

Table 1 Suppl. Primers used in this study. Nucleotides corresponding to restriction enzyme cut sites and site-directed mutation sites are *underlined*.

Primer	Sequence(5'-3')	Description
LEA3140F	<u>GCGGATCC</u> ATGCTAGGAGGAGCAAAGAAAAC	ORF cloning and expression profiling
LEA3140R	<u>GCGAGCT</u> CTCACAGCCAAACTGTCTCCT	
LEA3140MF	ACCAATTGGGG <u>C</u> AGGGTGGACA	Site-directed mutagenesis
LEA3140MR	TGTCCACC <u>TG</u> CCCCAATTGGT	
LEA3160F	<u>GCGGATCC</u> ATGCAAGGAGGAGCAAAGAA	ORF cloning and expression profiling
LEA3160R	<u>GCGAGCT</u> CCTATGCCCTATTTGAGCAGC	
LEA3170F	<u>GCGGATCC</u> ATGCAGGGAGCTAAGAAAGCT	ORF cloning and expression profiling
LEA3170R	<u>GCGAGCT</u> CTCATTATAAGTACCACCAAGTGGTGTA	
Medtr1g053970F	ATGCAGGCAGCAAGGAAAGCA	Expression profiling
Medtr1g053970R	CTAAATTATTAGTAGTAGTAGGTCC	
ActinF	TGCTTCTAACTGAGGCTCCACT	Internal control for expression profiling
ActinR	AAAGGACTTCTGGGCAACG	

**LEA3140**

A17	<b>ATGCTAGGAGGAGCAAAGAAAAACAGGAGAGTCCATTAAGGAGACAGCTGCCAACATTGGTCTTCAGCCAAATCTGGCATGGAAAAAGACC</b>	90
R108	<b>ATGCTAGGAGGAGCAAAGAAAAACAGGAGAGTCCATTAAGGAGACAGCTGCCAACATTGGTCTTCAGCCAAATCTGGCATGGAAAAAGACC</b>	90
A17	<b>AAGGCCACTCTTCAGGAGAACAGAGAACAGAGATGACGGCACATGATCCTTGCAAAAGGAGATGGCAACCCAAAAGAAAGAAGAAAGGGTT</b>	180
R108	<b>AAGGCCACTCTTCAGGAGAACAGAGAACAGAGATGACGGCACATGATCCTTGCAAAAGGAGATGGCAACCCAAAAGAAAGAAGAAAGGGTT</b>	180
A17	<b>AACCAAGGCTGAACATTGATAAAAGAGGCAGCGCGTGAAACACAACGCTGCAGCCACCCACCGGGCACCAATTGGGGCAGGGTGGACACCCATACC</b>	270
R108	<b>AACCAAGGCTGAACATTGATAAAAGAGGCAGCGCGTGAAACACAACGCTGCAGCCACCCACCGGGCACCAATTGGGGCAGGGTGGACACCCATACC</b>	270
A17	<b>ACGGAACTGGTGGGGCTGCTAAACGAGGAGACAGTTGGGCTGTGA</b>	318
R108	<b>ACGGAACTGGTGGGGCTGCTAAACGAGGAGACAGTTGGGCTGTGA</b>	318
	<b>*</b>	

**LEA3160**

A17	<b>ATGCAAGGAGGAGCAAAGAAAAACAGGAGAGTCCATTAAGGAGACAGCTGCCAACATTGGTCTTCAGCCAAATCTGGCATGGAAAAAAC</b>	90
R108	<b>ATGCAAGGAGGAGCAAAGAAAAACAGGAGAGTCCATTAAGGAGACAGCTGCCAACATTGGTCTTCAGCCAAATCTGGCATGGAAAAAAC</b>	90
A17	<b>AAGGCCACATTTCAAGAGAACAGAGAACAGGAGATGACGGCACATGATCCTTGCAAAAGAGATGGCAACCCAAAAGAAAGAAGAAAGGGTT</b>	180
R108	<b>AAGGCCACATTTCAAGAGAACAGAGAACAGGAGATGACGGCACATGATCCTTGCAAAAGAGATGGCAACCCAAAAGAAAGAAGAAAGGGTT</b>	180
A17	<b>AACCAAGGCTGAGCTTGTATAAAAGAGGCAGCGCGTGAAACACAACGCTGCAGCTCTGCCGGCACCAATTGGGGTGGGTGGACACCCACACC</b>	270
R108	<b>AACCAAGGCTGAGCTTGTATAAAAGAGGCAGCGCGTGAAACACAACGCTGCAGCTCTGCCGGCACCAATTGGGGTGGGTGGACACCCACACC</b>	270
A17	<b>ACGGAACTGGTGGGGCTGCTAAATAAGGGCATAG</b>	306
R108	<b>ACGGAACTGGTGGGGCTGCTAAATAAGGGCATAG</b>	306
	<b>*</b>	

**LEA3170**

A17	<b>ATGCAGGGAGCTAAGAAAGCTGGAGAGACCATTAAAGGAAACAGCTGCCAACATTGGTCTTCAGCCAAATCTGGTATGGAGAAGACCAAG</b>	90
R108	<b>ATGCAGGGAGCTAAGAAAGCTGGAGAGACCATTAAAGGAAACAGCTGCCAACATTGGTCTTCAGCCAAATCTGGTATGGAGAAGACCAAG</b>	90
A17	<b>GCCACCCCTCAAGAGAACAGACTGAGAACAGATGACAGCACGTGATCCTGTGCAAAAGAGATGGCAACCCATAAGAAAGAGGCAAGATGAAC</b>	180
R108	<b>GCCACCCCTCAAGAGAACAGACTGAGAACAGATGACAGCACGTGATCCTGTGCAAAAGAGATGGCAACCCATAAGAAAGAGGCAAGATGAAC</b>	180
A17	<b>CAGGCAGAGCTAGATAAAGCTGGCAGCACGTGAAACACAATGCCGGCTAACAGACGACCAACTGCTGCCGGCTGGCATATGGGTAGCCC</b>	270
R108	<b>CAGGCAGAGCTAGATAAAGCTGGCAGCACGTGAAACACAATGCCGGCTAACAGACGACCAACTGCTGCCGGCTGGCATATGGGTAGCCC</b>	270
A17	<b>CACCAACACAGGGACGACTTGAACCGGGACCCACATACTCTACCAACTGGAAATTATGGACATCCACTGGGCACATCAGATGTCA</b>	360
R108	<b>CACCAACACACAGGGACGACTTGAACCGGGACCCACATACTCTACCAACTGGAAATTATGGACATCCACTGGGCACATCAGATGTCA</b>	360
A17	<b>GCCATGCCTGGTCATGGAACTGGACAGCCCACGGGCCATGCTCGACGGTGGGTGGCTCACACCCATTGGGACTAATAGAGGCACA</b>	450
R108	<b>GCCATGCCTGGTCATGGAACTGGACAGCCCACGGGCCATGCTCGACGGTGGGTGGCTCACACCCATTGGGACTAATAGAGGCACA</b>	450
A17	<b>GATGGGACCGCCACGGCCATAATACCGTGTGGAAATCCAATGCCACAGGGTACACCACTGGGTACTTATAATGA</b>	534
R108	<b>GATGGGACCGCCACGGCCATAATACCGTGTGGAAATCCAATGCCACAGGGTACACCACTGGGTACTTATAATGA</b>	534
	<b>*</b>	

Fig. 1 Suppl. Alignments of *MtLEA* genes from *Medicago truncatula* genotypes A17 and R108. Single nucleotide polymorphisms responsible for the premature termination codon, amino acid substitutions, and synonymous substitutions are indicated by *red*, *green*, and *black asterisks*, respectively.

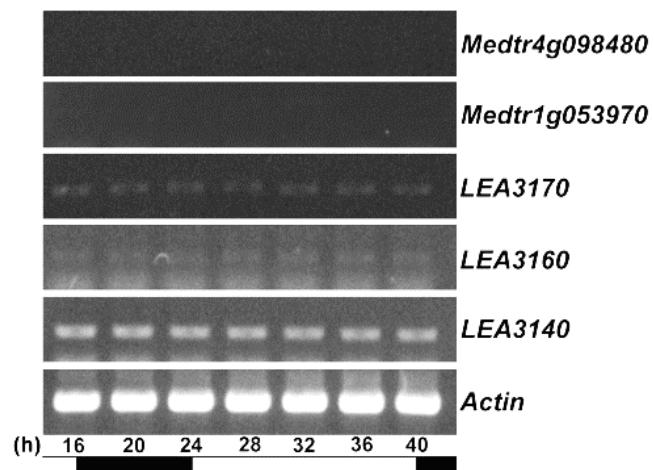


Fig. 2 Suppl. Reverse transcription PCR detection of the diurnal transcriptional patterns of *MtLEA* genes in *Medicago truncatula* genotype R108. The *black* and *white* bars indicate dark and light, respectively. Seedlings grown in *Vermiculite* for two weeks at 21 °C were collected at appropriate time points for transcription profiling.

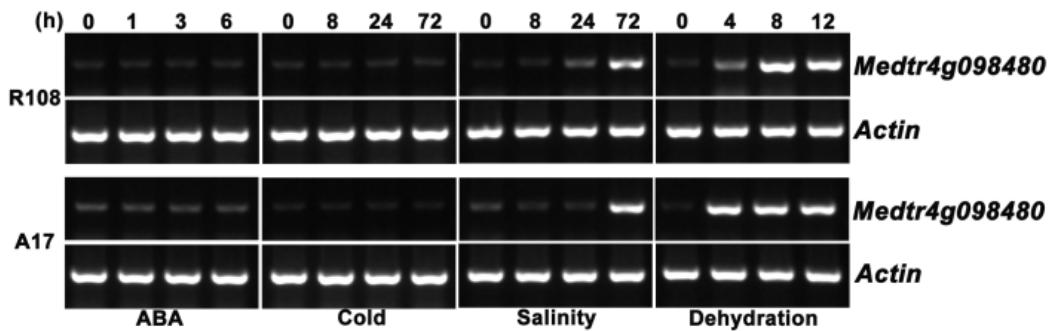


Fig. 3 Suppl. Reverse transcription PCR detection of abiotic stresses and abscisic acid induced transcriptional patterns of *Medtr4g098480*, which encodes a subgroup 4A LEA protein in *Medicago truncatula* genotypes A17 and R108. Specific primers for *Medtr4g098480* (LEA8480F: 5'-ATGCAATCTTCAATGGAGAAGCT-3', LEA8480R: 5'-CTACATGCGATTGTTCTGTGGAA-3') were used.