

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	GCGGATCCATGCTAGGAGGAGCAAAGAAAAC	ORF cloning and expression profiling
LEA3140R	GCGAGCTCTCACAGCCCAAAGTGTCTCCT	
LEA3140MF	ACCAATTGGGGCAGGGTGGACA	Site-directed mutagenesis
LEA3140MR	TGTCCACCCTGCCCCAATTGGT	
LEA3160F	GCGGATCCATGCAAGGAGGAGCAAAGAA	ORF cloning and expression profiling
LEA3160R	GCGAGCTCCTATGCCCTATTTTGAGCAGC	
LEA3170F	GCGGATCCATGCAGGGAGCTAAGAAAGCT	ORF cloning and expression profiling
LEA3170R	GCGAGCTCTCATTATAAGTACCACCAGTGGTGTA	
Medtr1g053970F	ATGCAGGCAGCAAGGAAAGCA	Expression profiling
Medtr1g053970R	CTAATTATTAGTAGTAGGTCC	
ActinF	TGCTTCTAACTGAGGCTCCACT	Internal control for expression profiling
ActinR	AAAGGACTTCTGGGCAACG	

# **LEA3140**

A17	ATGCTAGGAGGAGCAAAGAAAACAGGAGAGTCCATTAAGGAGACAGCTGCCAACATTGGTGCTTCAGCCAAATCTGGCATGGAAAAGACC	90
R108	ATGCTAGGAGGAGCAAAGAAAACAGGAGAGTCCATTAAGGAGACAGCTGCCAACATTGGTGCTTCAGCCAAATCTGGCATGGAAAAGACC	90
A17	AAGGCCACTCTTCAGGAGAAGACAGAGAAGATGACGGCACATGATCCTTTGCAAAAGGAGATGGCAACCCAAAAGAAAGAAAGGGTT	180
R108	AAGGCCACTCTTCAGGAGAAGACAGAGAAGATGACGGCACATGATCCTTTGCAAAAGGAGATGGCAACCCAAAAGAAAGAAAGGGTT	180
A17	AACCAGGCTGAACCTTGATAAAGAGGGCGCGCTGAACACAACGCTGCAGCCACCACCGGGCACCAATTGGGGCAGGGTGGACACCATACC	270
R108	AACCAGGCTGAACCTTGATAAAGAGGGCGCGCTGAACACAACGCTGCAGCCACCACCGGGCACCAATTGGGGCAGGGTGGACACCATACC	270
A17	TCGGGAACCTGGTGGGGCTGCTCAAAACGAGGAGACAGTTTGGGCTGTGA	318
R108	TCGGGAACCTGGTGGGGCTGCTCAAAACGAGGAGACAGTTTGGGCTGTGA	318

# **LEA3160**

A17	ATGCAAGGAGGAGCAAAGAAAACAGGAGAGTCCATTAAGGAGACAGCTGCCAACATTGGTGCTTCAGCCAAATCTGGCATGGAAAAGACC	90
R108	ATGCAAGGAGGAGCAAAGAAAACAGGAGAGTCCATTAAGGAGACAGCTGCCAACATTGGTGCTTCAGCCAAATCTGGCATGGAAAAGACC	90
A17	AAGGCCACATTTCAAGAGAAGACAGAGAAGATGACGGCACATGATCCTTTGCAAAAGAGATGGCAACCCAAAAGAAAGAAAGGGTT	180
R108	AAGGCCACATTTCAAGAGAAGACAGAGAAGATGACGGCACATGATCCTTTGCAAAAGAGATGGCAACCCAAAAGAAAGAAAGGGTT	180
A17	AACCAGGCTGAGCTTGATAAAGAGGGCGCGCTGAACACAACGCTGCACCTTCTGCCGGGCACCAATTGGGGGTGGGTGGACACCACACC	270
R108	AACCAGGCTGAGCTTGATAAAGAGGGCGCGCTGAACACAACGCTGCACCTTCTGCCGGGCACCAATTGGGGGTGGGTGGACACCACACC	270
A17	ACGGGAACCTGGTGGGGCTGCTCAAAATAGGGCATAG	306
R108	ACGGGAACCTGGTGGGGCTGCTCAAAATAGGGCATAG	306

# **LEA3170**

A17	ATGCAGGAGGCTAAGAAAGCTGGAGAGACCATTAAGGAAACAGCTGCCAACATTGGTGCTTCTGCCAAATCTGGTATGGAGAAGACCAAG	90
R108	ATGCAGGAGGCTAAGAAAGCTGGAGAGACCATTAAGGAAACAGCTGCCAACATTGGTGCTTCTGCCAAATCTGGTATGGAGAAGACCAAG	90
A17	GCCACCCCTTCAAGAGAAGACTGAGAAGATGACAGCACGTGATCCTGTGCAAAAAGAGATGGCAACCCATAAGAAAGAGGCAAGATGAAC	180
R108	GCCACCCCTTCAAGAGAAGACTGAGAAGATGACAGCACGTGATCCTGTGCAAAAAGAGATGGCAACCCATAAGAAAGAGGCAAGATGAAC	180
A17	CAGGCAGAGCTAGATAAGCTGGCAGCACGTGAACACAATGCGGGCGGTCAAACAGACGACCACTGCTGCGGCTGGGCATATGGGTACAGCCC	270
R108	CAGGCAGAGCTAGATAAGCTGGCAGCACGTGAACACAATGCGGGCGGTCAAACAGACGACCACTGCTGCGGCTGGGCATATGGGTACAGCCC	270
A17	CACCACACCACAGGGACGACTGGAACGGGGACCGCCACATACTCTACCACTGGGAATTATGGACATCCCACTGGGGCACATCAGATGTCA	360
R108	CACCACACCACAGGGACGACTGGAACGGGGACCGCCACATACTCTACCACTGGGAATTATGGACATCCCACTGGGGCACATCAGATGTCA	360
A17	GCCATGCCTGGTCATGGAACCTGGACAGCCACGGGCCATGTCGTCGACGGTGTGGTGGGCTCACACCCCTATTGGGACTAATAGAGGCACA	450
R108	GCCATGCCTGGTCATGGAACCTGGACAGCCACGGGCCATGTCGTCGACGGTGTGGTGGGCTCACACCCCTATTGGGACTAATAGAGGCACA	450
A17	GATGGGACCGCCACGGCCCATATAACCCGTGTTGGTGGAAATCCAAATGCCACAGGGTACACCACTGGTGGTACTTATAAATGA	534
R108	GATGGGACCGCCACGGCCCATATAACCCGTGTTGGTGGAAATCCAAATGCCACAGGGTACACCACTGGTGGTACTTATAAATGA	534

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.

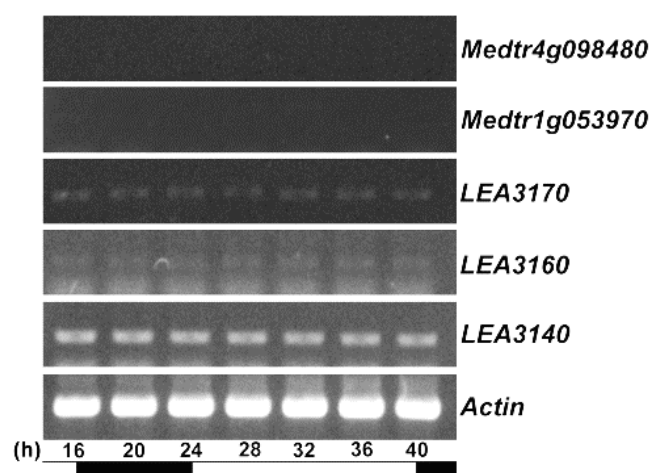


Fig. 2 Suppl. Reverse transcription PCR detection of the diurnal transcriptional patterns of *MtLEA* genes in *Medicago truncatula* genotype R108. The *black* and *white bars* indicate dark and light, respectively. Seedlings grown in *Vermiculite* for two weeks at 21 °C were collected at appropriate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

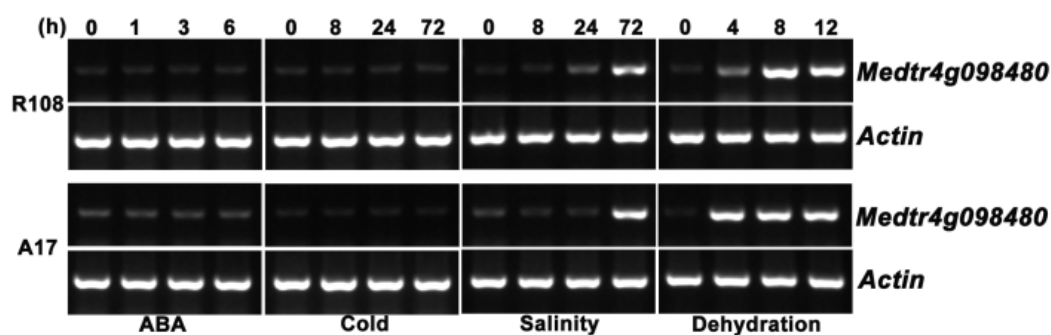


Fig. 3 Suppl. Reverse transcription PCR detection of abiotic stresses and abscisic acid induced transcriptional patterns of *Medtr4g098480*, which encodes a subgroup 4A LEA protein in *Medicago truncatula* genotypes A17 and R108. Specific primers for *Medtr4g098480* (LEA8480F: 5'-ATGCAATCTTCAATGGAGAAGCT-3',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