

Table 1 Suppl. Primers used in semi-quantitative RT-PCR assay and plasmid construction.

Primer name	Sequence (5'–3')	Comments
LtpII.3 – Fw	GGGATCGACCGATGTTATGT	RT-PCR analysis
LtpII.3 – Rv	TGTTGACAGTGACACGCAGA	
LtpII.5 – Fw	CACACGCACTGGTCATCAAT	RT-PCR analysis
LtpII.5 – Rv	AGCACGTACTGAGCCTGGAT	
LtpII.6 – Fw	AATGCTTGTGCAGTTTTGCT	RT-PCR analysis
LtpII.6 – Rv	CCCATTGAAGAGATAGCAAGC	
LtpV.1 – Fw	AAGGGCACTCGAACACTTTG	RT-PCR analysis
LtpV.1 – Rv	TCCAGGAGAAGTCACATCCTT	
LtpV.2 – Fw	GTATGCTGTTGTGCGTTCGT	RT-PCR analysis
LtpV.2 – Rv	CTCTGCATCCCTCCGAGATA	
LtpL1 – Fw	GCTCCTGATCGATTGATATGC	RT-PCR analysis
LtpL1 – Rv	CATCGCCGACACACTTACAC	
LtpL2 – Fw	CGATCGATTGACAGTGTGCT	RT-PCR analysis
LtpL2 – Rv	GGGGTCACAACCAACACTTAC	
Actin1 – Fw	ATGCTCTCCCCATGCTATC	RT-PCR analysis
Actin1 – Rv	TCTTCCTTGCTCATCCTGTC	
SpeI-LtpII.3 – Fw	GGTGAAGCAGCACTTTTCG	subcellular localization
SpeI-LtpII.3 – Rv	GCGCACAGTCATAAGAGTCCT	
SpeI-LtpII.5 – Fw	GGGATCGACCGATGTTATGT	subcellular localization
SpeI-LtpII.5 – Rv	TGTTGACAGTGACACGCAGA	
SpeI-LtpV.2 – Fw	CACACGCACTGGTCATCAAT	subcellular localization
SpeI-LtpV.2 – Rv	AGCACGTACTGAGCCTGGAT	
SpeI-LtpL1 – Fw	AATGCTTGTGCAGTTTTGCT	subcellular localization
SpeI-LtpL1 – Rv	CCCATTGAAGAGATAGCAAGC	
SpeI-LtpL2 – Fw	TGTGTGCAGCTGCCTAAGAC	subcellular localization
SpeI-LtpL2 – Rv	GCCAAAGGAGGTCATCGTTA	
DsRed – Fw	CTAGCTGATGGCAAGCACAA	subcellular localization
DsRed – Rv	GGCTCATCGATCGCATAGTA	
GFP – Fw	AAGGGCACTCGAACACTTTG	subcellular localization
GFP – Rv	TCCAGGAGAAGTCACATCCTT	

Table 2 Suppl. Nomenclature of the rice lipid transfer protein (*Ltp*) and *Ltp-like* (*LtpL*) genes in the literature and this study.

^a Rice Genome Annotation Project (Michigan State University; http://rice.plantbiology.msu.edu/analyses_nomenclature.shtml)

^b International Rice Genome Sequencing Project - Rice Annotation Project Database (IRGSP-RAP-DB; <http://rapdb.dna.affrc.go.jp/gene/nomenclature.html>)

Locus_ID MSU RGAP ^a (RAP-DB ^b)	García-Garrido <i>et al.</i> (1998)	Boutrot <i>et al.</i> (2008)	This study
LOC_Os03g02050 (Os03g0111300)	Ltp2	LtpII.3	
LOC_Os05g47730 (Os05g0550600)		LtpII.5	
LOC_Os06g49190 (Os06g0705400)		LtpII.6	
LOC_Os01g62980 (Os01g0849000)		LtpV.1	
LOC_Os04g33920 (Os04g0415800)		LtpV.2	
LOC_Os07g19000 (Os07g0290500)			LtpL1
LOC_Os10g40510 (Os10g0552600)			LtpL2

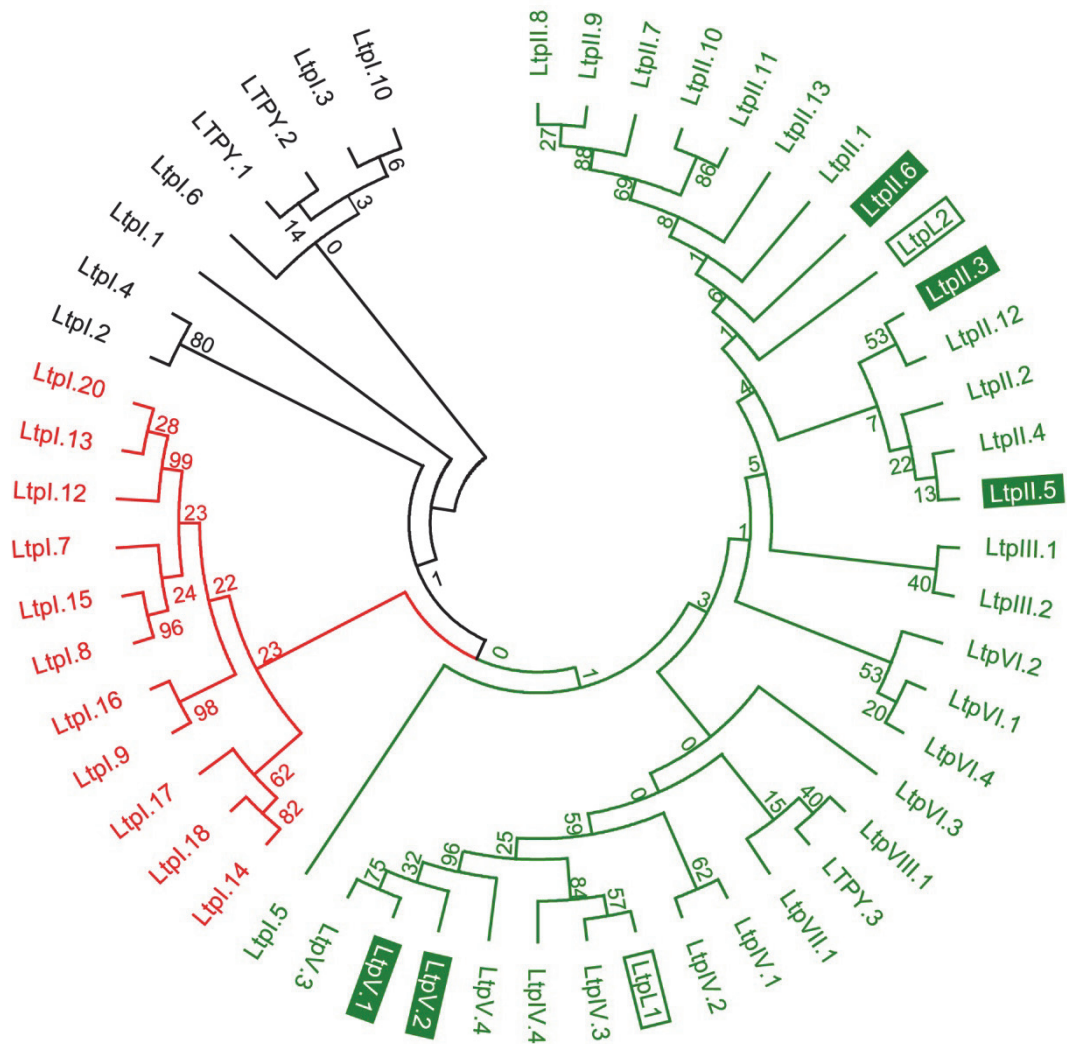


Fig. 1 Suppl. Phylogenetic relationship of lipid transfer protein (*Ltp*) and *Ltp*-like (*LtpL*) genes in rice. The phylogram was generated with the *MEGA 5* program (Tamura *et al.* 2011) from a multiple alignment of the deduced amino acid sequences of *Ltp* and *LtpL* proteins. Bootstrap values from 1 000 replicates were used to assess the robustness of the tree and are indicated. Filled green box indicates the *Ltp* genes induced by salinity, empty green box indicates the *LtpL* genes induced by salinity. Nomenclature of rice *Ltp* was according to (Boutrot *et al.* 2008).

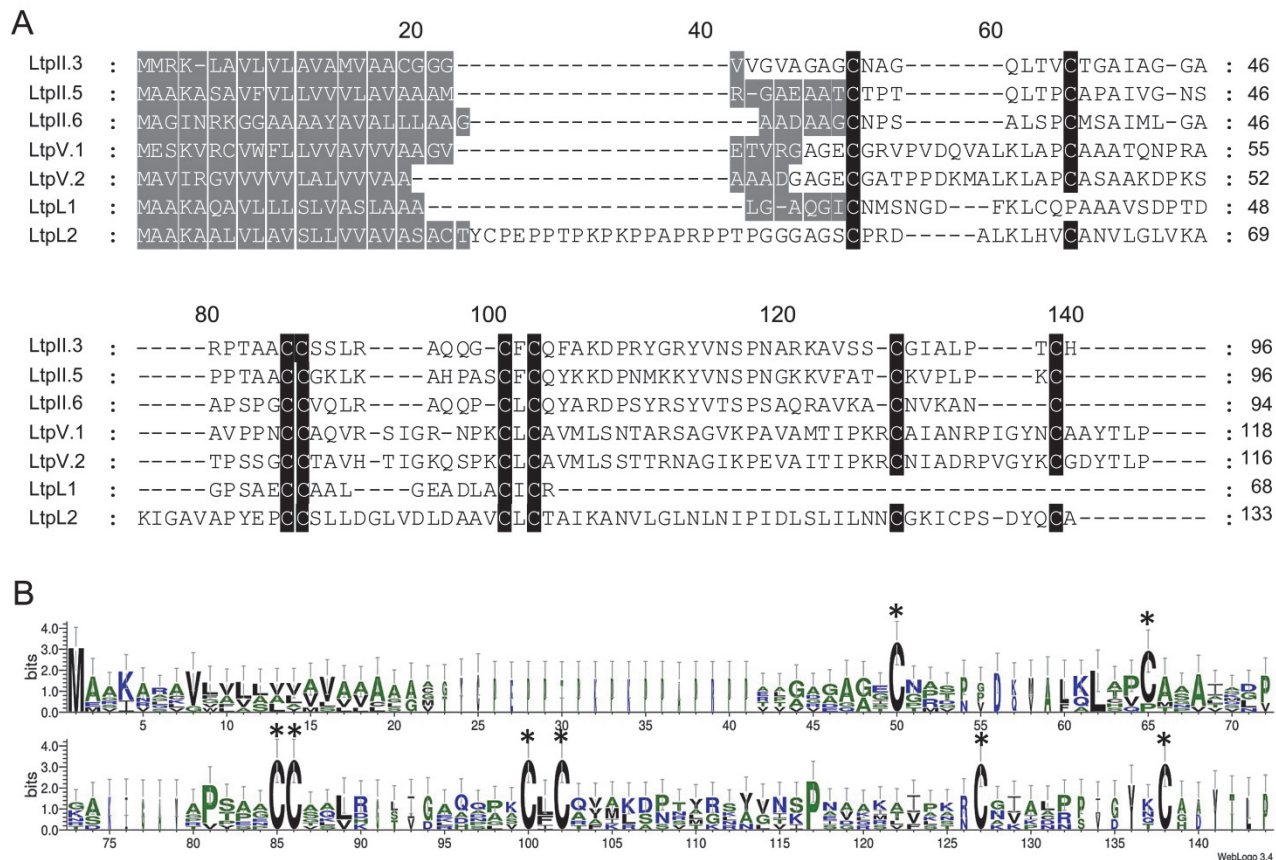


Fig. 2 Suppl. Sequence alignment and protein prediction of salt-inducible rice lipid transfer protein (*Ltp*) and *Ltp*-like (*LtpL*) genes. *A* - Amino acid sequence alignment of seven salt-inducible *Ltp* and *LtpL* genes by *Clustal W 2.0* (Larkin *et al.* 2007). The eight critical cysteine residues in the *Ltp*-related sequences are on a *black background*. The predicted signal peptide sites are on a *gray background* determined by *ChloroP 1.1* server (Emanuelsson *et al.* 1999). Numbers on the right indicate the positions of amino acid residues. *B* - *Weblogo* analysis of the rice salt-inducible lipid transfer proteins. The overall height of the stack indicates the sequence conservation at that position, and the height of each letter represents the relative frequency of the corresponding amino acid at that position. The cysteine residues are indicated by *asterisks*.