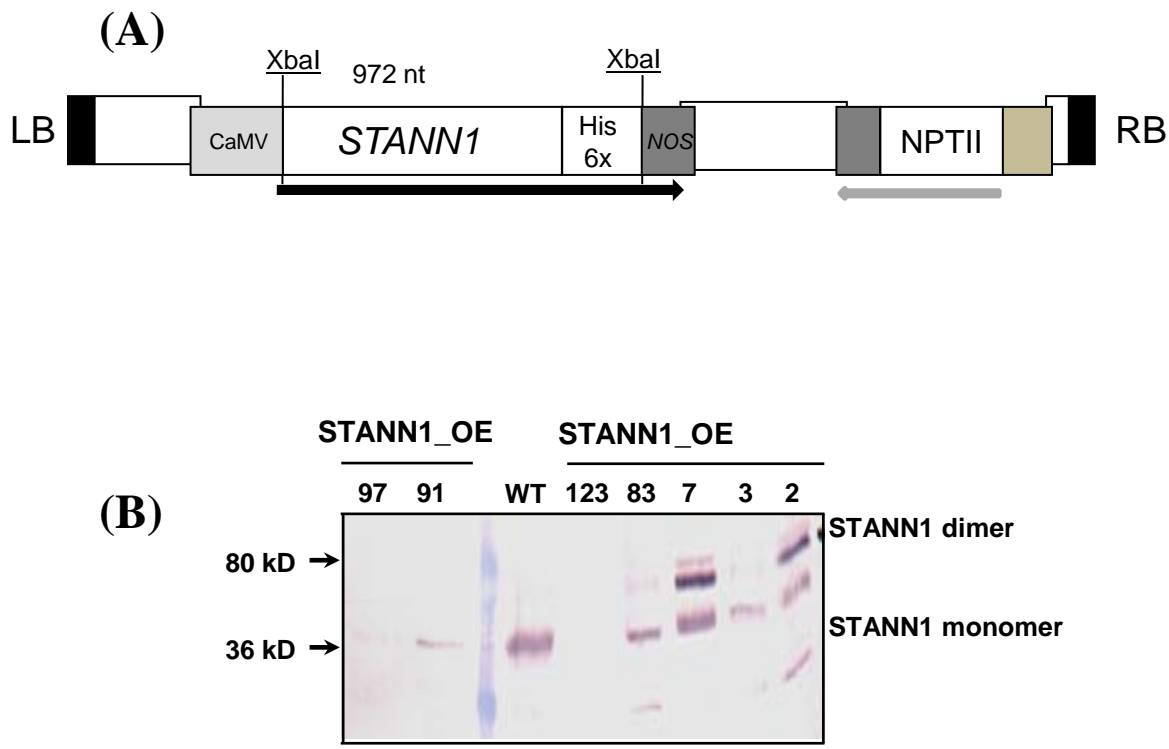


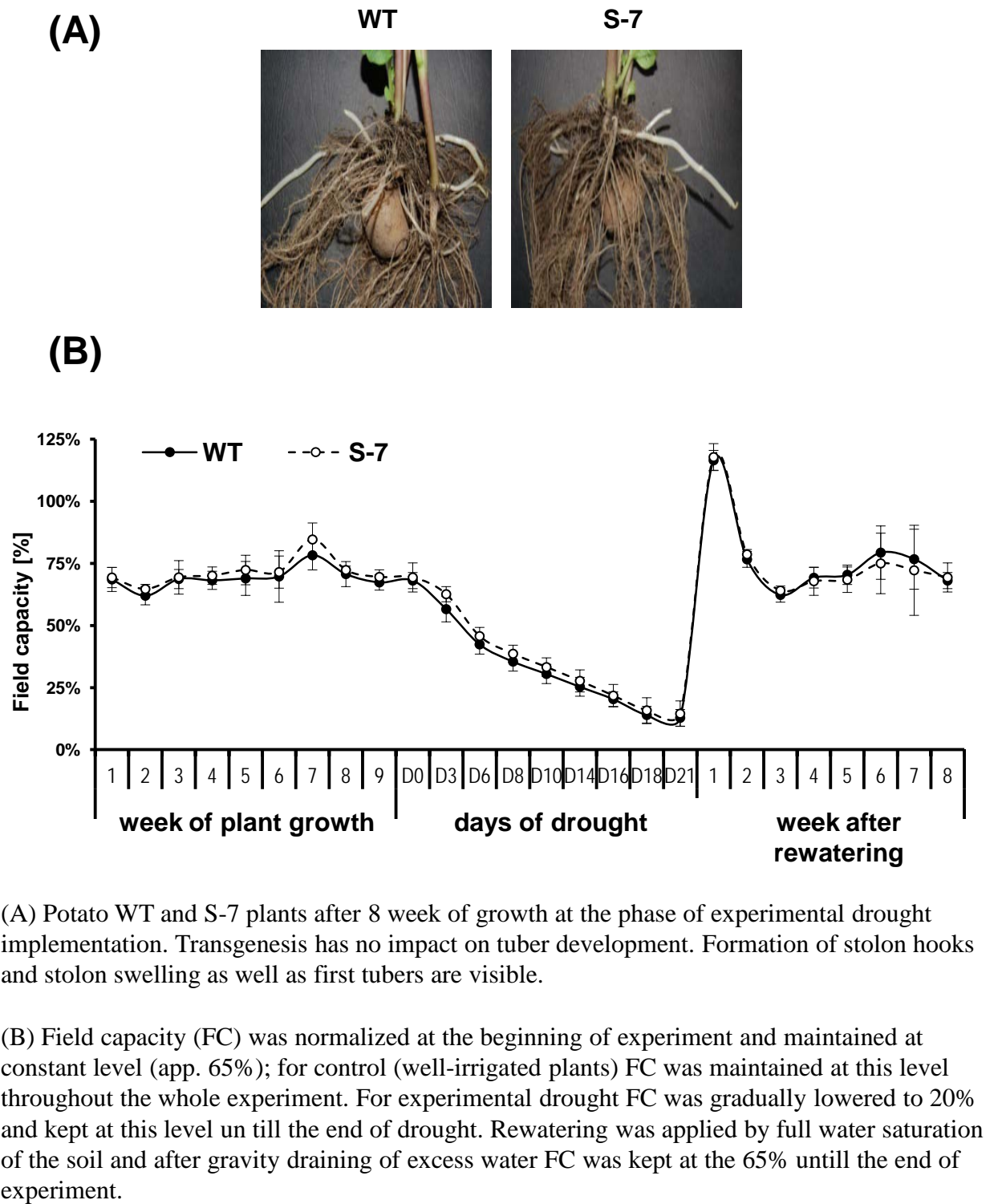
**Figure A.** Construction of transgenic plants.



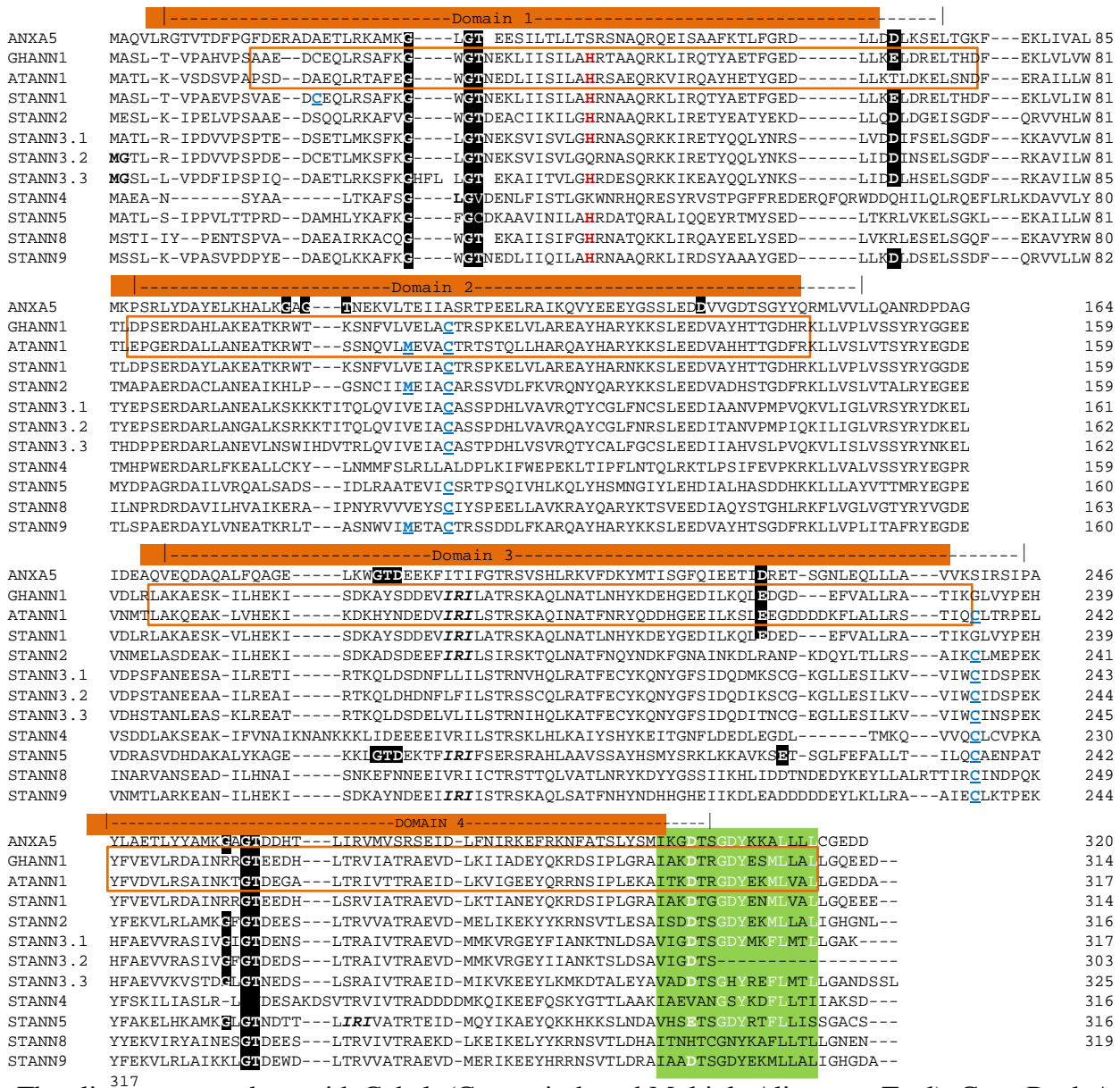
(A) Structure of the T-DNA region from pROK2 carrying STANN1\_His6x that was used for *Agrobacterium* -mediated transformation. LB – left border; RB – right border; NPTII – neomycin phosphotransferase II, CaMV – cauliflower mosaic virus 35S promoter; NOS – nopaline synthase terminator;

(B) Expression of STANN1\_His6x protein in F1 transgenic potato lines. Proteins were isolated from leaves of WT and F1 transgenic lines S-2, S-3, S-7, S-83, S-91, S-97 and S-123 grown *in vitro*. His-tagged proteins were purified with Ni-NTA agarose, subjected to SDS\_PAGE and blotting followed by detection with anti-His primary Ab. The band detected in WT represents *Arabidopsis* annexin ATANN1\_His6x (molecular weight *ca* 36 kD) produced in *Escherichia coli* that was added before purification to the ground protein to STANN1\_His6x easily dimerized hence the two bands were detected, the lower with molecular weight corresponding to monomer and the upper corresponding to dimer.

**Figure B.** Schematic characteristic of experimental drought.

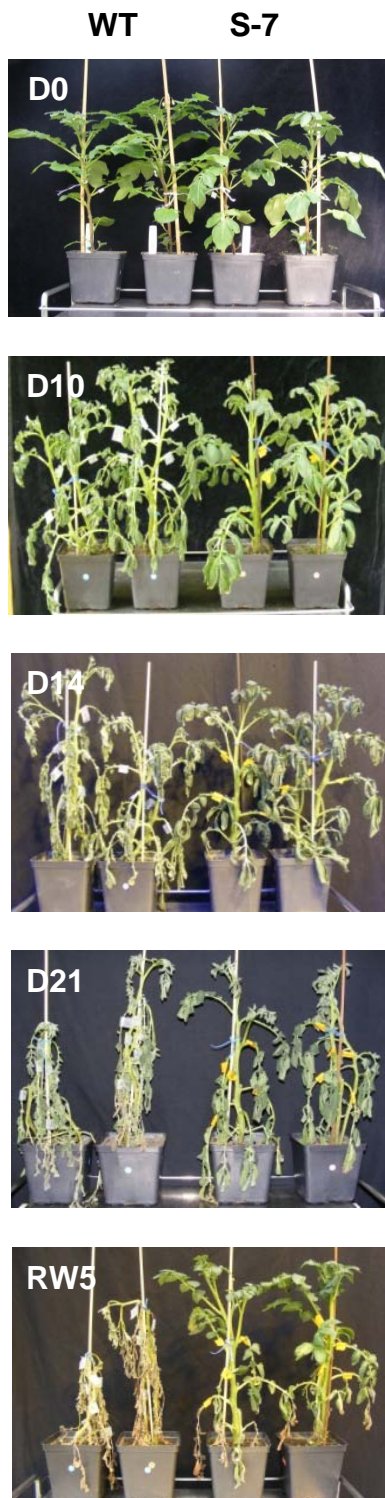


**Figure C.** Multiple alignment of amino acid sequences of putative annexins from potato and selected annexins from human, Arabidopsis and cotton.



The alignment was done with Cobalt (Constrain-based Multiple Alignment Tool). Gene Bank Acc Nos of sequences are: human AnxA5 (NP\_001145.1), cotton (*Gossypium hirsutum*) GHANN1 (1N00), *Arabidopsis thaliana* ATANN1 (2Q4C), *Solanum tuberosum* annexins: STANN1 (PGSC0003DMG4000177114), STANN2 (PGSC0003DMG40002817), STANN3.1 (PGSC0003DMG4000221817), STANN3.2 (PGSC0003DMG401019427), STANN3.3 (PGSC0003DMG402019427), STANN4 (PGSC0003DMG400019446), STANN5 (PGSC0003DMG400007966), STANN8 (PGSC0003DMG400007482) and STANN9 (PGSC0003DMG40001879). Boundaries of endonexin repeats (orange rectangles) were determined on the basis of crystallized plant annexins from cotton, GHANN1 and Arabidopsis ATANN1. Functional amino acid motifs (either predicted or previously indicated for plant annexins) are highlighted. Conserved histidine 40 residue is in red; methionine and cysteines from C3 cluster are in blue and underlined. Calcium binding motifs G-X-GTD-{38-40}-D/E are in green boxes; potential N-terminal acylation motif is in bold; putative actin-binding domains IRI are bolded in yellow boxes. C-terminal peptide similar to 14-3-3 proteins is marked by blue rectangle. Amino acid residues of high conservation are shown in red, medium - in blue.

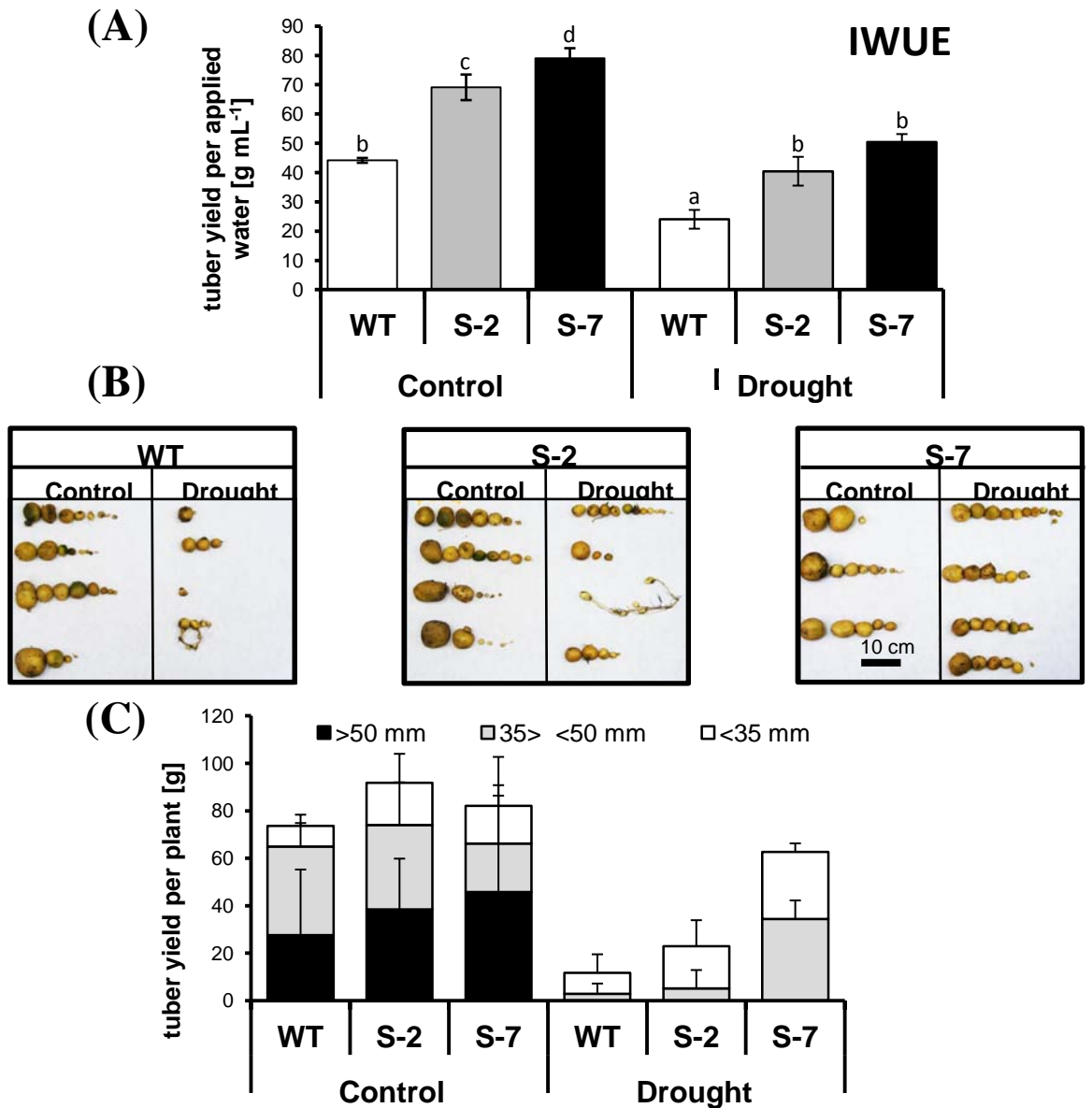
**Figure D.** Drought tolerant phenotype of transgenic S-7 potato plants.



Each image depicts two WT plants (left side) and two transgenic S-7 plants (right side) subjected to experimental drought. Drought was started on D0 and lasted 21 days. During that time watering was gradually reduced so as to lower the FC to 20%. After reaching that level it was maintained until 21 days after onset of experiment. The soil was then fully saturated with water (rewatering) and FC was maintained at 65% until the end of experiment. D10 - irrigation withheld for 10 days, D14 - irrigation withheld for 14 days, D21 - irrigation withheld for 21 days, RW5 – rewatered for 5 days. Experiments were repeated four times and similar results were obtained both in greenhouse and in growth chamber.

In WT symptoms of wilting clearly appeared after 10 days of drought; in S-7 they were apparent only after 2 weeks. On the 21<sup>st</sup> day WT were severely affected with damaged stems and dry leaves. At the same time in S-7 plants the upper leaves still maintained turgor. After rewatering only a few leaves in WT regenerated; instead, new shoots developed from below-ground parts after at least a week of regular irrigation. In contrast, the S-7 plants preserved their upper leaves and after rewatering returned to a normal healthy look within hours. The exact number of irreversibly damaged leaves varied between experiments, but it was always significantly lower than in WT.

**Figure E. Potato yield during drought.**

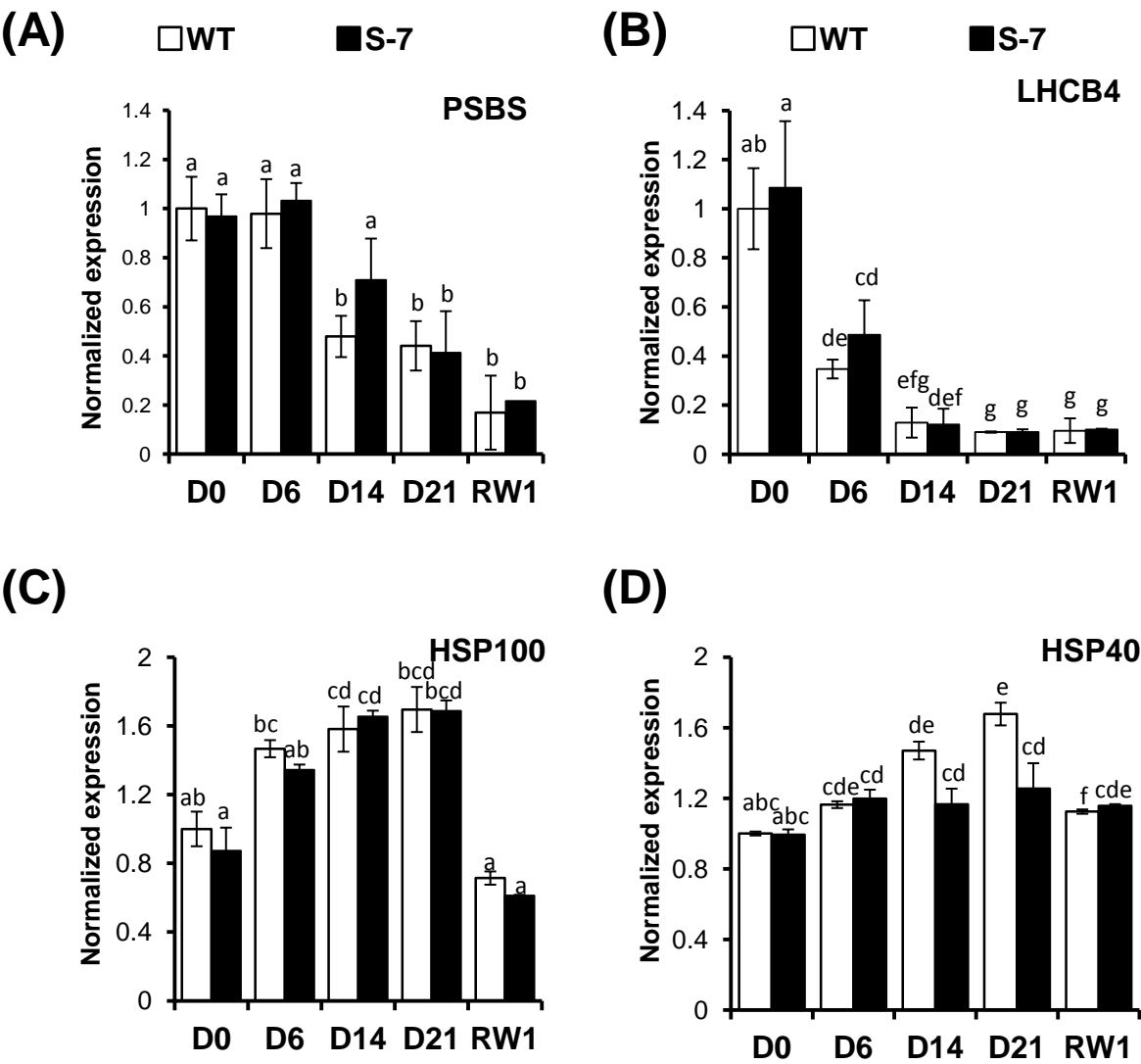


(A) Irrigated Water Use Efficiency (IWUE) is a quotient of crop produced per unit per amount of water supplied ( $IWUE = Y / W$  [g/pot/mL of water])

(B) An exemplary tuber yield per plant. Potato plants WT, S-2, and S-7 were grown in a greenhouse. After 8-10 weeks of growth plants were subjected to drought stress by restricting irrigation to achieve 20% FC and kept at this level until 14<sup>th</sup> day. After that time plants were rewatered and cultivated in optimal conditions for additional 10 weeks until physiological maturity. Tubers were lifted immediately after withering of haulms. The weight of all fresh tubers from single plant was determined immediately after harvesting. Experiments were repeated twice and gave similar results.

(C) Quantification of tuber yield experiments. Results are shown as mean  $\pm$  SD ( $n=10$ )

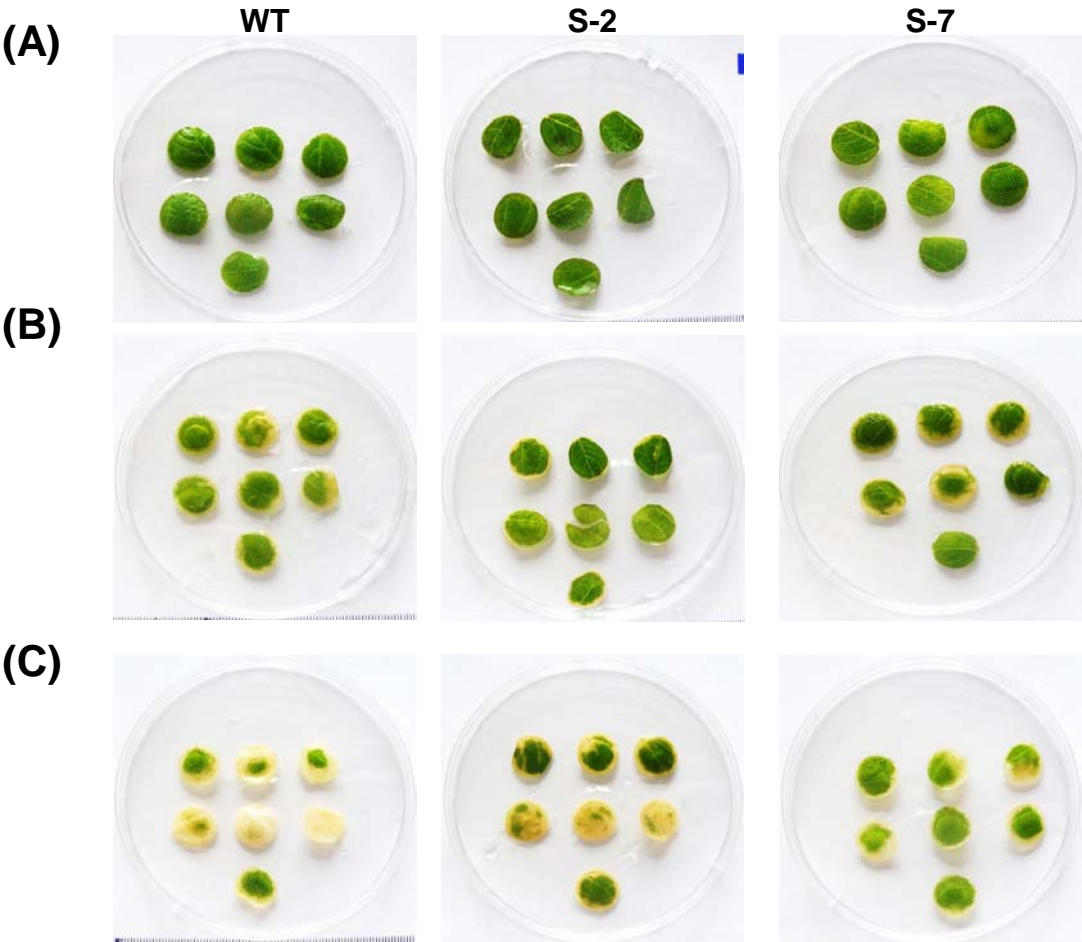
**Figure F.** Expression of genes coding for PSII proteins and HSPs.



Relative quantification of *PSBS* (A), *LHCB4* (B) *HSP100* (C) and *HSP40* (D) mRNAs in leaves of WT (white bars) and transgenic S-7 (black bars) potato plants during three-week drought and after rewatering. The data represents the mean  $\pm$  SE from at least four measurements. Homogenic groups are determined by Tukey HSD (Honestly Significant Differences) test, the same letters designate days which are not significantly different at  $P < 0.05$  and belong to the same homogenic group.



**Figure G.** The effect of photooxidative stress on potato leaves.



Leaf discs ( $\Phi \sim 1$  cm) were excised from leaves of WT or transgenic plants S-2 and S-7 and immediately infiltrated with (A) 50 mM Tris, pH 7.5 (B) 10  $\mu$ m MeV or (C) 50  $\mu$ m MeV. Subsequently, leaf discs were exposed to light of 150 PPFD for 30 h.