

Table S2. List of differentially expressed oxidative stress related transcripts in non-mycorrhizal *A*

Locus Name Mt4.0v1	Gene ID	Regulation in -K
Cytochrome P450 enzymes		
Flavonoid hydroxylase	Medtr3g024520	UP
Cytochrome P450 family 72 protein	Medtr0025s0110	UP
Cytochrome P450 family 76 protein	Medtr1g091010	DOWN
Cytochrome P450 family 71 protein	Medtr3g058210	DOWN
Cytochrome P450 family 71 protein	Medtr3g058220	DOWN
Cytochrome P450 family 722 protein	Medtr8g076940	DOWN
Cytochrome P450 family 71 protein	Medtr3g058110	DOWN
Cytochrome P450 family 72 protein	Medtr2g023680	DOWN
Cytochrome P450 family 76 protein	Medtr7g103450	DOWN
Cytochrome P450 superfamily protein	Medtr8g020960	DOWN
Cytochrome P450 family 71 protein	Medtr0554s0020	DOWN
Cytochrome P450 family 72 protein	Medtr2g055430	DOWN
Cytochrome P450 family 76 protein	Medtr1g116890	DOWN
Cytochrome P450 family 71 protein	Medtr3g057910	DOWN
Cytochrome P450 family 82 protein	Medtr4g018800	DOWN
Cytochrome P450 family 71 protein	Medtr0059s0170	DOWN
Cytochrome P450 family flavone synthase	Medtr4g062500	DOWN
Dehydrogenases		
Zinc-binding alcohol dehydrogenase family protein	Medtr3g089977	UP
Zinc-binding alcohol dehydrogenase family protein	Medtr3g089940	UP
L-lactate dehydrogenase A-like protein	Medtr5g012390	UP
NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	Medtr1g014320	UP
NAD-dependent aldehyde dehydrogenase family protein	Medtr3g078490	DOWN
Phenylpropanal double-bond reductase	Medtr2g088190	DOWN
Oxidases		
1-aminocyclopropane-1-carboxylate oxidase	Medtr6g092620	UP
Ubiquinol oxidase 1a	Medtr5g070680	DOWN
Cytokinin oxidase/dehydrogenase-like protein	Medtr2g039410	DOWN
Amine oxidase	Medtr4g117670	DOWN
Oxygenases		
Prolyl 4-hydroxylase alpha-like protein	Medtr8g074810	UP
Flavin containing monooxygenase-like protein	Medtr2g044140	UP
2OG-Fe(II) oxygenase family oxidoreductase	Medtr5g055800	UP
Gibberellin 2-beta-dioxygenase	Medtr1g034120	UP
Flavin-binding monooxygenase-like protein	Medtr7g107710	UP
1-aminocyclopropane-1-carboxylate oxidase-like protein	Medtr8g009090	UP
2OG-Fe(II) oxygenase family oxidoreductase	Medtr2g437380	DOWN
2OG-Fe(II) oxygenase family oxidoreductase	Medtr2g069090	DOWN

2OG-Fe(II) oxygenase family oxidoreductase	Medtr3g092890	DOWN
Aminocyclopropanecarboxylate oxidase	Medtr1g070120	DOWN
2OG-Fe(II) oxygenase family oxidoreductase	Medtr7g062550	DOWN
Peroxidases		
Cationic peroxidase	Medtr1g086490	UP
Cationic peroxidase	Medtr1g066640	UP
Peroxidase family protein	Medtr5g074740	UP
Cationic peroxidase	Medtr2g008710	UP
Cationic peroxidase	Medtr3g466180	UP
Cationic peroxidase	Medtr1g038680	UP
Class III peroxidase	Medtr4g127670	DOWN
Cationic peroxidase	Medtr7g026990	DOWN
Redox proteins		
Monothiol glutaredoxin-S2 protein	Medtr1g088920	UP
Glutaredoxin-C1 protein	Medtr1g088910	UP
Monothiol glutaredoxin-S2 protein	Medtr7g108200	UP
Thioredoxin	Medtr5g037950	DOWN
Thioredoxin	Medtr5g037930	DOWN
Reductases		
Oxidoreductase/ferric-chelate reductase	Medtr8g028780	UP
Dihydrodipicolinate reductase	Medtr8g028145	DOWN
Aldo/keto reductase family oxidoreductase	Medtr8g070115	DOWN
Aldo/keto reductase family oxidoreductase	Medtr7g114990	DOWN
NADP-dependent alkenal double bond reductase P1	Medtr0011s0280	DOWN
Others		
NAD(P)-binding rossmann-fold protein	Medtr7g063270	UP
FAD-dependent urate hydroxylase-like protein	Medtr1g112740	UP
Stearoyl-acyl-carrier desaturase	Medtr1g029150	UP
Lipoxygenase	Medtr8g018590	DOWN
fatty acid/sphingolipid desaturase	Medtr1g016070	DOWN
Lipoxygenase	Medtr8g018650	DOWN

V. truncatula roots under continuous potassium deprivation. Transcripts were annotated with

Log₂ ratio
+K vs -K

- 1.09907
- 0.750407
- 0.598016
- 0.624218
- 0.650619
- 0.697923
- 0.701513
- 0.742794
- 0.762278
- 0.794491
- 0.806191
- 0.827122
- 0.851278
- 0.949323
- 0.982724
- 1.16453
- 1.96034

- 1.11583
- 0.90046
- 0.834419
- 0.828013
- 0.635433
- 0.719258

- 1.06868
- 0.655484
- 0.667991
- 0.907592

- 1.27321
- 1.1374
- 0.976077
- 0.914764
- 0.78409
- 0.620523
- 0.610726
- 0.646106

-0.665597
-0.88131
-1.8818

2.78538
1.07482
1.01871
0.661104
0.656326
0.59106
-0.676641
-1.12505

1.52612
1.27882
0.755123
-0.629741
-0.718586

0.863287
-0.615699
-0.657931
-0.83325
-1.16771

1.8338
0.990197
0.897026
-0.669985
-0.784028
-0.859605

† the Mt4.0v1 version of *M. truncatula* genomic database (<http://jcvi.org/medicago/index.php>).