

Supplementary information for

Isolation and characterization of an atypical *LEA* gene (*IpLEA*) from *Ipomoea pes-caprae* conferring salt/drought and oxidative stress tolerance

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Supplementary Fig. S1. The simple map of *IpLEA*-PRO/pBI101.2 (A) and *IpLEA*/pBIIm (B).

Supplementary Fig. S2. The 3D structural diagram of IpLEA predicted by PHYRE² (<http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index>).

Supplementary Fig. S3. The confirmation for *IpLEA*'s over-expression in Arabidopsis plants.

(A) DNA agarose gel electrophoresis for semi-quantitative RT-PCR and genomic PCR confirmation and (B) Quantitative RT-PCR test for *IpLEA* OX lines.

Supplementary Table S1. Primer sequences used in this study.

Supplementary Table S2. The physical and chemical properties of IpLEA protein.

Fig S1

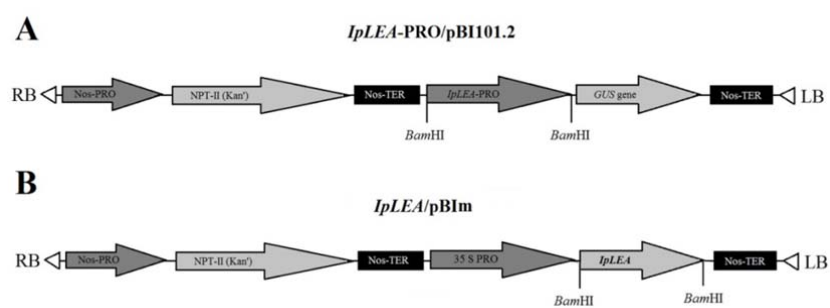


Fig S2

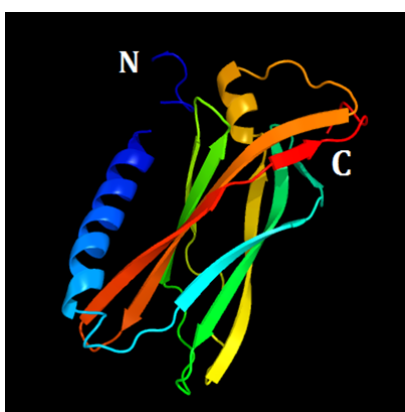
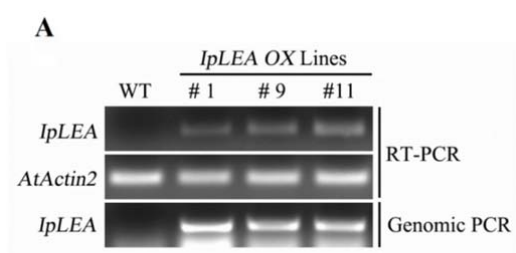
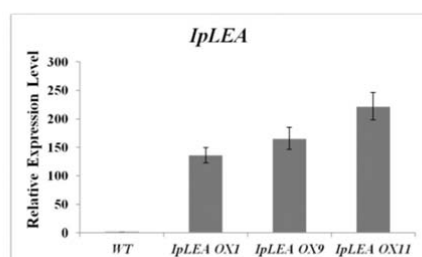


Fig S3



B



Tab. S1 Primer sequences used in this study.

Primer ID	Sequence (from 5' to 3')	Feature
IpLEAF	ATGGCATCGTCTGATAATCC	gene primer pair for sequence of <i>IpLEA</i>
IpLEAR	TCAATCCTCCTCATCATCAT	genomic DNA
IpLEASP1	GGGATCAGCCCCGAGATCAG	IpLEA gene-specific primers for genome walking to amplify promoter sequence of <i>IpLEA</i>
IpLEASP2	ACAGGATTGGATTCTTCAC	
IpLEASP3	AATCTCGGACACATCTGCAG	
IpLEAPEF	AATGGGTCGCGGATCCATGGCATCG TCTGATAATCC	gene primer pair for construction of <i>IpLEA</i> -pET 28a, <i>Bam</i> HI site was underlined
IpLEAPER	GCTCGAATTGCGATCCTCAATCCTCC TCATCATCAT	
IpLEAGF	CTTGCTCCGTGGATCCATGGCATCGT CTGATAATCCA	gene primer pair for construction of <i>IpLEA</i> -pUC/EGFP, <i>Bam</i> HI site was underlined
IpLEAGR	TGCTCACCATGGATCCATCCTCCTCA TCATCATCTCC	
IpLEARTF	ACCAACTGCAGATGTGTCCG	gene primer pair for qRT-PCR of <i>IpLEA</i>
IpLEARTR	CGTTCCAGCATCAGGGATCA	
IpUBQRTF	TCGACAATGTGAAGGCAAAG	gene primer pair for qRT-PCR of reference gene <i>IpUBQ</i>
IpUBQRTR	CTTGATCTTCTTCGGCTTGG	
CAT1RTF	CGCCATGCCGAAAAATACCC	gene primer pair for qRT-PCR of <i>CAT1</i> (At1g20630) in <i>Arabidopsis</i>
CAT1RTR	CTTGCTGTCTGAATCCCAGGAC	
CSD1RTF	TGATGGAAGTCCACCTTCACA	gene primer pair for qRT-PCR of <i>CSD1</i> (At1g08830) in <i>Arabidopsis</i>
CSD1RTR	ATGGCCTCCCTTTCCGAGGT	
APX1RTF	GGACGATGCCACAAGGAT	gene primer pair for qRT-PCR of <i>APX1</i> (AT1G07890) in <i>Arabidopsis</i>
APX1RTR	CGACCAAAGGACGGAAAA	
ERD5RTF	GTCCTCTCTACCACAAAACTC	gene primer pair for qRT-PCR of <i>ERD5</i> (AT3G30775) in <i>Arabidopsis</i>
ERD5RTR	TGGACTCTTGGCATTTCCTAC	
ANAC19RTF	CAACTGTGGCTACCTGAAGACGG	gene primer pair for qRT-PCR of <i>ANAC19</i> (At1g52890) in <i>Arabidopsis</i>
ANAC19RTR	CAAACGAGTCAACACCATAACCCT	
NCED3RTF	GCTGCGGTTTCTGGGAGAT	gene primer pair for qRT-PCR of <i>NCED3</i> (At3g14440) in <i>Arabidopsis</i>
NCED3RTR	TTGAGAAGACGATAATGGCGG	
HAI2RTF	ACGGGCTATGGGACGTAGTG	gene primer pair for qRT-PCR of <i>HAI2</i> (At1g07430) in <i>Arabidopsis</i>
HAI2RTR	ACACATGCGCACCATCGTA	
RD26RTF	AGTTCGATCCTTGGGATTG	gene primer pair for qRT-PCR of <i>RD26</i> (At4g27410) in <i>Arabidopsis</i>
RD26RTR	ACCCGTTGCTTTCCAATAAC	
RD29ARTF	GATATCGACAAGGATGTGCCG	gene primer pair for qRT-PCR of <i>RD29A</i> (At5g52310) in <i>Arabidopsis</i>
RD29ARTR	GTATCCAGGTCTTCCCTTCGC	
RD29BRTF	AAGGAGACGCAACAAGGG	gene primer pair for qRT-PCR of <i>RD29B</i> (At5g52300) in <i>Arabidopsis</i>
RD29BRTR	ACGGTGGTGCCAAGTGAT	
ACT2RTF	GGTAACATTGTGCTCAGTGGTGG	gene primer pair for qRT-PCR of reference gene <i>AtActin2</i> (At3g18780)
ACT2RTR	AACGACCTTAATCTTCATGCTGC	
IpLEAOXF	GGACTCTAGAGGATCCATGGCATCG TCTGATAATCCA	for cloning the full-length ORF of <i>IpLEA</i> and construction of <i>IpLEA</i> -pMD, <i>Bam</i> HI site was underlined
IpLEAOXR	GTCGACCCGGGATCCTCAATCCTC	

	CTCATCATCAT	
IpLEAProF	CGACTCTAGAGGATCCAATCTCGGA	for cloning the full-length promoter and
	CACATCTGCAG	construction of IpLEA-Pro:GUS, <i>Bam</i> HI site
IpLEAProR	ACCTACCCGGGGATCCACCTTCTCA	was underlined
	CAAGCTGAGAT	

Tab. S2 The physical and chemical properties of IpLEA protein.

Physical and chemical properties	IpLEA
No. of amino acids	313
Molecular weight (kD)	34.92
Theoretical pI	4.78
Total no. of negatively charged residues (D+E)	61
Total no. of positively charged residues (R+K)	39
Grand average of hydropathicity(GRAVY)	−0.373
instability index (II)	29.09

Figure 3A The full-length gels/blots of this manuscript.

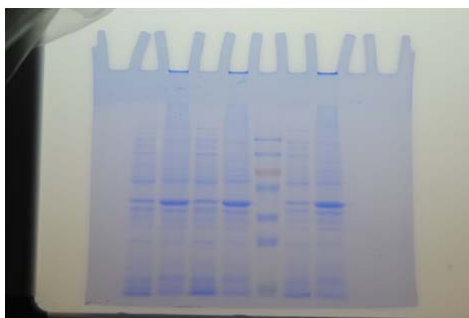


Fig S3 The full-length gels/blots of this manuscript.

