Total		12,074	9,007	9,393	9,025	6,218

The genes encoding polypeptides longer than 100 amino acids are used for the analysis. The genes having homology to ≥ 2 COGs are counted redundantly in each COG.

¹The genes having homology to COGs other than R/S are excluded.

²The genes having no homology to any COGs including the genes having homology to R/S.

Table S3. Classification of the polyketide synthase related genes in *Aspergillus oryzae*

	<i>A. oryzae</i>	<i>A. nidulans</i>	<i>A. fumigatus</i>
Aflatoxin biosynthesis related PKS genes	2	1	0
WA PKS orthologue gene	1	1	1
WA-like PKS genes	10	3	4
Lovastatin PKS-like genes	15	12	7
Others	2	11	2
Total	30	28	14

*Gray columns indicate that the number of the genes is ≥ 2 -fold of the minimum number among the three *Aspergilli*.

Table S4. Redundancy of the transporter genes

	<i>A. oryzae</i>	<i>A. nidulans</i>	<i>A. fumigatus</i>	<i>N. crassa</i>	<i>S. cerevisiae</i>
Total Transporter Proteins:	610	474	548	339	286
ATP-Dependent	61	54	74	55	42
ABC family	52	46	37	34	23
P-ATPase family	2	2	26	19	16
Ion Channels	18	26	22	10	13
Annexin family	3	14	3	0	0
Secondary Transporter	529	389	444	270	222
AAAP family	5	8	17	4	7
APC family	75	39	47	15	24
DMT family	5	5	13	6	9
MC family	18	12	26	33	34
MFS family	365	278	251	142	84
Unclassified	1	4	7	3	6

*Gray columns indicate the redundancy of ≥ 10 . Thick framed values indicate the number of genes of ≥ 1.4 -fold of the minimum numbers among the three Aspergilli when the numbers of genes of all the three Aspergilli are ≥ 10 .

Table S5. Redundancy of genes encoding hydrolytic enzymes.

	<i>A. oryzae</i>	<i>A. nidulans</i>	<i>A. fumigatus</i>
Pectinolytic enzymes			
Pectin methylesterase	5	3	4
Pectin/pectate lyase	15	13	9
Family PL1 (PF00544; IPR002202)	11	8	6
Family PL3 (PF03211; IPR004898)	4	5	3
Polygalacturonase	20	9	11
Glycosyl hydrolases with substrate-binding domains			
Cellulose-binding domain (CBM1)	5	7	14
Starch-binding domain (CBM20)	1	4	3
Chitin-binding domain (CBM18)	6	14	5

*Gray columns indicate that the number of the genes is ≥ 1.5 -fold of the minimum number among the three Aspergilli.

Table S6. Redundancy of secretory protease genes

	EC number	<i>A. oryzae</i>	<i>A. nidulans</i>	<i>A. fumigatus</i>
Exopeptidase				
Aminopeptidase	3.4.11.-	19	15	14
Dipeptidase	3.4.13.-	3	1	2
Dipeptidyl or tripeptidyl peptidase	3.4.14.-	9	6	6
Serine-type carboxypeptidase	3.4.16.-	12	5	8
Metalloprotease	3.4.17.-	12	7	7
unknown peptidase		14	10	11
Total		69	44	48
Endopeptidase				
Oryzin	3.4.21.63	2	2	2
Aorsin	3.4.21.-	2	1	1
Kexin	3.4.21.61	1	1	1
ATP-dependent proteinase	3.4.21.51	6	6	6
Cysteine proteinase	3.4.22.-	4	3	4
Ubiquitin-specific proteinase	3.4.22.-	7	7	7
PalB	3.4.22.-	1	1	1
Aspartic proteinase	3.4.23.18	11	7	7
Pepstatin insensitive proteinase	3.4.23.19	3	2	2
Saccharolysin	3.4.24.37	3	0	1
Metalloprotease	4.2.24.-	12	5	8
Insulinase	3.4.24.-	4	4	4
Unknown	3.4.99.-	10	7	7
Total		66	46	51
Exopeptidases + Endopeptidases		135	90	99

*Gray columns indicate that the number of the genes is ≥ 1.5 -fold of the minimum number among the three *Aspergilli*.

Table S7. Genes responsible to protein folding

<i>Aspergillus sp.</i>	<i>A.oryzae</i>	<i>A.nidulans</i>	<i>A.fumigatus</i>
PDI	AO070229000008	AN7436.1	57.m05906
TIG (Erp38)	AO070311000141	AN0075.1	71.m15353
PRP	AO070338000241	AN0248.1	54.m06701
<i>S.cerevisiae ERO1</i> homolog	AO070334000228	AN1510.1	55.m03022
PPI (-H(E/N)EL)	AO070305000123	AN4467.1	58.m07853
PPI (-CGEL)	AO070311000012	AN3814.1	57.m05668
PPI (-AGEL)	AO070328000042	-	-
BiP	AO070341000205	AN2062.1	57.m05760
Other ER-resident Hsp70	AO070216000006	AN0847.1	70.m15446
Calnexin	AO070342000144	AN3592.1	58.m07392

*Gray columns indicate presence only in *A. oryzae* genome.

Table S8. Genes responsible to protein translocation for secretion

	<i>A.oryzae</i>	<i>A.nidulans</i>	<i>A.fumigatus</i>
SBH1/2	AO070338000265	AN0417.1	54.m06659
SSS1	AO070329000042	AN4589.1	-
SEC61/SSH1	AO070325000136	AN7721.1	71.m15748
SEC62	AO070304000007	AN6269.1	72.m19366
SEC63	AO070255000011	AN0834.1	70.m15804
SEC66	AO070232000005	AN1442.1	55.m02942
SEC72	AO070294000021	AN7623.1	71.m15860