

**Transcriptome analysis of *mfs2*-defective *Penicillium digitatum* mutant to reveal importance of *Pdmfs2* in developing fungal prochloraz-resistance**

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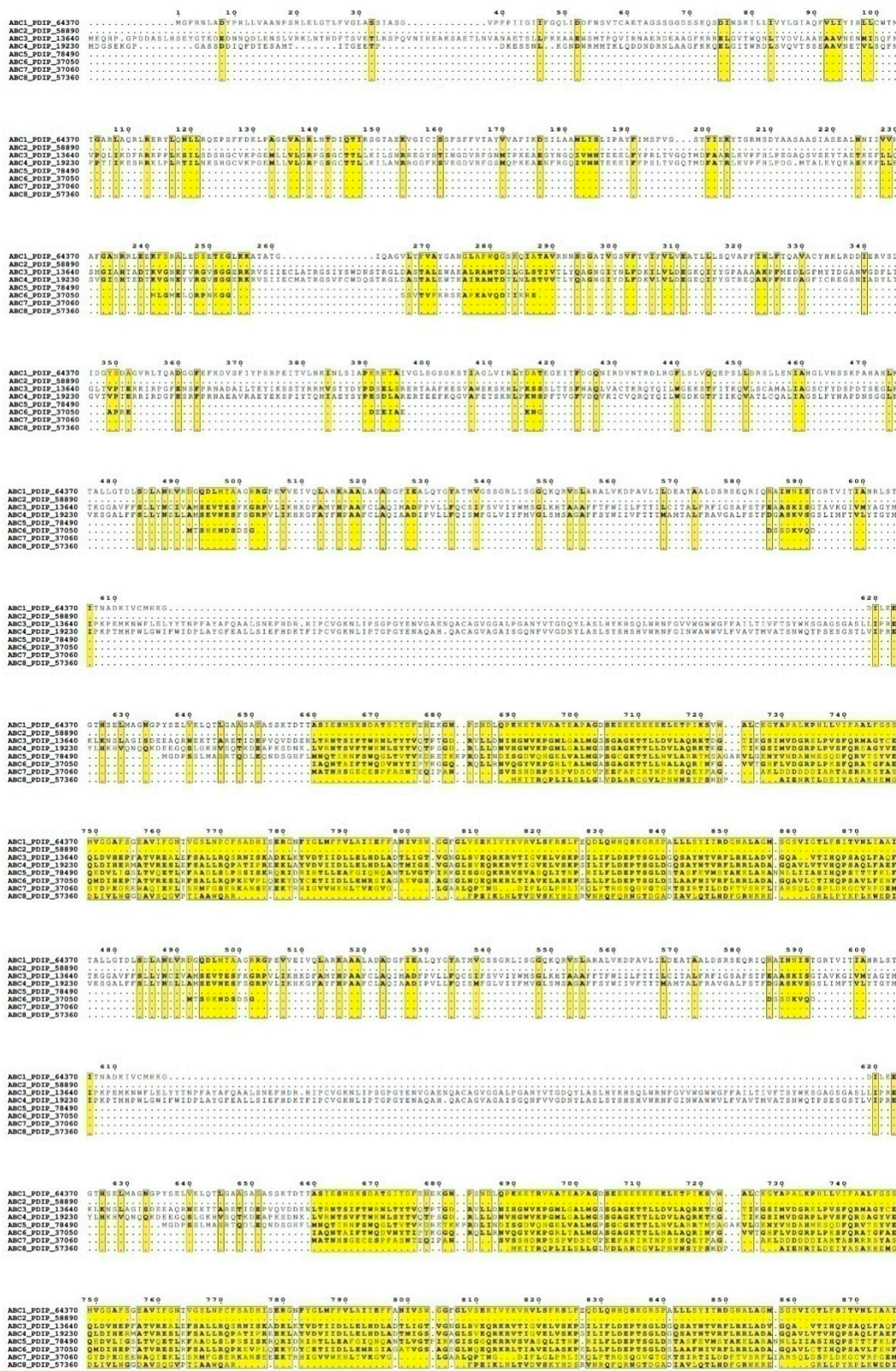
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## Supplementary Materials



**Figure S1.** Protein homology alignments for multiple isoforms of MFS (MFS1-33), ABC (ABC1-8), and MATE (MATE1-3) in the present study.





**Figure S1 (continued).** Protein homology alignments for multiple isoforms of MFS (MFS1-33),

ABC (ABC1-8), and MATE (MATE1-3) in the present study.



**Table S1** Primers used in the present qRT-PCR.

Gene name	Primer	Sequence (5'→3')	Fragment size amplified
<i>MFS1</i>	F	GCCCACAGCACAAACCAAAG	108
	R	CATGCGCAAGGGTTGTTTCAG	
<i>MFS2</i>	F	ACATCTTCCGGCGATTTCCAT	109
	R	GAACCTTAGCCCAAGTGCCA	
<i>MFS3</i>	F	CGATCATCGTACGTGAAACCC	106
	R	CTGCGACGGTTGACTGTTTG	
<i>MFS4</i>	F	AATGCTTCCTGAGTCTCCGC	107
	R	TGATTTCTGCGAACACGGA	
<i>MFS5</i>	F	TGCATCCAGAGAGCATGACC	106
	R	ATCCCACAGCAAGAAGAGCC	
<i>MFS6</i>	F	CTGTGAGCTTTTGCAATGGGA	108
	R	CCCATTGTTGATGGCAAGC	
<i>MFS7</i>	F	GCTAACACCAAGCACAGGGA	104
	R	CAGCCCTAGTGATGAGAACCA	
<i>MFS8</i>	F	CTTCACGGGCTTCGTCTACC	108
	R	TGGATCGCACATACCCATCG	
<i>MFS9</i>	F	CAAACCTGGACAACGCTGACG	104
	R	GCAAGCTCACCTCGTCGATA	
<i>MFS10</i>	F	CGCTCCCCGCTTCATCTTAT	105
	R	GCCAGGTGTCCTTGACGTAG	
<i>MFS11</i>	F	GTGTGATGGACGAGGGGAC	110
	R	TGCAGACGTACACATCACCG	
<i>MFS12</i>	F	GGAGCTCTTATCACTGGGGG	107
	R	TGGATGCACAGCCCACTTAG	

<i>MFS13</i>	F	TAGCAACGCCAGCAGTATCT	105
	R	CTGGGATCCCCAGAAAGACA	
<i>MFS14</i>	F	ATCGGTTGGGTACTGTCTGTG	102
	R	AATGGCTGAGACACAGGTCG	
<i>MFS15</i>	F	ATGCTAAACCGCCTCAACCA	106
	R	TCAGCGTGAAGAATGGCAGA	
<i>MFS16</i>	F	GGACCCTGTGTTCCCTGAAG	105
	R	TTCGTGGATGGAACAGAGCC	
<i>MFS17</i>	F	GTGAGCTCATGGCTTTCCGA	108
	R	ACGCACGTTAGGGTAAGACAC	
<i>MFS18</i>	F	TGGTTGGAGCGTTTGCTACT	106
	R	TGCCCCTGGAAACCAATCAA	
<i>MFS19</i>	F	AGCCATGGGGCTATGAATGG	106
	R	AGTGCTCGGGTGAATGACAC	
<i>MFS20</i>	F	GCTCCTTACGGCAAGGTGAA	104
	R	ACTGGTTCAAAAGCCACTGGA	
<i>MFS21</i>	F	GTCGGCGGTACTTTTGGAGA	105
	R	GTAGATGGGAGCACCGACTG	
<i>MFS22</i>	F	TGACCCGAATTCCATTGCCA	110
	R	CGTCCGGATCGAATCTGTGT	
<i>MFS23</i>	F	TCACTGTGTATCTTGGCCGC	103
	R	AAAGTGAGCACGTCAACGGA	
<i>MFS24</i>	F	CGAGTGTTGTCGGTATTGCAC	109
	R	TCTTTGCGGAGGAAAAGGCT	
<i>MFS25</i>	F	TGGGTAGGTCCCACTCACAT	103
	R	TCTTCATGGCGAGGATACCG	
<i>MFS26</i>	F	AGCAGTGGATCAACGCCATT	106
	R	ACGGACGGTAGAATTGCAGC	

<i>MFS27</i>	F	CCCAGAGCGCAGCTAATACT	109
	R	TCCTTCTCCAAATCGGCATCC	
<i>MFS28</i>	F	CTCACCTACTCCATTGGCCC	107
	R	CCCAAATTCCAGGCTAGGCA	
<i>MFS29</i>	F	TCGCGGTAAGACTTCGACTC	109
	R	CAGTGGAGCCCAGAGCAATG	
<i>MFS30</i>	F	GCGCCAAATCAACATTGGGA	108
	R	AGTCCCCGTTTCACCAAACA	
<i>MFS31</i>	F	CGTTTTCACATCGTGCCTGG	109
	R	CGTCCGGAGTTATACTCGCC	
<i>MFS32</i>	F	AAACACCCCAACTCGCCAAT	108
	R	AGACAGTGAGGAGAGGGAACT	
<i>MFS33</i>	F	CTCCTCGTATGCTCTACCGC	107
	R	GCAATGGCTGTAGAAACTGACA	
<i>ABC1</i>	F	AGGTGCCACTGTTGGATCTG	108
	R	GGGTAGCTGTCGGTGATGTT	
<i>ABC2</i>	F	GCGCTCTACAGAAGGTACGA	107
	R	GCAGAGGAGTTGCTTTTGGC	
<i>ABC3</i>	F	TCTGGTAAGCTGTCGTCTTCC	103
	R	AGCGGACCCGATAAATCGAA	
<i>ABC4</i>	F	CCTGGGCGTAAGTTTTCTTCA	110
	R	CTATTTGGGCGTAGGGGACC	
<i>ABC5</i>	F	TTCACCAAAGAGCGAGCCAA	106
	R	TGGCAGGAGATAGTGAGGACA	
<i>ABC6</i>	F	ATTTGCACGGTGTGAGCAAC	105
	R	GCGCAGCATAGAAGACACGA	
<i>ABC7</i>	F	GGTAATCAACGAGCGGGCTA	106
	R	AGAAACACACACCTTCAGACCT	

<i>ABC8</i>	F	AAACACGAGATGGGTGACCTC	108
	R	GCTTACAGCTTTTCAACCGTGT	
<i>MATE1</i>	F	ACTGGCACTTATCTGTGGCT	102
	R	GGCCAGTCTTACCTGGATTGT	
<i>MATE2</i>	F	GACGCGAGAACAATTTGCGA	105
	R	AGCCCATCGGCAATCTGAAA	
<i>MATE3</i>	F	GTGCAAGGCAAACGATGTGA	109
	R	AGTGCTTTACAACGCAGGGA	
<i>1,3,6,8-Tetrahydroxynaphthalene reductase</i>	F	TCCAAGCCGACCTGACAAAT	105
	R	TCTCAGTTCCTGCGTTCGAC	
<i>4-Hydroxyphenylpyruvate dioxygenase</i>	F	CAGTTGTCGACGAGGCATCT	111
	R	CAGTTGTCGACGAGGCATCT	
<i>60S Acidic ribosomal phosphoprotein</i>	F	CGAGAAGGTCATCTCCGAGC	108
	R	CAGCTATGGAAAGGGTCAGCA	
<i>60S Ribosomal protein</i>	F	TCCGCCGTCTGAGTTGTATG	106
	R	GACCTTAAGGGCTGCTCAGAA	
<i>40S Ribosomal protein</i>	F	CCGCAAGAAGATCCACGAGT	103
	R	ATCCGCTCTAAGGTGACGGA	
<i>Ribosomal protein</i>	F	CGAACAGTCAACTGGGGTGA	106
	R	TCTGGAAGCCGTTCTGGAAG	
<i>Acetyl-CoA carboxylase</i>	F	GGCTTATGAGACCTTCGGCA	104
	R	ATTGGTCGGCCATGCGAATA	
<i>Alcohol dehydrogenase</i>	F	GCGTCGGAGTACCACGTATT	109
	R	GGATGAGGCTCGTG TAGTCG	
<i>Aldehyde dehydrogenase</i>	F	TGGTTAGTCGTGTGCAGCAT	103
	R	CCCGTATTACCGATCCGCTC	
<i>Aldehyde reductase</i>	F	GTGCACCAGATGGAGTGTCA	107
	R	TTCTGGTTACCAAACGGCGA	



<i>Amine oxidase</i>	F	GGTGTCTCCTTCAAGGTCCG	106
	R	GAGTGCGCACATCGGAGATA	
<i>Amino acid permease</i>	F	AGGGCTTTTCGTTACTGGAGC	109
	R	CCAGCTTGAATAAGCACCGC	
<i>ATP synthase subunit 6</i>	F	CAGGTTGTCCTTTAGCTTTATTACC	113
	R	GTGACCACTTAATATGTTAGCAGC	
<i>Erg1</i>	F	GAGCAGAAAGTCGGTCCCAA	108
	R	CTCGGTGATACTGGCGTGAA	
<i>Erg3</i>	F	AACGAAGATGGGCGATGAGG	106
	R	CTTCGTGTCGGAGGAGTAGC	
<i>Erg24</i>	F	CAATGGTATGGCAACGGCAG	103
	R	ATGATGGCAGAGGAGAACGC	
<i>Erg25</i>	F	TGGCATTACTTCTCCCACCG	107
	R	GCATATTCAGCAGCCAAGCC	
<i>Carnitine acetyl transferase</i>	F	GGCCATGAGCTCGTATCAGT	104
	R	CGACGATGTGCTGGTTTTTCG	
<i>Catalase</i>	F	TTCTGGGATTTCCACGCGAA	106
	R	TACCGAACCCTGTCATTTCGG	
<i>Cytochrome b</i>	F	TAATCGACGCACCAACACCA	109
	R	TGCATAGCTAATGTAACCTCCTGT	
<i>Cytochrome c oxidase</i>	F	TGGTACTGGTTTCCACGGTT	111
	R	TCGTAACCAAGGTGATGGTGA	
<i>RNA helicase</i>	F	AGGTGAGTTTGCACGAGAGG	101
	R	GAGACGAACGTTCTCCAGCA	
<i>Dienelactone hydrolase</i>	F	TACGGTGATGCTGTGCCTTT	106
	R	CAACGGTTGAGGGGAGATGA	
<i>Epoxide hydrolase</i>	F	CCCACGGCCAAGTATTCCT	108
	R	CGACCGAACAACCTTCTCCA	

<i>Exopolygalacturonase</i>	F	TGTAAAGCGCATTGGGGGAT	103
	R	TGCTTGCCAGTAATCGGTGT	
<i>Exo-<math>\beta</math>-1,3-glucanase</i>	F	ATCGATTTTTTGACGCCGCTG	103
	R	GCTCCAGTGTTGGGACAGAA	
<i>Fatty acid synthase <math>\beta</math> subunit</i>	F	CGCAGCATCTACACCACGTA	105
	R	GTAGAGCTTGCTAGCCTCGG	
<i>Fatty acyl-CoA oxidase</i>	F	GTGACTCTCCGGAACAAGG	107
	R	CCGTGGCCCAATTCTGTTTG	
<i>FMN dependent dehydrogenase</i>	F	GCGGCGCTGATATTGTGAAG	106
	R	TGGCTCACTCCATGTTCAAC	
<i>Glutathione S-transferase</i>	F	CTCGGGCTATTGCGAGGTAT	103
	R	CTTGCTGCTTGCTCGAAGAG	
<i>Glycerol kinase</i>	F	ATCAAGGCACTACGAGCACC	102
	R	ACCCCGGGATCGGGTATATT	
<i>Glyoxylate reductase</i>	F	CTTTGTCGTTGCACCGTTGA	107
	R	TTGCCGATGACTCGACTAGC	
<i>Maleylacetoacetate isomerase</i>	F	GCGGCTTGGTGTTGACTTG	101
	R	CCTGTGACCTCCAATGTCCC	
<i>MAP kinase kinase kinase</i>	F	CATTGGATCGCGTGCTTCTG	104
	R	AAGCTCGAGGAAATCAGCCC	
<i>NADH dehydrogenase subunit 1</i>	F	TGCATTTGTAACTATAGCCGAACG	106
	R	AGCATCAGCAAATGCTTGTAAT	
<i>NADH dehydrogenase subunit 4</i>	F	TCTGTATCTCACGCAGCTGTA	108
	R	TGCTGGTGATACAAAACCGT	
<i>NADH-ubiquinone oxidoreductase</i>	F	AGCCCAATCCGATTCAACCA	109
	R	CCTCGTACTGGCACTTCTCG	
<i>Nitrate reductase</i>	F	CCAGATCATGGCCGTCCTTT	102
	R	ATTGCTTGGGGCATCAGTCA	

<i>Nitrite reductase</i>	F	TGCAGGATCGTTGGTCACTC	107
	R	TGCCATCCACATTCTTCCCC	
<i>Oxaloacetate hydrolase</i>	F	ACTGTACGCTGACGGTGTTT	105
	R	AGCGTTGGTCTTCATGTCGT	
<i>Pectate lyase</i>	F	CTCCAAGGCCATTTTGAGCG	104
	F		
	R	CGTTGGTCTCTCCCTTGACC	
<i>Phenyloxazoline synthase</i>	F	GGCTCCATTGATGCCCCATA	106
	R	TCCGGTTTGACGACCCAAAA	
<i>Phosphatidylserine decarboxylase</i>	F	GGTCATCGGGATCTCACAGC	103
	R	CATGATTTGGCGCAGATGGG	
<i>Phospholipase C</i>	F	GACCCTCGGTTACTTGTGGG	108
	R	AGAGTCGGAGGAGTAGAGCG	
<i>Pre-mRNA-splicing factor</i>	F	AAGGAAATCGAAGAGGGCCG	104
	R	CGGTAGTACGGTTCGCTGTT	
<i>Protein-L-isoaspartate O-methyltransferase</i>	F	TTATCACTGGCGATGGACGG	109
	R	CGCAACTGATCCACCAGAGT	
<i>Superoxide dismutase</i>	F	CAGGAAGCGTTTGTCAAGGC	103
	R	TCTCAAGCCGTCCTTAGGA	
<i>Thioredoxin</i>	F	CATCGCACCCAAGATCGAAG	103
	R	TACACCCAGCTCTTGTCCGA	
<i>Ubiquitin carboxyl-terminal hydrolase</i>	F	ATGGTTCGACAGCTACCACG	101
	R	CACTCCTCGTGCATCTCCTC	
<i><math>\alpha</math>-L-Rhamnosidase</i>	F	CATGGGTACTGGCAGCAAGA	106
	R	AGACGTGCCATGGTTTGGAT	
<i><math>\beta</math>-actin</i>	F	TGTCACCAACTGGGACGATA	101
	R	GAGCTTCGGTCAAGAGGATG	

F and R indicated forward primer and reverse primer, respectively.

**Table S2** Summary of the reads quality in the present study.

Sample name	Clean reads	Clean bases	GC Content (%)	Q30 (%)
Pd-d-I	21847213	6536999320	54.06	94.83
Pd-d-NI	23870541	7141474368	53.98	95.00
Pd-wt-I	23294756	6966924166	53.62	94.85
Pd-wt-NI	22149643	6621791146	54.01	94.84

**Table S3** Summary of percentages of reads mapping to the reference genome in the present four samples.

Sample name	Pd-d-I	Pd-d-NI	Pd-wt-I	Pd-wt-NI
Total reads	43694426	47741082	46589512	44299286
Mapped reads	41903504 (95.90%)	44888991 (94.03%)	40876823 (87.74%)	41656928 (94.04%)
Unique Mapped reads	40979275 (93.79%)	44103959 (92.38%)	40232931 (86.36%)	40744683 (91.98%)
Multiple mapped reads	924229 (2.12%)	785032 (1.64%)	643892 (1.38%)	912245 (2.06%)
Reads map to '+'	20296757 (46.45%)	21930967 (45.94%)	20120079 (43.19%)	20160549 (45.51%)
Reads map to '-'	20669287 (47.30%)	22221843 (46.55%)	20257660 (43.48%)	20554396 (46.40%)

**Table S4** SNP analysis in the present four samples.

Sample name	SNP Number	Genic SNP	Intergenic SNP	Transition	Transversion	Heterozygosity
Pd-d-I	2,458	1,592	866	61.92%	38.08%	33.52%
Pd-d-NI	2,527	1,609	918	61.65%	38.35%	35.30%
Pd-wt-I	2,311	1,511	800	62.48%	37.52%	31.03%
Pd-wt-NI	2,580	1,675	905	61.94%	38.06%	35.47%

**Table S5** DEG numbers in the present four comparative groups.

Comparative group	DEG Number		
	All	Up-regulated	Down-regulated
Pd-wt-(I/Ni)	460	240	220
Pd-d-(I/Ni)	147	50	97
I-(Pd-d/Pd-wt)	1,221	608	613
Ni-(Pd-d/Pd-wt)	717	366	351

**Table S6** Number summary of the DEGs functionally annotated in the eight public databases.

Database	Pd-wt-(I/Ni)	Pd-d-(I/Ni)	I-(Pd-d/Pd-wt)	Ni-(Pd-d/Pd-wt)
COG	147	32	409	258
KOG	170	35	486	288
GO	243	68	689	408
KEGG	73	18	299	162



Pfam	258	65	750	434
Swiss-Port	196	51	586	346
eggNOG	364	104	1044	577
Nr	426	128	1167	676
Total	427	128	1169	676