

GmLATE	1	MDLNYPEECYSKSSCE-----ETNDDMGIGRSYECIFCKRGFTTAQALGGHMNIHRKERA	55
		M+ +Y E+ SS E E ND+ G GRS+EC+FCKRGF TAQALGGHMNIHRK RA	
GmSM	1	MEFSYQEDSSKSSSNEIDRSSEQNDETGTGRSFECVFCKRGFNTAQALGGHMNIHRKARA	60
GmLATE	56	NKTKAsfssshpsssNNVD--GINNVADLGFYSQIPSL-STAPD-----ANSYREVFF	104
		N +KA + PSSS+ VD NNYA+ + ++ ST PD N Y +++F	
GmSM	61	NNSKAKPNFPSSSSKVDHESNNYANPSYLTRGNHYSSTLPDHREVDDVYNYVYHQLYF	120
GmLATE	105	PTAAPSVIRPS----SHEVLCVENQRGHH-VFEQDWKRNLSLYTNPLGFHEIKDKFE-E	158
		P+ A PS S EVLCVENQR H +F QDWR+R LSLYTNPL HE KDK E	
GmSM	121	PSPACGAKSPSHVQYSSEVLCVENQRDPHLLFGQDWRQRGLSLYTNPLCVHENKDKIENN	180
GmLATE	159	SEDNGLDLELRLGHHP	174
		SE++ LDLELRLG+HP	
GmSM	181	SEEDDLDELRLGYHP	196

Fig. S1 BLAST analysis of GmLATE in soybean protein sequence database.

Amino acid sequences of GmLATE were used for BLAST analysis in protein sequence database of *Glycine max*. BLAST was performed in NCBI BLAST tool. Alignment results between GmLATE and GmSM were displayed. Note that identical amino acid sequences were annotated between GmLATE and GmSM sequences. Amino acid sequences which are different between two proteins but are conservative substitutions were marked as “+”. The conserved QALGGH motif is marked as a red line.

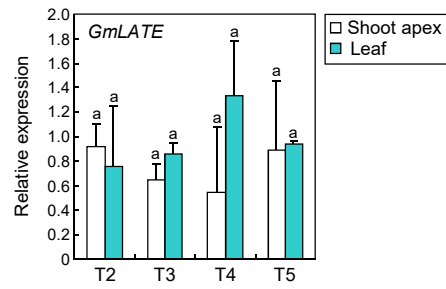


Fig. S2 Expression of *GmLATE* in leaf and shoot apex.

Leaves and shoot apices were harvested from the plants developing T2, T3, T4, and T5 leaves. Expression of *GmLATE* was analyzed ($n = 3$, Tukey's test, $P < 0.05$).

Primers	Sequences	Usage
GmSM SnaBI F	5'-ccgtacgtaTCCAACCTCCTTCTTCGAGT	Cloning & RT-PCR
GmSM SnaBI R	5'-ccgtacgtaGATGACCCGTTG6TTTTCC	"
GmLATE SnaBI F	5'-ccgtacgtaACAAGCCTTAGGTGGACACA	"
GmLATE SnaBI R	5'-ccgtacgtaCTAATAACACTTGGTGCAGCGG	"
GmPDS SnaBI F	5'-CCGTACGTAATAACTGGAAAGG	"
GmPDS SnaBI R	5'-CCGTACGTAAACCAACTCTAAC	"
Nb Actin F	5'-TGGACTCTGGTGATGGTGTC	RT-PCR
Nb Actin R	5'-CCTCCAATCCAACACTGTA	"
GmLATE F	5'-GCCCTTCTCCCATGAGGTTTTG	RT-qPCR
GmLATE R	5'-ATGACCAAGCCTCAGCTCCAA	"
GmCOL1 F	5'-TGTTGCTACTACTACGGACCAT	"
GmCOL1 R	5'-GAAACTGAAACACTTTGATTAAACA	"
GmCOL2 F	5'-CCTAACACCAATAACAATAACA	"
GmCOL2 R	5'-GATCAGTAGTAGCAGCAG	"
GmCOL13 F	5'-AACACAACCAACCACAAGATAAGC	"
GmCOL13 R	5'-GGGAGAATCAAGAGTGCCAACG	"
GmCOL5 F	5'-CCACTAACTTGCTGCCACGATG	"
GmCOL5 R	5'-TGGAGGAAGAGAAGTGAGTGTGAG	"
GmFTL2 F	5'-ATCTCTTCTGTTAATGTACCAAAAGTG	"
GmFTL2 R	5'-GTGACCCATGAGTGTTATTATATGTAG	"
GmFTL3 F	5'-GGTTCTGGTGGAAGGAGGTTATAC	"
GmFTL3 R	5'-ACTACTAAAGAGTGTGGGAGATTGC	"
GmFTL4 F	5'-GGACAGAAGCAAAATTAAAGCAGATG	"
GmFTL4 R	5'-ACTATATACTATGATGTTTGTGTTTGGG	"
GmFTL5 F	5'-GCGACAAGCACAAAGCGATTTC	"
GmFTL5 R	5'-TGTTATGACACCAACTATGATGAGG	"
GmACT11 F	5'-CGGTGGTTCTATCTTGGCATC	"
GmACT11 R	5'-GTCCTTCGCTTCAATAACCCTA	"

Table S1 Primers used in this work.

The primers used were designed using the NCBI primer blast (<https://www.ncbi.nlm.nih.gov/tools/primer-blast>). F, forward primer; R, reverse primer. Note that RT-qPCR primers for *GmCOL* and *GmFTL* genes were previously reported (Fan et al., 2014).