



Table S1. Gene specificity primers used in this study.

Gene Name	Primer	Primer Sequence (5' to 3')
<i>pgaX</i>	pgaX-F	TGGATGGTAACGGTCAGGTCTGG
	pgaX-R	GCGAGTAACGAAGGTTGAGAGGTC
<i>eglB</i>	eglB-F	CACTGTCACTGCCACTGCCAAG
	eglB-R	GGTCCAGTTGATGCCACCACAC
<i>CELB</i>	CELB-F	CGATGCCTCACTCACCAACTG
	CELB-R	CAGCACGCAGGAGATGTCAAGAC
<i>cbhA</i>	cbhA-F	GTTGGCTCTCGTCTGTTCTGATG
	cbhA-R	GCTCCATTGAGTCCGCAAGGC
<i>galA</i>	galA-F	TTGCGGCAATCATCTCGATGTG
	galA-R	TGTTGCTGTAGCTGCTTGTTCCTC
<i>manA</i>	manA-F	CCTGGACTATGTTGTTGCCTCTGC
	manA-R	TAGGCGGCCATACCTCCATAATCC
<i>xyn2</i>	xyn2-F	CGATCACCACGAGCCAGCAAG
	xyn2-R	TCACCTGAAGCACCGTTGTTGTAG
<i>abnA</i>	abnA-F	CCGCCAGCGGAGCAGAATAC
	abnA-R	CAGGACCGTATACTGTGCCATGAC
<i>btgE</i>	btgE-F	GCTTCCTTCATCCAGTCCGCTTC
	btgE-R	GATGTCAACGGCACCGCAGAG
<i>brlA</i>	brlA-F	CGATGCCTCAGTACAACCAGATGG
	brlA-R	ATCGGACGAGACAAGCAAGGATTG
<i>abaA</i>	abaA-F	CCGTAACCTTCTTCCGCTCCTTGTC
	abaA-R	GCCATACGCTTGCTCTCATCACC
<i>wetA</i>	wetA-F	GCCTTCTCAGTACGACGCAAGAC
	wetA-R	TGGCTGCCGTGCTGACATTG
<i>VEA1</i>	VEA1-F	CCACCGCCGATGATACGATTGC
	VEA1-R	GCCGATGTCAAGTTGGACGAGTAG
<i>CCC1</i>	CCC1-F	GGTGGTATTGCCGCTGGTTCTG
	CCC1-R	GTCATGCTTGTGGTCCTCGTGAG
<i>FET5</i>	FET5-F	GTCCACAAGCCAGCATCCAGATC
	FET5-R	TGCTGCATCGACGCTGTCAAC
<i>FET3</i>	FET3-F	GTGGATGTTGCCTCTGACCTTGTC
	FET3-R	CCGCACCGTTCCGTAGATTGTTC
<i>Mic-33</i>	Mic-33-F	ACGCAACCAAGACCGCTATTGAG
	Mic-33-R	GCCAGTCCGCCATTGAAGAAGG
<i>gdh-1</i>	gdh-1-F	AACGAGCACGACGAGATGGTTATG
	gdh-1-R	CGGAACTCAGAGCTGATGACAAGG
<i>NoxA</i>	NoxA-F	GGCTACGACGTGTGCGAGTTCATC
	NoxA-R	CAGCGGTGTCAGCGTCAAGG

<i>pacC</i>	pacC-F	CGCACAGTCATACACCTCCAACC
	pacC-R	GGTCATACGCAACGCTCAGAGTAG
<i>β-tublin</i>	Tub-F	GATTGTCTTGAGAAATACTG
	Tub-R	TGTACCAGTGCAAGAAAGCC

Table S2. Number of differentially expressed genes annotated.

DEG Set	Total	Swiss-Prot	GO	KEGG	COG	KOG	Pfam	NR
A vs B	4582	3100	3278	1219	1891	2360	3061	4565

Table S3. The DEGs related to growth of *Penicillium digitatum* spores.

Gene ID	Gene Name	Function Classification	Description	Fold Change
PDIP_05330	<i>brlA</i>	growth	conidiophore stalks	-3.35
PDIP_20340	<i>abaA</i>	growth	phialides	-2.35
PDIP_44350	<i>wetA</i>	growth	conidiospore	-2.92
PDIP_21430	<i>VEAI</i>	growth; oxidative stress	growth; oxidative stress	1.76
PDIP_64730	<i>VelB</i>	growth; oxidative stress	growth; oxidative stress	1.63
PDIP_33270	<i>vosA</i>	growth	conidiospore	-1.58

Table S4. The up-regulated DEGs related to pH.

Gene ID	Gene Name	Function Classification	Description	Fold Change
PDIP_57180	<i>gox</i>	Organic acid	Glucose oxidase	2.53
PDIP_86430	<i>patE</i>	Precursors for organic acid	glucose-methanol-choline oxidoreductase	5.72
PDIP_54170	<i>xptC</i>	Precursors for organic acid	glucose-methanol-choline oxidoreductase	2.33
PDIP_23540	<i>patE</i>	Precursors for organic acid	glucose-methanol-choline oxidoreductase	2.08
PDIP_84520	<i>citC</i>	Precursors for organic acid	glucose-methanol-choline oxidoreductase	1.05

Table S5. The DEGs related to iron transport.

Gene ID	Gene Name	Function Classification	Description	Fold Change
PDIP_76510	<i>CCC1</i>	Iron storage	Transport protein	7.81
PDIP_65530	<i>FET5</i>	Iron uptake rate	Iron transport multicopper oxidase	7.45
PDIP_59000	<i>FET3</i>	Iron uptake rate	Iron transport multicopper oxidase	4.51
PDIP_44440	<i>NRPS12</i>	Synthesis of iron carrier	Non ribosome peptide synthetase	3.35
PDIP_39920	<i>NRPS11</i>	Synthesis of iron carrier	Non ribosome peptide synthetase	-1.03

Table S6. The up-regulated DEGs related to ethylene.

Gene ID	Gene Name	Function Classification	Description	Fold Change
MSTRG.6263	<i>AAT2</i>	Ethylene synthesis	Aspartate amino transferase	3.35
PDIP_36570	<i>Mic-33</i>	Precursors for ethylene	2-oxoglutarate carrier protein	5.62
PDIP_06610	<i>htyE</i>	Ethylene forming enzyme (EFE)	2-oxoglutarate	1.70
PDIP_83100	<i>encD</i>	Ethylene forming enzyme (EFE)	2-oxoglutarate-Fe(II)	1.93
PDIP_08660	<i>citB</i>	Ethylene forming enzyme (EFE)	2-oxoglutarate-Fe(II)	1.14
PDIP_32270	<i>gdh-1</i>	Precursors for ethylene	generate 2-oxoglutarate	1.93

Table S7. The up-regulated DEGs related to anti-oxidative stress.

Gene ID	Gene Name	Function Classification	Description	Fold Change
PDIP_07850	<i>tef3</i>	Glutathione S-transferase	Elongation factor 1-gamma	8.20
PDIP_64830	<i>hpm2</i>	Glutathione S-transferase	Transferase activity	5.11
PDIP_62390	<i>GTT1</i>	Glutathione S-transferase	Transferase activity	3.37
PDIP_06860	<i>ustS</i>	Glutathione S-transferase	Glutathione S-transferase-like protein	3.15
PDIP_12980	<i>FUS2</i>	Glutathione S-transferase	20-hydroxy-prefusarin hydrolase	2.99
PDIP_26410	<i>mtx1</i>	Glutathione S-transferase	Metaxin-1	2.08
PDIP_11910	<i>FUS3</i>	Glutathione S-transferase	Glutathione S-transferase-like protein	1.43
PDIP_77260	<i>gedE</i>	Glutathione S-transferase	Glutathione S-transferase-like protein	1.34
PDIP_74290	<i>tpcF</i>	Glutathione S-transferase	Glutathione transferase activity	1.32
PDIP_74730	<i>tpcF</i>	Glutathione S-transferase	Glutathione S-transferase-like protein	1.32
PDIP_80930	<i>gto2</i>	Glutathione S-transferase	Glutathione S-transferase omega-like	1.10
PDIP_86820	<i>unknow</i>	Catalase	oxidation-reduction process	3.15
PDIP_67580	<i>catB</i>	Catalase	Inorganic ion transport and metabolism	2.76
PDIP_05940	<i>PXP9</i>	Catalase	Peroxisomal catalase	1.63

Table S8. The up-regulated DEGs related to effectors.

Gene ID	Gene Name	Function Classification	Description	Fold Change
PDIP_77830	unknow	Necrosis inducing protein	Necrosis inducing protein	7.23
MSTRG.1774	unknow	Necrosis inducing protein	Necrosis inducing protein	6.25
PDIP_06030	unknow	LysM domain	Killer toxin subunits alpha/beta	4.55
PDIP_59730	unknow	LysM domain	Killer toxin subunits alpha/beta	1.11
MSTRG.8292	<i>chiA1</i>	Chitinase	Chitinase activity	6.00
PDIP_36560	<i>chiA</i>	Chitinase	Chitinase activity	5.62
PDIP_53900	<i>ctcA</i>	Chitinase	Chitinase activity	5.06

MSTRG.3881	<i>DAN4</i>	Chitinase	Chitinase activity	4.72
PDIP_79160	<i>chiA</i>	Chitinase	Chitinase activity	4.49
PDIP_84020	<i>chiA</i>	Chitinase	Chitinase activity	3.17
PDIP_85490	<i>chiA</i>	Chitinase	Chitinase activity	2.27
PDIP_16610	<i>chiA1</i>	Chitinase	Metal ion binding	2.06
PDIP_06200	<i>chiA</i>	Chitinase	Chitinase activity	1.70
PDIP_09650	<i>CH11</i>	Chitinase	Chitinase activity	1.63
PDIP_83360	<i>chiB</i>	Chitinase	Chitinase activity	1.55
PDIP_53760	<i>CH11</i>	Chitinase	Chitinase activity	1.39
PDIP_82800	<i>chiA1</i>	Chitinase	Chitinase activity	1.05

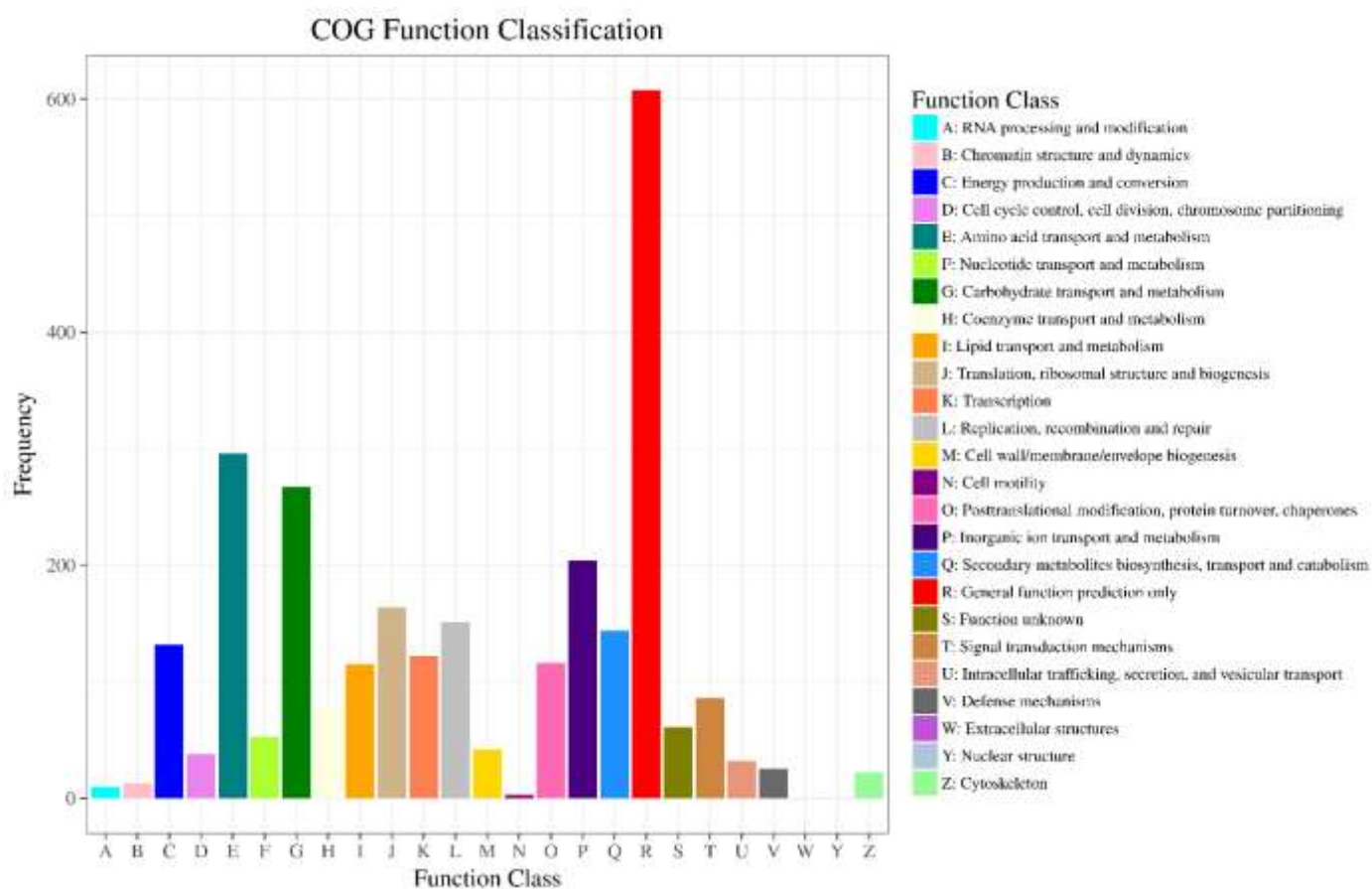


Figure S1. COG function classification of DEGs.