Table 1. Suppl. Sequences of the oligonucleotide primers used for Real time quantitative PCR. In the first column GenBank accession No. of each sequence is specified.

| mRNA | Forward primers | Reverse primers |
|---|---|---|
| *preLegrp1a* (AK246918) | 5'-ATCGGTTTTGAAGTTTCTGTTTTA-3' | 5'-GCCATCAAGTTCCTGACCAT-3' |
| *mLegrp1a* (JQ613215) | 5'-AAGTAGTCGACTCGAAGATCATT-3' | 5'-TTGTCTTCCACCACCGAAACCA-3' |
| *asLegrp1a* (AK323933) | 5'-TTATACCATTCCTTGAAACGATCA-3' | 5'-TTGTCTTCCACCACCGAAACCA-3' |
| *preLegrp1b* (AK320592) | 5'-ATGTTTCTCCCCCTCATGC-3' | 5'-CCCTTCAATAGCATCCCTCA-3' |
| *mLegrp1b* (AK224744) | 5'-GTGGTCGAATCCAAGATCATC-3' | 5'-GTAACCACCCCCGCCTCTT-3' |
| *asLegrp1b* (JQ613216) | 5'-ATTCCAATTCCCCGAAACGATCATC-3' | 5'-GTAACCACCCCCGCCTCTT-3' |
| *preLegrp1c* (AK324061) | 5'-TTTTGTGTTTATTCACCATC-3' | 5'-TGATGTTACGACCATCAAGG-3' |
| *mLegrp1c* (AK323723) | 5'-AATGTGGTCGACTCCAAGATT-3' | 5'-CAAAACCGCCGCCGCCGCCG-3' |
| *asLegrp1c* (JQ613217) | 5'-ATTCCATTCCTTTATACGATT-3' | 5'-CAAAACCGCCGCCGCCGCCG-3' |
| *LeEF1α* (X14449) | 5'-GCTGGTATCTCCAAAGATGGTC-3' | 5'-CATGTTGTCTCCTTCAAAACCA-3' |

Table 2 Suppl. Program employed for the separation of phenylisothiocyanate (PITC) derivatized amino acids. Run time was 64 min with 7 min column regeneration time. Buffer A: 19 g of sodium acetate trihydrate was dissolved in 1 $dm^3$ of HPLC grade water. To this, 0.5 $cm^3$ of triethylamine (TEA) was added and the contents were mixed properly, adjusted to pH 6.4 with glacial acetic acid and filtered. Acetonitrile (60 $cm^3$) was added to the filtrate (940 $cm^3$). Buffer B: acetonitrile:$H_2O$ (6:4).

| Run time [min] | Buffer A [%] | Buffer B [%] |
|---|---|---|
| 0 | 100 | 0 |
| 0.1 | 96.5 | 3.5 |
| 1 | 96.5 | 3.5 |
| 22 | 94.8 | 5.2 |
| 24 | 69 | 31 |
| 46 | 64.6 | 35.4 |
| 50 | 0 | 100 |
| 57 | 0 | 100 |
| 59 | 100 | 0 |
| 64 | 100 | 0 |

Table 3 Suppl. Calibration parameters of amino acid PITC derivatives. The slope, the intercept, and the regression coefficient (*R*) for each amino acid is shown.

| AA | Slope | Intercept | *R* | AA | Slope | Intercept | *R* |
|---|---|---|---|---|---|---|---|
| Asp | 4390 | -0.35 | 0.93 | Pro | 4978 | 1.32 | 0.92 |
| Glu | 4502 | -0.17 | 0.98 | Tyr | 5677 | 3.08 | 0.98 |
| OH-Pro | 5147 | 0.76 | 0.99 | Val | 5042 | 1.33 | 0.99 |
| Asn | 5075 | 1.95 | 0.97 | Met | 5866 | 1.22 | 0.99 |
| Ser | 4841 | 2.68 | 0.97 | Cistine | 5568 | -3.59 | 0.96 |
| Gln | 5661 | 1.67 | 0.97 | Ile | 5079 | 0.99 | 0.99 |
| Gly | 5755 | 1.98 | 0.98 | Leu | 5420 | 1.66 | 0.96 |
| Citrulline | 4666 | 1.15 | 0.98 | Phe | 5639 | 2.37 | 0.99 |
| Arg | 6011 | 0.35 | 0.98 | Trp | 5762 | 5.64 | 0.88 |
| Thr | 6840 | 0.22 | 0.95 | Orn | 5915 | 1.87 | 0.92 |
| Ala | 4701 | 1.91 | 0.90 | Lys | 7234 | -1.33 | 0.79 |

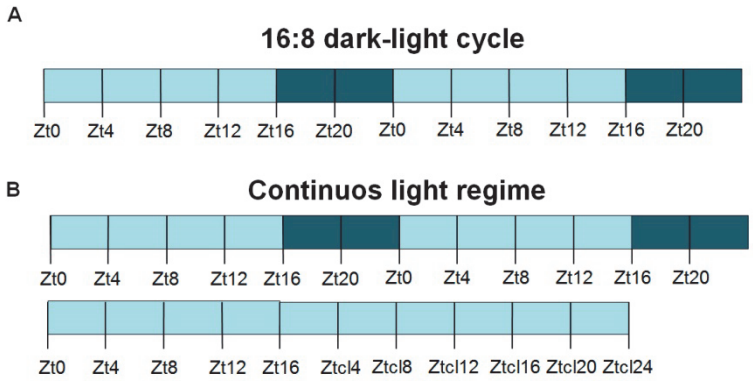


Fig. 1 Suppl. Schematic representation of the 16-h photoperiod cycles and the continuous irradiance. The boxes represent a 4-h periods; *light blue* boxes correspond to light periods whereas *dark blue* boxes to dark periods. Plants under 16-h photoperiod (*A*) were transferred to a continuous irradiance (bottom part of *B*) and fruits were harvested at 4-h intervals. The Zeitgeber times (Zt) of the continuous irradiance are named "Ztcl" to differentiate them from the normal Zt.

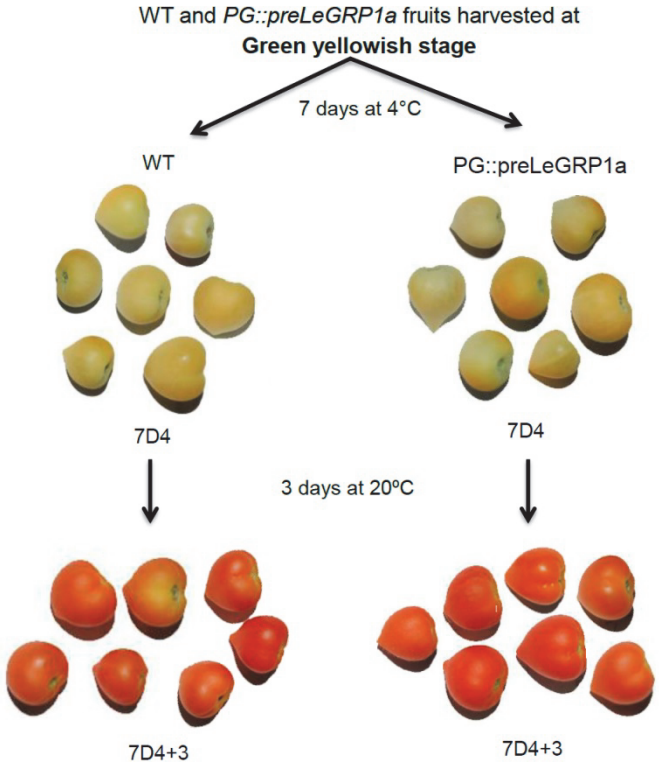


Fig. 2 Suppl. Schematic representation of cold-stress treatments applied to fruits of tomato cv. Micro-Tom wild type and transgenic *PG::preLeGRP1a* plants. The tomatoes were harvested at the green yellowish stage (37 - 39 DPA) and stored at 4 °C for 7 d. The fruits were then maintained at 20 ºC for 3 d more. The picture is representative of the treatments performed to more than 30 fruits per treatment.

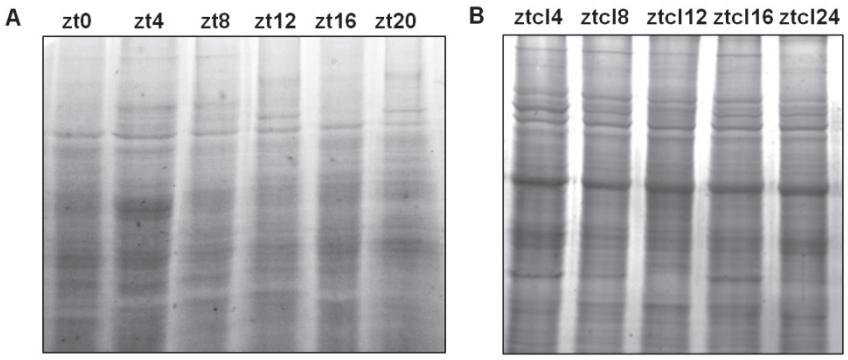


Fig. 3 Suppl. Total protein loading control. SDS-polyacrylamide gel (12 %, m/v) electrophoresis of pericarp proteins of tomato WT and transgenic *PG::preLeGRP1a* plants grown under continuous irradiance. They were extracted from fruits at the red ripe stage (*A*) and at the immature green stage (*B*). Ten and 25 µg of total protein were loaded in each lane in (*A*) and (*B*), respectively. *A* - *lanes* 1 to 6: zt0, 4, 8, 12, 16, and 20. *B* - *lanes* 1 to 5: ztcl4, 8, 12, 16, and 24. One representative image of three replicates is shown.

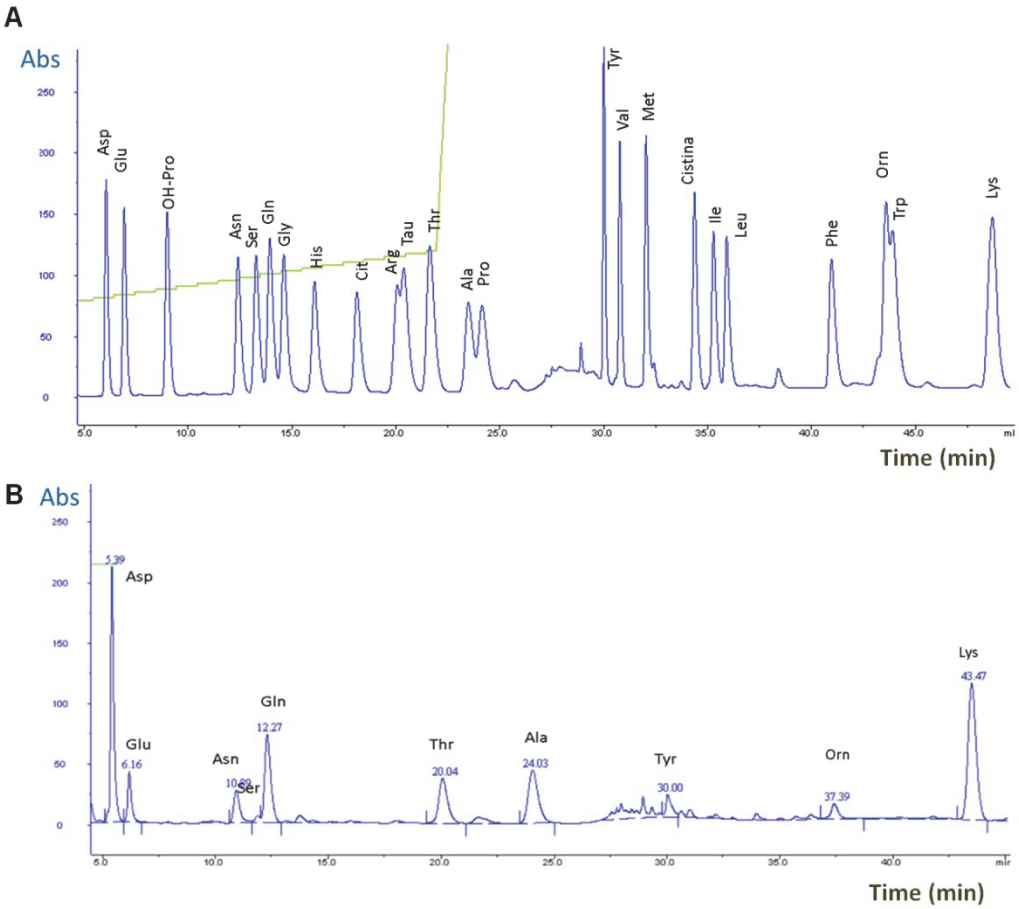


Fig. 4 Suppl. Chromatogram of amino acid derivatives resolved on reverse phase-HPLC with pre-column phenylisothiocyanate (PITC) derivatization. The reverse phase C18 column (5 µm, 250 × 4.6 mm, *LUNA Phenomenex*) with a C18 guard security pre-column (4 × 3 mm) was connected to an *ÄKTA* purifier equipment. *A* - Individual 23 amino acid standards (cysteine, arginine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, tyrosine, threonine, valine, alanine, aspartic acid, glutamic acid, glycine, proline, serine, asparagine, glutamine, cystine, ornithine, citrulline, and tryptophan). The *green line* represents the buffer gradient in the run. *B* - Typical chromatogram of free amino acids from tomato fruits after 7 d of storage at 4 ºC and 3 d at 20 ºC.

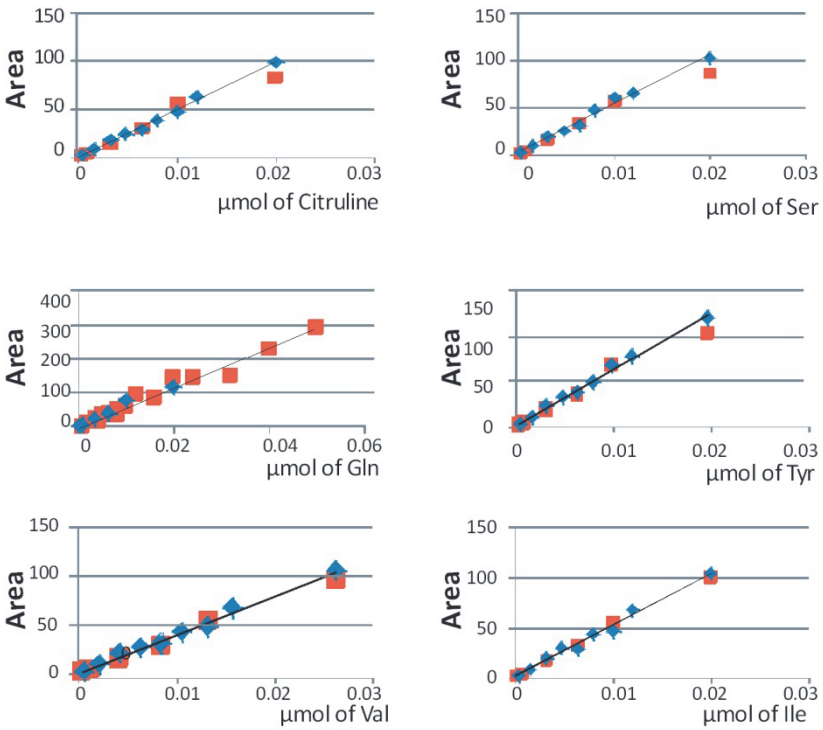


Fig. 5 Suppl. Calibration curves of standard amino acids. Curves of each amino acid were done using concentrations between 0 and 0.03 µmol and repeated two times using two standard amino acids mixtures of the same composition prepared indepently times, *red* and *blue squares*, respectively. Working standard amino acid composition: cysteine, arginine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, tyrosine, threonine, valine, alanine, aspartic acid, glutamic acid, glycine, proline, serine, asparagine, glutamine, cystine, ornithine, citrulline and tryptophan. Representative curves of some amino acids are shown.

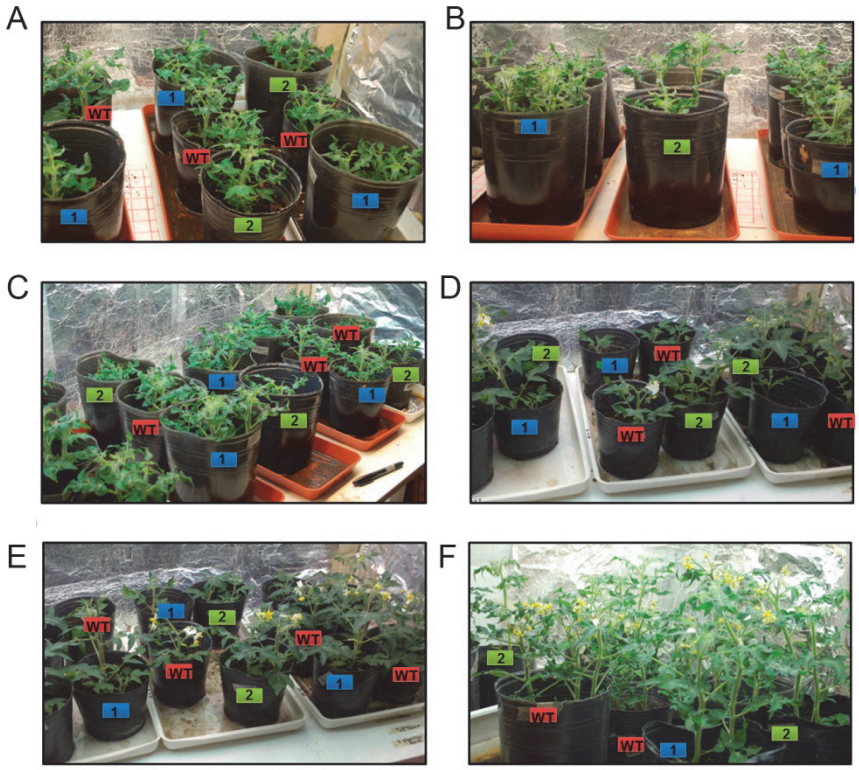


Fig. 6 Suppl. Pictures of tomato plants cv. Micro-Tom (WT) and transgenic *PG::preLeGRP1a* (lines 1 and 2) of different age: 30 d (*A*, *B*), 45 d (*C*) and in flowering stage (*D*, *E*, and *F*). Coloured boxes indicate wild type (*red*, "WT") and transgenic *PG::preLeGRP1a* (line 1: *blue*, "1"; line 2: *green*, "2") plants.

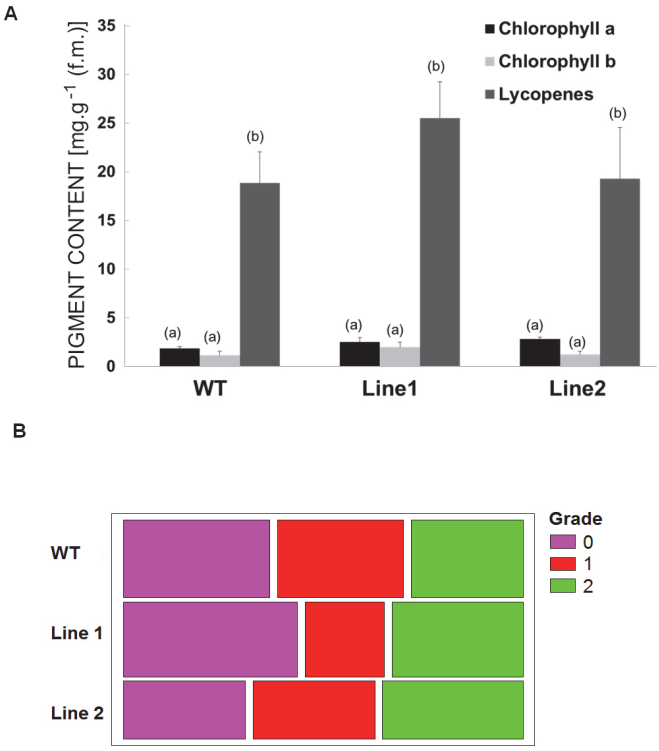


Fig. 7 Suppl. Pigment content in fruits of WT and transgenic *PG::preLeGRP1a* plants after storage for 7 d at 4 ºC and 3 d at 20 ºC. The experiment was repeated in three consecutive harvests. *A* - Chlorophyll *a*, chlorophyll *b*, and carotenoid lycopene. Means ± SDs, $n = 30$. Bars with the same letters are not significantly different among the treatments ($P < 0.05$). *B* - Dehydration visually evaluated using the following scale: 0 - 20 % of visually dehydrated fruits = no dehydration (grade 0), grade 1 = 20 - 60 %, grade 2 = more than 60%. No significant differences were observed using Score testing.

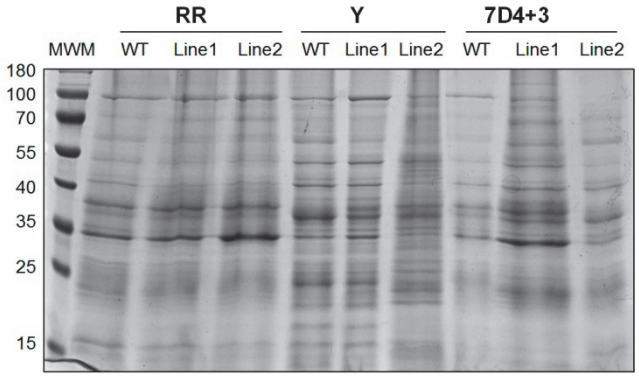


Fig. 8 Suppl. SDS-polyacrylamide gel (15 %) electrophoresis. Protein extracted from 0.32 g of fruit pericarp of WT and transgenic *PG::preLeGRP1a* lines 1 and 2 were loaded in each lane. RR - red ripe fruits; Y - green yellowish fruits, and 7D4+3 - fruits after storage for 7 d at 4 ºC and 3 d at 20 ºC. MWM - molecular mass marker in kDa. One representative image of three replicates is shown.

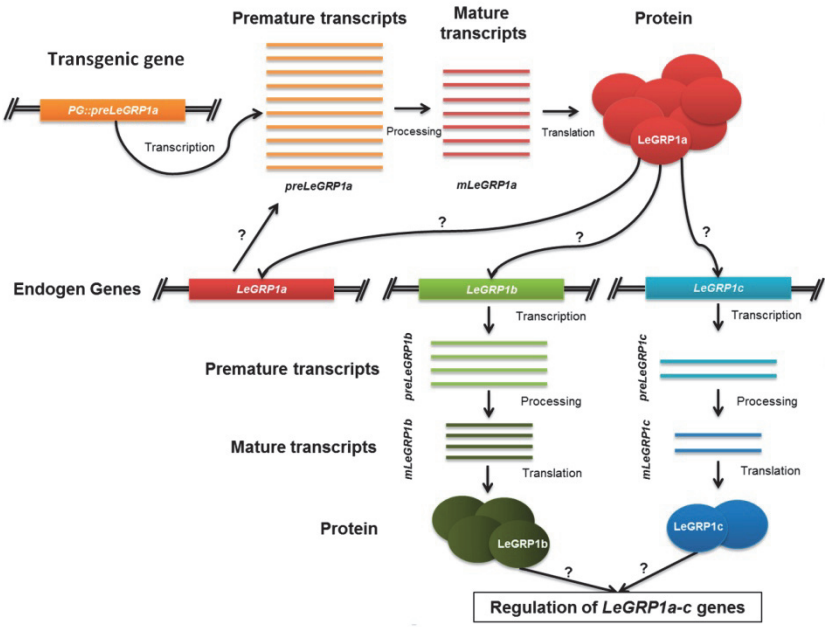


Fig. 9 Suppl. Schematic representation of proposed regulation model. The overexpression of *preLeGRP1a* under PG promoter in red ripe fruits (RR; *orange boxes*) generates the accumulation of preLeGRP1a trascript which is processed to mature form mLeGRP1a and it may conduct to an increment of LeGRP1a protein (*red ovals*). This protein would activate the expression of genes *legrp1b-c* (*green and blue boxes*, respectively) and possibly the endogen *legrp1a* gene (*red box*) through an unknown mechanism (?). Immature transcripts *preLeGRP1b* and *c* (*green* and *blue* lines) would be processed to *mLeGRP1b* and *c*, and finally transduced to protein contributing with the increment of LeGRP1 protein displayed.