

Table 1 Suppl. Abiotic stress resistance genes-specific primers used in this study.

Name	Primer sequence	Gene IDs
<i>AtUBQIN</i>	F: TTCAGGCGAGTGAGTGAGCAGT R: TCCGCAGTTGCATCTTGGTATT	AT4G05320
<i>RD19A</i>	F: CGACTCATGGTGTACGCAGTT R: TTGTTGGCATCTTTAGGAA	AT4G39090
<i>RD29A</i>	F: CCGTGACGACGAAGTTACCTAT R: CTGAAGTTTCTCGGCAACCATA	
<i>COR47</i>	F: ATCATGCCAAGACCACTG R: AATCAACGAAAGCCACAATAAC	AT1G20440
<i>P5CS1</i>	F: AGATGGTTTCCGATTT R: CCACTACATAAGCGAGGGTTTC	AT2G39800
<i>DREB2A</i>	F: GCTGAGCGAGTTTGAACAT R: CTGCAACAGATAGCGAA	AT5G05410
<i>KINI</i>	F: CTGGAGCTGGAGCACAACA R: ATTTGACCCGAATCGCTACTTG	AT1G14370

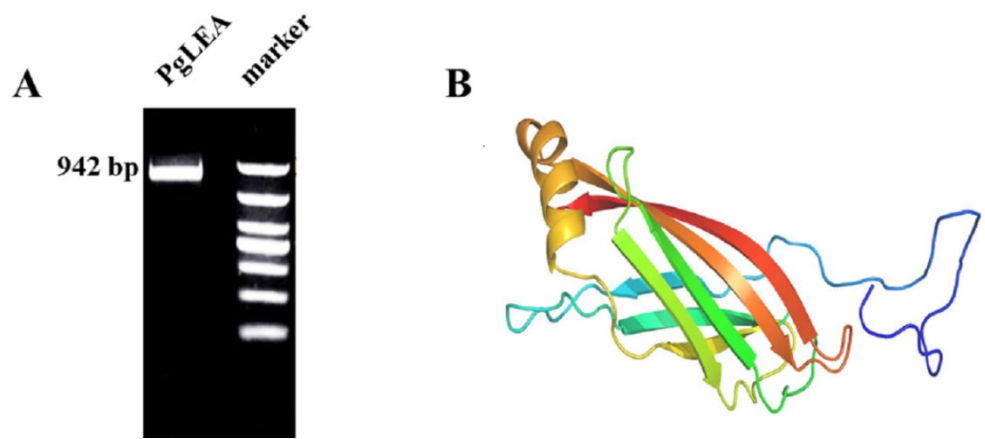


Fig. 1 Suppl. Detection of the *PgLEA* gene and structure prediction. *A* - PCR amplification of *PgLEA* by RT-PCR from total mRNA of ginseng. *B* - Predicted three-dimensional structural model of *PgLEA* by *SWISS-MODEL* server.

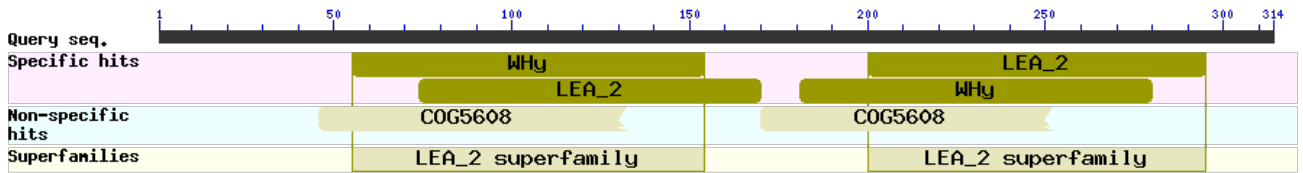


Fig. 2 Suppl. Conserved domains of *PgLEA* from *Panax ginseng*

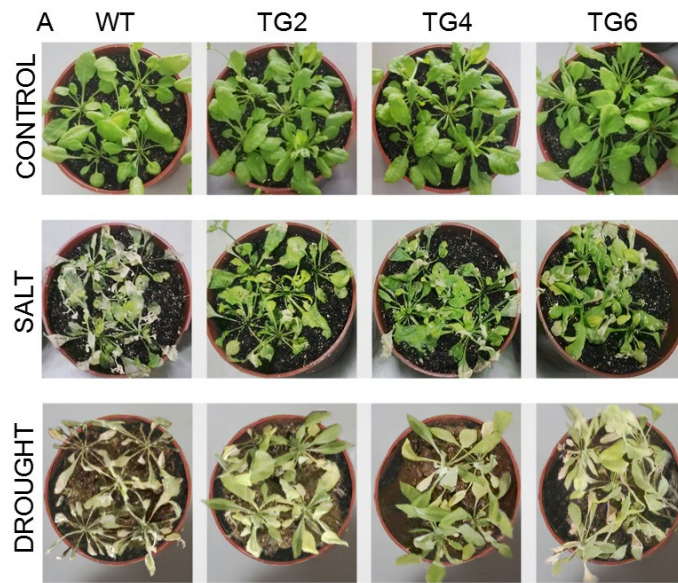


Fig. 3 Suppl. Phenotype of *PgLEA* transgenic and WT plants under normal, salt (300 mM NaCl for 24 h), and drought (10 % PEG for 24 h) stress conditions. WT - wild-type *Arabidopsis*, TG2, TG4, and TG6 - transgenic *Arabidopsis* lines.