Title

Hypoxia Responsive MicroRNAs and Trans-Acting Small Interfering RNAs in Arabidopsis

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Legends for Supporting Information

Fig. S1 Relative expression of ADH expression during hypoxia stress. Expression of ADH in 2.5 week old Col-0 plants exposed to 0.1% O_2 for 5 h compared to the control as measured by QRT-PCR.

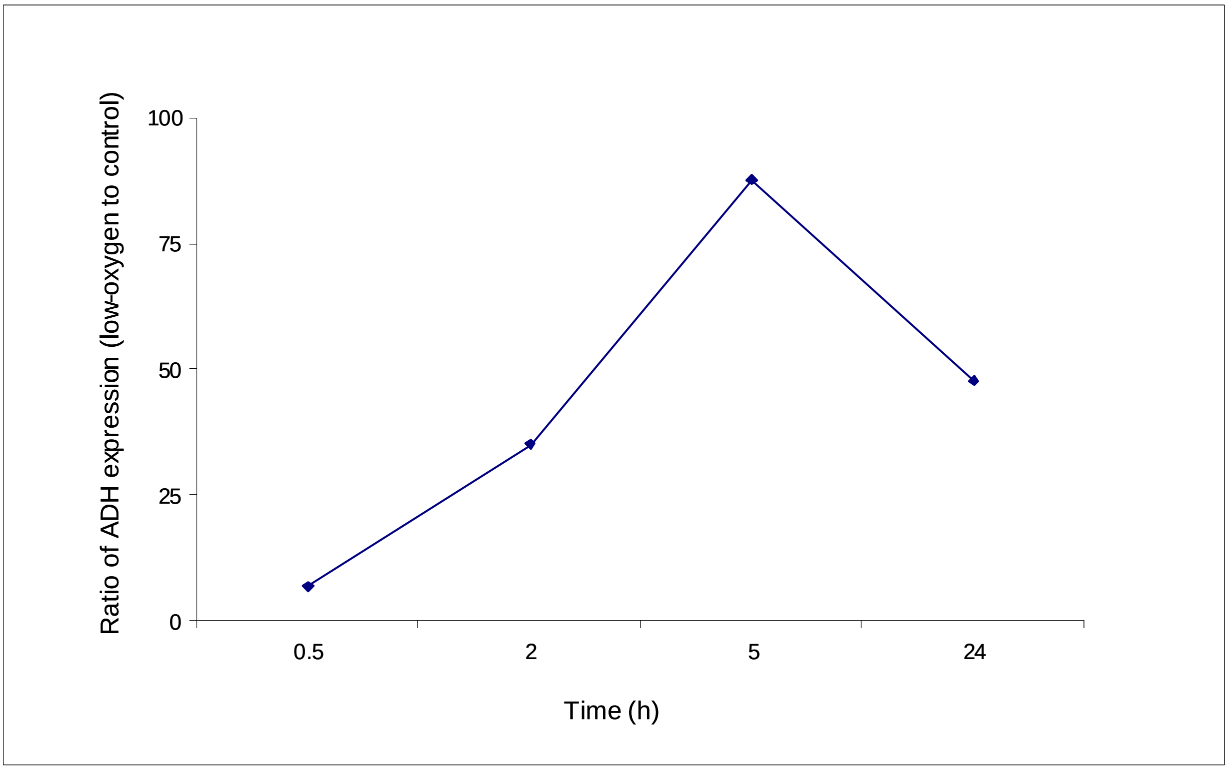

Fig. S1 Relative expression of ADH expression during low oxygen stress.

Table S1. Summary of the origin of small RNA sequencing data

Feature	Reads	Sequences
Arabidopsis genome	420,360	1,915,426
CDS	179,442	64,689
Sense	108,938	42,907
Antisense	69,053	21,016
Both	1,451	766
UTR	12,327	5,721
Intron	92,705	33,334
Transposons (Retro)	211,752	104,490
Intergenic	2,854,266	305,282
Mitochondrial/chloroplast	17,827	13,485

Table S2. Comparison of read numbers of miRNAs from different tissues.

miRNA	Reads/million		
	Roots#	Leaf	Whole Plant
156a,b,c,d,e,f	2043	129	53
156g	13	0	0
156h	1	0	1
157a,b,c	2258	99	20
157d	61	0	1
158a	1876	18	100
158b	19	0	0
159a	42	666908	187933
159b	5	196763	28615
160a,b,c	1	3572	2426
161	44	12214	9878
162	0	203	393
163	1	5476	3562
164a,b	993	449	500
164c	181	4	2
165a,b	5537	61	131
166a,b,c,d,e,f,g	29631	1222	1170
167a,b	565	21379	14835
167d	1	7789	3471
168a,b	3156	32666	7867
169a	2	6923	1649
169b,c	2	24	22
169d,e,f,g	28	27	25
169h,i,j,k,l,m,n	2	715	218
170	0	234	767
171a	0	154	664
172a, b	19	5131	4849
172c,d	1	1	41

172e	1	19	23
173	106	2	9
319a,b	0	1688	13807
390a,b	861	935	396
391	18	152	213
393	0	54	10
394	0	295	889
395a,d,e	1	8	18
395b,c,f	1	1	23
396	0	6585	2928
397	0	685	1015
398	0	443	234
399a	0	0	1
399b,c	1	9	16
399d	1	0	0
399f	4	0	4
400	1	23	12
402	0	2	4
403	1	55	74
408	47	1452	557
447a,b	1	68	50
472	0	22	15
771	0	1	22
773	0	195	186
774	0	0	0
775	6	202	190
776	0	5	1793
777	0	12	7
778	0	0	5
779	0	0	0
780	0	0	90
781	0	26	24
822	43	207	74

823	3	30	31
824	11	3170	976
825	0	596	141
826	0	0	3
827	5	10	12
828	0	2	11
829	503	0	0
830	0	4	5
831	0	0	1
832	0	0	0
833	0	3	3
834	0	0	1
835	0	0	0
836	0	0	0
837	7	5	10
838	0	26	9
839	0	6	131
840	0	18	46
841	0	84	5
842	8	44	9
843	0	136	71
844	0	14	11
845	0	4	112
846	1	1492	729
847	0	483	47
848	4	22	16
849	0	1	4
850	0	1	1
851	0	0	4
852	1	10	9
853	0	5	0
856	0	0	2
857	0	7	17

858	0	2	9
859	0	2	16
860	0	11	15
861	0	9	5
862	1	14	4
863	0	0	0
864	0	57	59
865	0	4	3
866	0	2	2
867	0	0	81
868	0	0	1
869	19	3	111
870	0	2	3
1888	0	NA*	

[#] Combined total from control and hypoxia stressed samples

*No data available

Table S3. Stem-loop RT & QRT-PCR primer sequences

smRNA	Primer sequence
miR157d/miR156g - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGTGCTC
miR156g - QRT-PCR	CCGGCGACAGAAGAGAGT
miR157d - QRT-PCR	GCGGTGACAGAAGATAGAG
miR158a - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTGCTTT
miR158a - QRT-PCR	CGGCGTCCCAAATGTAGAC
miR159a - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTAGAGC
miR159a - QRT-PCR	GCGGTTTGGATTGAAGGGA
miR166g - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACGGGGAA
miR166g - QRT-PCR	GGTCGGACCAGGCTTCA
miR172a - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACATGCAG
miR172a - QRT-PCR	GCGGGAGAATCTTGATGATG
miR391a - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTGGCGC
miR391a - QRT-PCR	GCGGTTCGCAGGAGAGATA
miR775 - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTGGCAC
miR775 - QRT-PCR	GCCGGTTCGATGTCTAGCA
ta-siR2140 - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACCAGATG
ta-siR2140 - QRT-PCR	GCGGGATATCCCATTTCTAC
ta-siR289 - RT	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGACTATGCT
ta-siR289 - QRT-PCR	CCGGCCTTCTAAGTCCAACAT
Universal Reverse	GTGCAGGGTCCGAGGT

Table S4. Primers for U6 loading control for QRT-PCR analysis of mature smRNAs

Target Gene	Forward Primer	Reverse Primer
U6	GATAAAATTGGAACGATACAG	ATTTGGACCATTTCTCGATTT

Table S5. Target genes and primers used for QRT-PCR analysis

Gene Assayed	Forward Primer	Reverse Primer
AT1G15940	GGAAAGCCGAGGTTATTCTTG	CAAGCACCAGTTGAGGATGAT
AT1G27360	TTTCAACTTCATGGCGAAGAT	GAGTAGAGAAAATGGCTGCACA
AT1G27370	TCAAACATCTGGTGGGTTCTC	GATCCCTTGTGAATCCGAAGT
AT1G50990	CACTGTTTATGCACGAAGAAGC	GTAAAATGCAGTTGGCCAGTC
AT1G51670	GAGCAAAACTGCATGTGTTCA	CCATGGACTTTCCTTGGATCT
AT1G53160	AGGTGGTGATGCAGAATCAAG	CCACAATTTTAGGATTCTAAGAGAGAA
AT1G53290	GCTCAGAAGAGAAATCGCAGA	CAGCTTTGAAGAAAGCCAAAG
AT1G64100	TTTCTGCGACTGCCATAAGTT	GGAGCAGCGTGTTAAAGGTAA
AT1G68840	TTTTCCGATTTTATGCTTTCG	TTTCCACAAAACCATTGTTCC
AT1G69170	CCACGGAAGTATCCTCCATTT	GGGTGATTGAGAACGTTGTGT
AT2G26950	CAGCCATTTGTTTGGAAATGT	TTGTTCTGCTCCAAAACTGCT
AT2G26960	TCTCCTCCTGGACCTCTTGTT	GGCATTGGGTTAGGTTGATCT
AT2G28550	AAACAAGCGCCGTGAGAC	TAACCACGTGTTGCATTGTCA
AT2G32460	TCGAGTTCTTTCCCTTTAGGA	TCAAGATGGACACCATTGTCA
AT2G33810	ATCCCGGTTTGAAGGTTAATG	GGCTTGAAATAACATTTGACAAG
AT2G34010	TCTCCAGGAGCAGGAAGATTT	TGGCCTCTTCTTAGCAGTGAA
AT2G39250	CGGGATATCTACCGATCACAG	TCACCTCATGGATCAAAACAAG
AT2G42090	ACGTCTCCATGCAATCTGTTC	GGGAGTGCGTAACCTTCGTAT
AT2G42200	AGGGACAAGCTTCTCATCTCC	GTTGTCATGTGGTTGATGTGG
AT3G03580	CAGATTCCTTCACGGTTTCAA	ACCACCACAACGGAATTAACA
AT3G11440	TGATGATGGTTCCTGATAGCC	CGTCTTCCACTGATCAAATGC
AT3G15270	ACTCATCATTCAAGCGACCAC	CCATGACCAACTTTTCTTGACA
AT3G27230	GCAAGGAATGTGTTGGTTGTT	ATCCACCGCTAATATCGAACC
AT3G54990	TATTTTTACCCATGGCAACCA	AATTGGACATGGAGGAAGAGG
AT3G57920	GAAACCCATCCACACATGAAT	TGTTGGTGTCTGAAGTTGCTG
AT3G60460	GAAAGCCGAAGAAGACGAAGT	TATTGACCCAACGAAGACGAC
AT3G61320	CATTGGATTGTTGTTCCTGCT	CTATGCACAAGATCGCAAAGC
AT4G05360	TGCAGTCATGAGGGTTTAAGG	CTTCAAATCTCCCCCTTTTTG
AT4G29760	AGGGAGTTTACAAAGGCCTCA	ACAGAATCTCCCTCGAACTCC
AT4G29770	AAGCTGGGTATGCAACAACC	CTTGATCTTCTCCGCCTCAAC

AT4G36920	CTCGACGAACCAAGTGTTGAC	CAGCCAATTTTGATGAGGAGT
AT4G37770	TTATCATGGCCTTCCTTCCTT	GAGAGTCTCGTTAGCCGGAGT
AT5G06100	ATAGCCATACCCCTACGGATG	TGTGGAGGAGATGACGATTTC
AT5G18040	CCATGTGTTCAGTCCAGACCT	CCTCGGACTTATTCACTGCAA
AT5G18065	TCCATGTCTTCAGTCCAGAGC	TTTCCCTCGGACTTATCCACT
AT5G18100	CTGGCTTCCATGGATTTCATA	CCTGCAAGAATGTTACCCAAA
AT5G42670	GAGAGGAGCCGAACCTAAAGA	CCACTCGAAACGAACAATCAT
AT5G43270	CACATGGGTGCTTCTCAAGAT	AGGGATGGTGATCAAGGGTAA
AT5G50570, AT5G50670	CGTTGTGTGAGAGAATGACGA	AAGTGGTGGTTGAAGCAAATG
AT5G52070	TATGGAATCGGATGGAATTGA	TCACATTCCAGAGGAAGATGG
AT5G55020	CCAACCCAGTTTACTCCATGA	CTTCTATGAGCACCGGAACTG
AT5G60120	GCATGATCAGTCCAGTGGTG	GCTGATTCAGATTGACGAAGG
AT5G67180	TAGCAATGATGACGACGACTG	GATGATGAATCAGGGACGAGA