Supplementary materials

Table S1 Primer sequences used in this study

Gene	Purpose	Forward primers (5'–3')	Reverse primers (5'–3')
PtrLEA7-pBI121	Overexpression	GCTCTAGAATGGCATCCCACGATCAGAG	CGGGATCCTTAACCCTTTGTATAAGTGT
PtrLEA7-101LYFP	Subcellular localization	CGGAATTCATGGCATCCCACGATCAGAG	CGGGATCCACCCTTTGTATAAGTGTTCC
35S-F	Transgenic identification	TCCTCGGATTCCATTGCCCAGC	
NPT II		CGGCTATGACTGGGCACAACA	CGGCAGGAGCAAGGTGAGATG
PtrLEA7-qPCR	qPCR	GAAAACCCAGGAGACGGGAC	CCGAAAGTGTTCTTCACGGC
CAT		CTGCCAGTTCTTTCAACGCC	AAACCCTTAGCACTGGCTCC
SOD		CAAGCCGCAATAGCAGCCAT	CCGTGGAATGCAGAGTGAAG
POD		TGCTGGACAGCACTAACACC	CCAATGGAACTGCCCATGAC
ACTIN	Internal reference	CCGACCGTATGAGCAAGGAAA	TTCCTGTGGACAATGGATGGA
Ubiquitin		GGTGTTTCCAGTGGCGGACG	TCCTCCCCTCAGCTACGGGGTAT

Note: Underlines indicate enzyme site.

Table S2 Prediction of subcellular localization of PtrLEA7 by two online tools

Location	Plant-mPLoc	YLoc^{+}
Cytoplasm	–	43.3%
Nucleus	Nucleus	51%
Extracellular space	–	5.6%

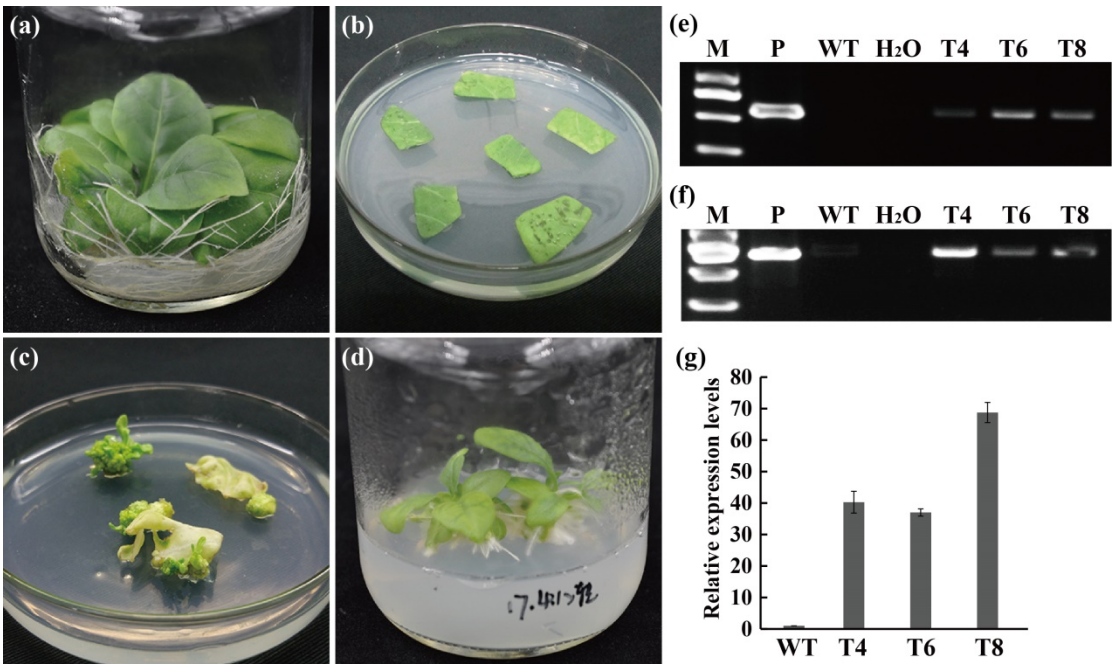

Fig. S1 Genetic transformation and molecular identification of transgenic tobacco plants overexpressing *PtrLEA7*. (a) Wild type tobacco plants used for transformation. (b) Leaf discs on the selection medium. (c) Regenerated buds on the selection medium for 40 d. (d) Representative rooted plants. (e,f) Transgenic identification of three transgenic lines (T4, T6, T8) by PCR using *35S*-forward + *PtrLEA7*-reverse primers (e) and *NPT II* primers (f). M, marker; P, plasmid; WT, wild type. (g) Gene expression levels of *PtrLEA7* in three transgenic lines and wild type by qPCR.

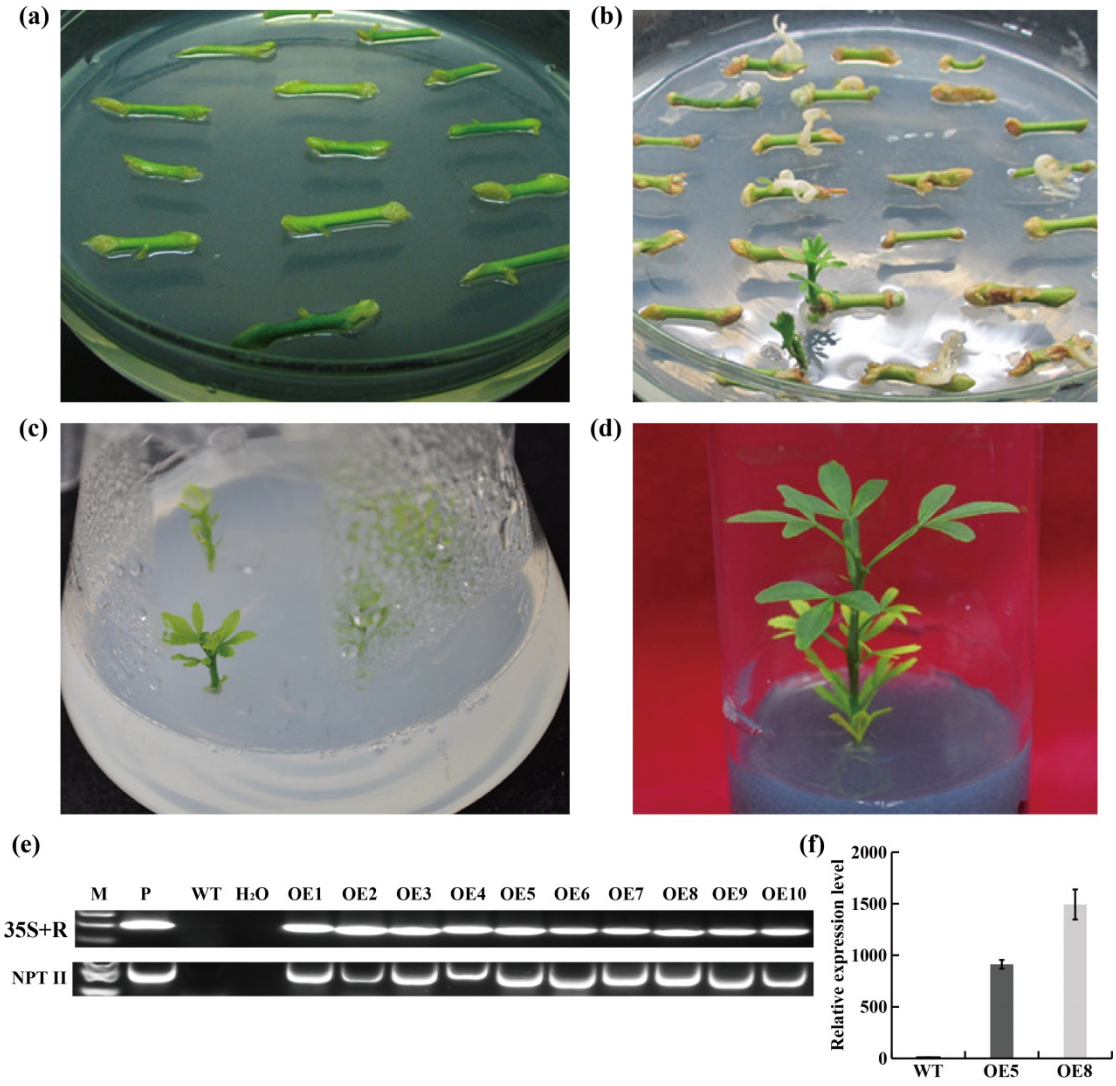

Fig. S2 Genetic transformation and molecular identification of transgenic trifoliate orange overexpressing *PtrLEA7*. (a) Co-culture of the shoot segments. (b) Regenerated shoots on the selection medium. (c) Regenerated plants on the shooting medium. (d) Representative rooted plants. (e) Genetic identification of ten transgenic lines (OE1-OE10) and wild type by PCR using two pairs of primers. M, DNA marker; P, plasmid; WT, wild type. (f) Relative expression levels of *PtrLEA7* in two transgenic lines and wild type by qPCR.