

Table 1 Suppl. Classification and functional analysis of late embryogenesis abundant (LEA) protein family genes in *Lepidium apetalum* based on conserved domains.

Serial number	Group	Structure characteristics	Representative proteins	Expression characteristics
-	group 1 LEA_5/D-19	proteins are generally composed of 80 - 153 amino acid sequences, rich in charged amino acids and glycine.	<i>Gossypium hirsutum</i> LEA D19, <i>Triticum aestivum</i> Em, <i>Zea mays</i> E564, <i>Hordeum vulgare</i> B19	auxiliary protein folding, the members of the group have strong hydrophilicity
c12286_g1 c10995_g1	group 2 dehydrin /D-11	proteins are generally composed of 80 - 620 amino acid sequences, there are conserved fragments of Y, S, K and Ψ, rich in polar amino acids.	<i>Gossypium hirsutum</i> LEA D11, <i>Zea mays</i> DHN1, <i>Arabidopsis thaliana</i> COR15a	it has molecular chaperone, high hydrophilicity and thermal stability, and protects cell membrane function.
c36763_g1 c23918_g1 c15290_g1 c37384_g1 c10628_g1	group 3 LEA_4/D-7	proteins are generally composed of 170 - 555 amino acid sequences, rich in basic and hydrophilic amino acids, formation of α-helix.	<i>Gossypium hirsutum</i> LEA D7, <i>Hordeum vulgare</i> HAV1, <i>Glycine max</i> pGmPM2, <i>Arabidopsis thaliana</i> ECP63	induced by drought, high salinity and low temperature, it has the function of stabilizing cell membrane.
c35254_g1 c8434_g1 c23990_g1 c34997_g1 c14252_g1	group 4 LEA_1/D-113	proteins are generally composed of 80 - 120 amino acid sequences, rich in glycine or alanine, formation of α-helix.	<i>Gossypium hirsutum</i> LEA D113, <i>Solanum lycopersicum</i> LE25	maintenance of lactate dehydrogenase activity, closely related to cold and salt resistance
c10119_g1 c18705_g1 c5774_g1	group 5 LEA_4/D-29	structure of this protein is similar to that of the third group, a repeating sequence consisting of 11 amino acids.	<i>Gossypium hirsutum</i> LEA D29, <i>Daucus carota</i> DCECP31, <i>Arabidopsis thaliana</i> AtEC31	they have the function of neutralizing ions.
c26899_g1 c6277_g1 c12355_g1 c29783_g1	group 6 SMP/D-34	low molecular mass and high conserved C-terminal sequence	<i>Gossypium hirsutum</i> LEA D34	they have high hydrophilicity and thermal stability.
c13858_g1 c10900_g1 c13993_g1	group 7 LEA_3/D73	proteins contains five conserved domains, the fifth domain has Zn ²⁺ dependent DNA binding activity.	<i>Gossypium hirsutum</i> LEA D73	they have strong thermal stability
	additional group	most of them are atypical LEA proteins, low homology with other species.	<i>Arabidopsis thaliana</i> LEA14	expression induced by drought, low temperature, salt and strong irradiance

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c15049_g1 c11524_g1 c17381_g1	LEA_2			
c29526_g1	additional group	only in the <i>Brassicaceae</i>	<i>Arabidopsis thaliana</i> At2g41260	free from abiotic stress or ABA induction
c12672_g1	AtM			
-	additional group PvLEA-18	proteins has low molecular mass and contains five conserved domains.	<i>Phaseolus vulgaris</i> PvLEA-18	they have high hydrophilicity and thermal stability

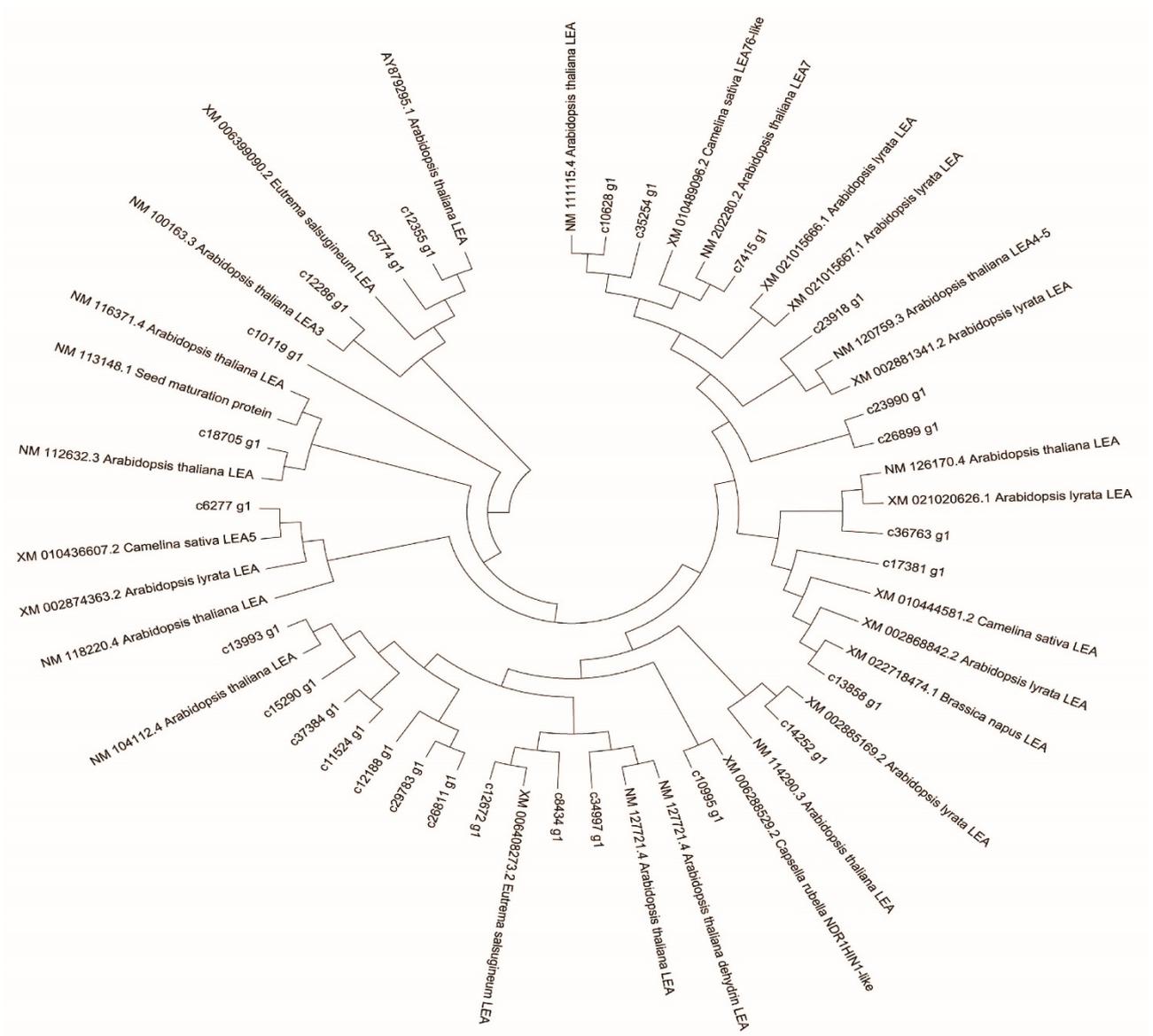


Fig. 1 Suppl. A phylogenetic tree of late embryogenesis abundant (LEA) proteins from *Lepidium apetalum* and other species.

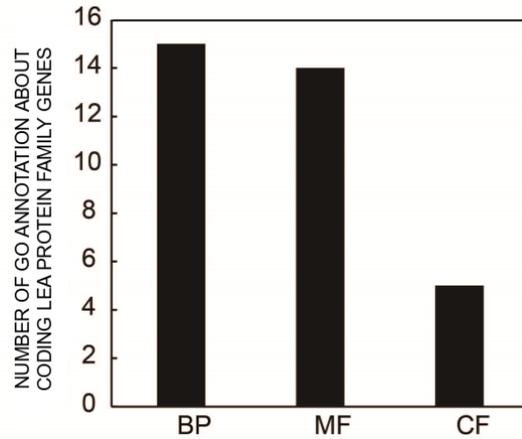


Fig. 2 Suppl. Classification of *Lepidium apetalum* late embryogenesis abundant (LEA) protein family unigenes using gene ontology (GO) annotation. BP - biological process, MF - molecular function, CC - cellular component.

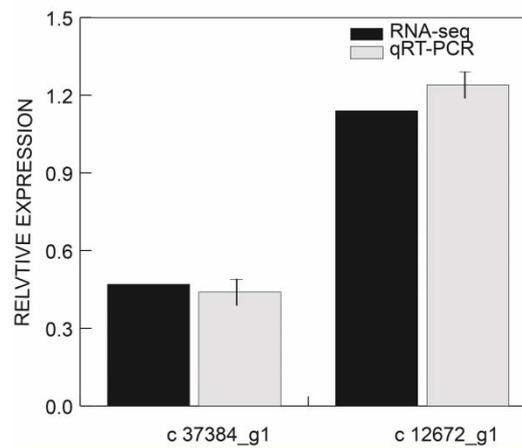


Fig. 3 Suppl. Verification of the transcriptome by quantitative reverse transcription PCR; RNA-seq - transcriptome sequencing, qRT-PCR - real-time quantitative PCR.

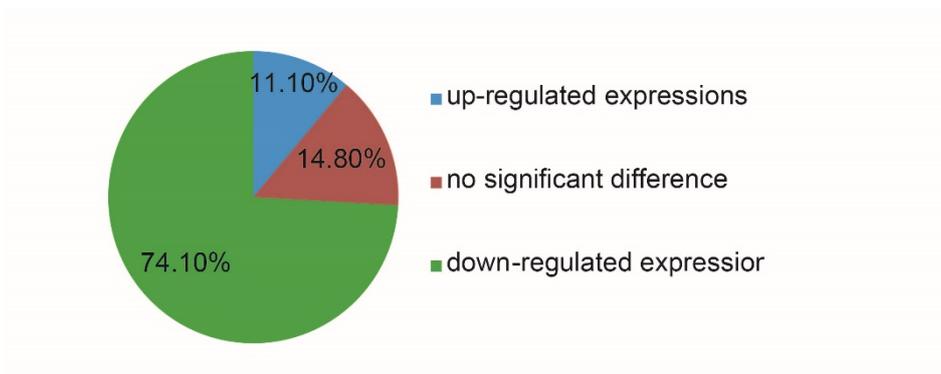


Fig. 4 Suppl. Relative expression difference of late embryogenesis abundant (LEA) protein family genes between controls and seedlings stressed by low temperature (4 °C for 9 d).

1 atggcgtctcaccaacagagttacaaggctgggaaaccagaggcaagggccaggaagactggacaagctatgggaacagtggaggacaaggctgaggaaaggtaaggacaagactcaa
 I M A S H Q Q S Y K A G E T R G K A Q E K T G Q A M G T V R D K A E E G K D K T Q
 121 gcaacggctcaatcagcaaaaggataaagacttctcaactaccaaaacgctcaacaaaaggccatgagacggcccaatcagcaaaaggacaaaacatctcaaacgctcaaacggcccaa
 41 A T A Q S A K D K T S Q T T Q T A Q Q K A H E T A Q S A K D K T S Q T A Q T A Q
 241 caaaaggccatgatacagactcaagcagcaaaagacaagacatctcaagctgctcagacggctcaagacaagctcgtgagtcgaaggacaagaccggggagctactgtctgcgacagga
 81 Q K A H D T T Q A A K D K T S Q A A Q T A Q D K A R E S K D K T G S Y L S A T G
 361 gaagccataaagaacaaggctcaagacgcgctcagtagcacaagaggagacggccgaagttggtagagacaagaccgggtgggttcttgagccagaccgggtgagcatgtaaacagatggct
 121 E A I K N K A Q D A A Q Y T K E T A E V G R D K T G G F L S Q T G E H V K Q M A
 481 atgggtgcagctgatcagctgaagcatactttgggatggctacagagacgaagacaggagcattatccaggaactactacgaccactactgtacaactcggaccactgatccact
 161 M G A A D A V K H T F G M A T E D E D R E H Y P G T T T T T T A T T R T T D P T
 601 caccagacttatcagaggaagtga
 201 H Q T Y Q R K *

Fig. 5 Suppl. Sequence of cDNA and the putative amino acid sequence of *Lepidium apetalum* late embryogenesis abundant 1 (*LaLEA1*).

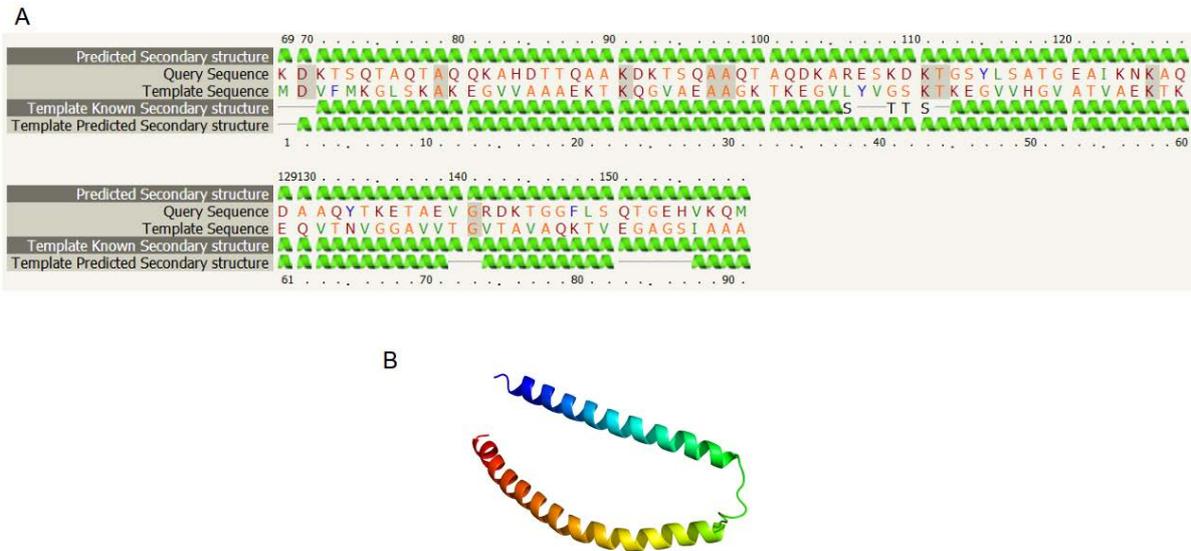


Fig. 6 Suppl. The predicted structure of *Lepidium apetalum* late embryogenesis abundant 1 (*LaLEA1*) encoded protein. *A* - The secondary structure prediction of *L. apetalum* *LaLEA1* encoded protein. *B* - The tertiary structure prediction of *L. apetalum* *LaLEA1* encoded protein. Polar amino acids A, S, T, G, and P are *yellow*; hydrophobic amino acids M, I, L, and V are *green*; charged amino acids K, R, E, N, D, H, and Q are *red*; and aromatic amino acids W, Y, F, and C are *purple*.

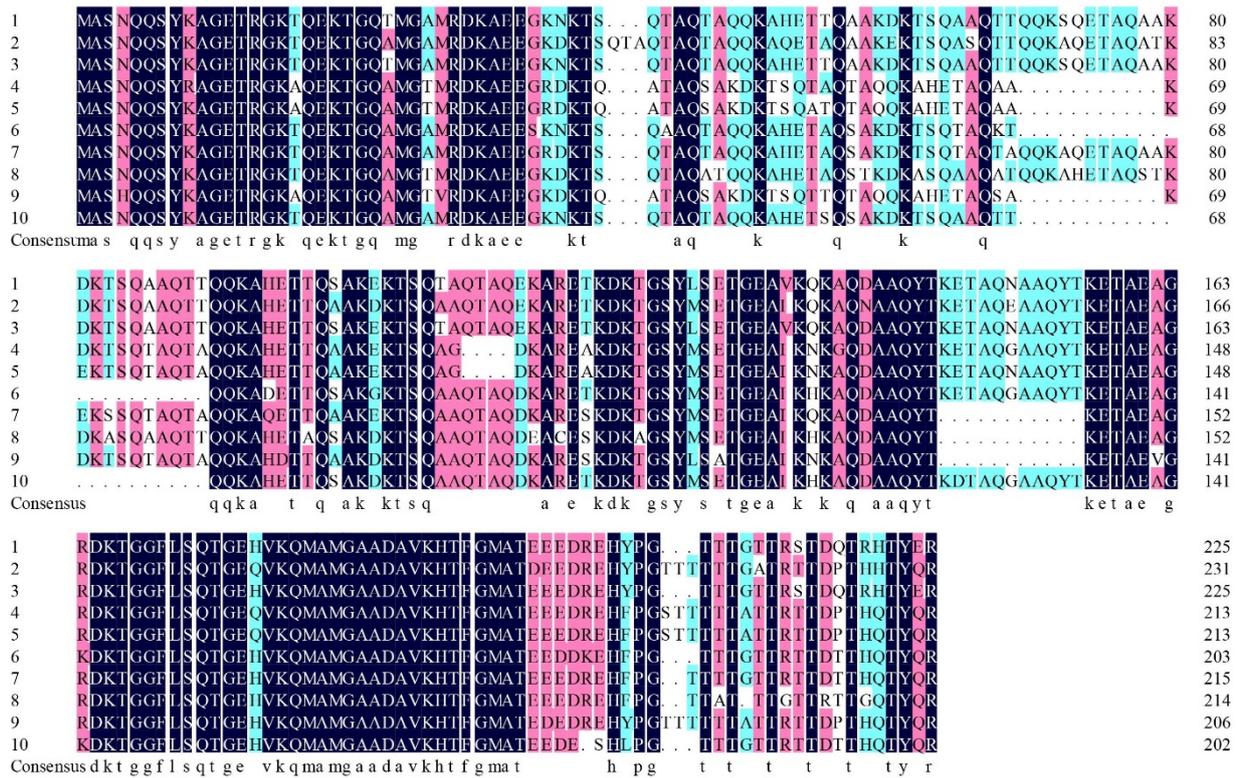


Fig. 7 Suppl. Multiple alignments of *Lepidium apetalum* late embryogenesis abundant 1 (*LaLEA1*) and nine homologous proteins from other plant species. 1 - *Brassica napus* LEA 29-like, 2 - *Brassica napus* LEA 76-like, 3 - *Brassica oleracea* var. *Oleracea* LEA 76, 4 - *Brassica rapa* LEA 76, 5 - *Camelina sativa* LEA 76-like, 6 - *Capsella rubella* LEA 29, 7 - *Eutrema salsugineum* LEA 29 8 - *Isatis tinctoria* LEA, 9 - *Lepidium apetalum* LaLEA, 10 - *Raphanus sativus* LEA.