

# Overexpression of glycine-rich RNA-binding protein in tomato renders fruits with higher protein content after cold storage

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## Abstract

Glycine-rich RNA-binding proteins (GR-RBPs) are involved in RNA processing and also some of them are output signals of the circadian clock. In tomato, one *GR-RBP* gene family (*LeGRP1*) is composed by three highly homologous genes (*LeGRP1a-c*); each one rendering three transcriptional products: the un-spliced pre-RNA (*preLegrp1a-c*), the mature mRNA (*mLegrp1a-c*) and the alternatively spliced mRNA (*asLegrp1a-c*). To get insight into their regulation and impact on RNA metabolism in fruits, *Solanum lycopersicum* cv. Micro-Tom was transformed with *preLeGRP1a* fused to the polygalacturonase promoter, which drives expression to fruits from the mature green stage. Our results demonstrated a complex positive regulation of *LeGRPs*, in which *LeGRP1a* overexpression led to the induction of the others *LeGRP1* members. Even though the *LeGRP1* transcription and the content of three *LeGRPs* proteins were affected, the overall *LeGRP* protein circadian rhythm profile was similar in transgenic and wild type (WT) fruits. However, when the fruits were kept at a chilling temperature after harvest, total protein content was significantly higher in transgenic than in WT fruits, and the content of some free amino acids was modified. The results obtained suggest a probable role of *LeGRP1s*: structural rearrangements and/or stabilization of mRNA to allow efficient processing of fruits under cold conditions.

*Additional key words:* amino acids, circadian rhythm, polygalacturonase promoter, RNA stabilization.

## Introduction

In order to respond and adapt to the changing environment, living organisms regulate gene expression. Transcriptional and post-transcriptional control of RNA content as well as RNA splicing, capping, polyadenylation, transport, stability, and translation have important roles in growth, development, and in the response to numerous stresses (Lorković 2009, Jung *et al.* 2013). RNA binding proteins (RBPs) are proteins that bind to RNA molecules enabling its processing and metabolism, such as splicing, polyadenylation, editing, stabilization, localization, and translation. At low temperatures, RBPs are essential, because RNA molecules adopt misfolded-stabilized structures and

RBPs allow them to acquire native conformation (Phadtare 2011, Kang *et al.* 2013).

Plants genomes encode hundreds of RBPs (Cook *et al.* 2011). Among these proteins, glycine-rich RNA-binding proteins (GR-RBPs) function as RNA chaperones during growth, development, and under stress conditions (Lorković 2009, Kim *et al.* 2010, 2012, Kang *et al.* 2013, Ambrosone *et al.* 2015). GR-RBPs contain an *N*-terminal RNA recognition motif (RRM) domain involved in RNA recognition and a glycine-rich (GR) *C*-terminal domain implicated in protein-protein interactions (Sachetto-Martins *et al.* 2000). Plant GR-RBPs were mainly studied in *Arabidopsis thaliana* and *Oryza sativa*. Over-

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*Abbreviations:* CI - chilling injury; CSD - cold shock domain; DAA - days after anthesis; GR-RBPs - glycine-rich RNA-binding proteins; IG - immature green; MG - mature green; PG - polygalacturonase; PITC - phenylisothiocyanate; RT-qPCR - reverse transcription - quantitative polymerase chain reaction; RBP - RNA binding protein; RR - red ripe; RRM - RNA recognition motif; TEA - triethylamine; WT - wild-type; Y - green yellowish.

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expression of GR-RBPs in *Arabidopsis* enhances its tolerance to salinity, cold, and oxidative stress (Kim *et al.* 2007a,b, 2008, Sahi *et al.* 2007, Ayarpadikannan *et al.* 2014, Tan *et al.* 2014). However, to our knowledge, no studies analyzing GR-RBPs overexpression in fruits were performed.

In our previous work, a GR-RBP family, which was called *LeGRP1*, was characterized in tomato fruits (Müller *et al.* 2014). Three highly homologous *LeGRP1* genes (*LeGRP1a-c*) were identified. For each gene, three transcriptional products have been found, corresponding to the un-spliced pre-RNA, the mature mRNA, and the alternatively spliced mRNA (*preLeGRP1a-c*, *mLeGRP1a-c*, and *asLeGRP1a-c*, respectively). *LeGRP1s* harbored *in vivo* RNA-melting abilities and complemented the cold-sensitive phenotype of a particular *Escherichia coli* strain. Differential circadian profiles of expression, dependent on the fruit developmental stage, have been found for each *LeGRP1* form. During ripening of fruits harvested at the mature green (MG) stage of the vine, the content of all *Legrp1a-c* forms increases considerably; however, incubation at 4 °C prevents such an increase (Müller *et al.* 2014).

Tomato is one of the most important vegetable crops.

## Materials and methods

**Plasmid construct and plant transformation:** A 4.8 kbp promoter region of the *Solanum lycopersicum* Mill. polygalacturonase gene (*PG*, Gene Bank: FJ465170) and the full-length sequence of the *preLegrp1a* cDNA (*preLegrp1a*, Gene Bank: FJ465170) were cloned between the *NotI* and *PstI* restriction sites of a modified version of the pGreen II vector (Fahnenstich *et al.* 2007) bearing the kanamycin resistance gene. Full length of *PG* promoter (Lau *et al.* 2009) was obtained through PCR using genomic DNA from leaves of tomato cv. Micro-Tom (PG1F 5'-GCGGCCGCCCTGCAGGTC AACGG-3' and PG3R 5'-GGTACCTAGTCTATT GAAAAAGATTATT-3') and the full-length sequence of the *preLegrp1a* was achieved from PCR using immature green (IG) fruit cDNA (GRP1aF 5'-GGATCCTTA GGGTTCTCTTCTGG-3' and GRP1aR 5'-CTG CAGACATGCTTTACTTGATTCC-3').

*Agrobacterium tumefaciens* (strain GV3101) containing the “helper” pSOUP plasmid was transformed with the *pGreenII::PG::preLeGRP1a* construct by the freeze thaw method (An *et al.* 1988). Thus, *S. lycopersicum* cv. Micro-Tom *PG::preLeGRP1a* transgenic lines were generated by *Agrobacterium*-mediated transformation (Fernandez *et al.* 2009). When the plantlets had a root of 2 cm length, they were transferred to soil. After several rounds of selection on plates containing 100 mg dm<sup>-3</sup> kanamycin, homozygous lines were obtained (*PG::preLeGRP1a* plants) and seeds were collected.

**Plants and storage conditions:** *S. lycopersicum* WT and

Commercial tomatoes are subjected to a postharvest handling system that chills fruit to extend shelf life (Lana *et al.* 2005). Low-temperature storage is widely used to slow ripening and reduce decay. However, the fruits are sensitive to chilling injury (CI) at temperatures below 10 °C (Jackman *et al.* 1988, López Camelo 2004, Zhang *et al.* 2016).

Considering the role of GR-RBPs in RNA metabolism during stress conditions, such as cold (Kim *et al.* 2010, Kwak *et al.* 2011, Sasaki and Imai 2012), the working hypothesis is that GR-RBP overexpression in tomato may modify fruit quality by inducing RNA structural rearrangements and/or processing during postharvest cold storage. To test this hypothesis, *Solanum lycopersicum* cv. Micro-Tom was transformed with the complete sequence of the *preLeGRP1a* fused to the polygalacturonase promoter, which drives expression in fruits from the mature green (MG) stage (Lau *et al.* 2009). The effect of *LeGRP1a* overexpression on circadian oscillation of all *LeGRPs* family members was analyzed. In addition, total protein content and content of some free amino acids was compared in fruits of transgenic and wild-type (WT) tomato after cold storage.

*PG::preLeGRP1a* transgenic lines were grown from seeds as described in Müller *et al.* (2014). Flowers were tagged after pollination and fruits were allowed to develop until different stages according to the number of days after anthesis (DAA) and harvested for analysis or used for the postharvest treatments.

Transgenic tomatoes (*PG::preLeGRP1a*) were harvested at the immature green (IG, 16 DAA) and red ripe (RR, 47 DAA) stages. For time course analysis, IG and RR fruits were harvested from the vine grown in 16-h photoperiod at 4 h intervals (zeitgeber time - zt 0, 4, 8, 12, 16, 20). In addition, *PG::preLeGRP1a* tomato plants with IG or RR fruits grown under a 16-h photoperiod were transferred to continuous irradiance for 24 h, and fruits were harvested at 4 h intervals (zeitgeber time ztcl 4, 8, 12, 16, 20, and 24; Fig. 1 Suppl.). Therefore, the expression analysis was done comparing fruits subjected to 16-h photoperiod with those exposed to continuous irradiance. The following comparisons were conducted: ztcl4 with zt20, ztcl8 with zt0, ztcl12 with zt4, ztcl16 with zt8, and ztcl24 with zt16 (Fig. 1 Suppl.). Time course analyses were performed on fruits collected from different plants and repeated at least three times.

To analyze the effect of *preLegrp1a* overexpression during storage at chilling temperatures, WT and transgenic *PG::preLeGRP1a* fruits were harvested at green yellowish stage (Y; 38 - 40 DAA, first visible carotenoid accumulation) and stored at 4 °C for 7 d (7D4, Fig. 2 Suppl.). Then, the fruits were transferred to 20 °C for several days, each day was named as +1, +2, +3, +4 in fruits 7D4 (7D4+1, +2, +3, +4; respectively; Fig. 2

Suppl.). Each treatment was performed with at least five fruits and was repeated at least five times.

At each sampling point, fruits were cut into pieces; pulp and seeds were removed and the remaining pericarp was frozen in liquid nitrogen and stored at -80 °C for extraction of chlorophyll, lycopene, protein, and RNA.

Firmness, coloration, and fresh mass were determined according to Müller *et al.* (2013). Percentage of soluble solids in tomato juice was tested using a refractometer *Atago NI* for 0 - 32 °C (USA; Borsani *et al.* 2009). Dehydration was visually evaluated using the following scale: 0 - 20 % = no dehydration, 1 = 20 - 60 % of the fruit visibly dehydrated, 2 = more than 60 % of the fruit dehydrated. Total chlorophyll and carotenoids were extracted and quantified according to Nagata and Yamashita (1992).

**Protein extraction and quantitation, SDS-PAGE and Western blot analysis:** Total soluble proteins from the different samples were extracted as previously described by Müller *et al.* (2014). Protein content was determined by the method of Bradford (1976) using the *Bio-Rad* (Hercules, CA, USA) protein assay reagent and bovine serum albumin as standard. Coomassie brilliant blue stained SDS-PAGE was conducted for protein loading control before Western blot analysis (Fig. 3 Suppl.). SDS-PAGE was carried out using 15 % (m/v) polyacrylamide gels according to Laemmli (1970). Proteins were visualized with Coomassie brilliant blue or electroblotted onto a nitrocellulose membrane for immunoblotting according to Burnette (1981). Bound antibodies were located by linking to alkaline phosphatase-conjugated goat anti-rabbit IgG according to the manufacturer's instructions (*Bio-Rad*). Purified antibodies raised against LeGRP1a protein (1:1000) were used (Müller *et al.* 2014). These antibodies detect LeGRP1a, LeGRP1b, and LeGRP1c proteins corresponding to 16 and 17 kDa immunoreactive bands (Müller *et al.* 2014). Immunoreactive 16 and 17 kDa bands were semi-quantified by densitometric analysis. For this, images were scanned and the area of the bands was integrated by use of a *BioChemi System UVP* (*BioImaging System*, Upland, CA, USA). In integrating peak areas, a rectangular bar covering ~80 % of each lane was drawn. Each densitometric analysis was determined in triplicate to minimize experimental errors.

**RNA isolation, reverse transcription (RT)-PCR, and quantitative real-time PCR:** Total RNA, RT-PCR and quantitative real-time PCR were previously described in Müller *et al.* (2014). Oligonucleotide primers are listed in Table 1 Suppl. Each pair of primers detected each isoform specifically as it was reported in Müller *et al.* (2014).

**Free amino acid analysis:** The amino acid content of tomato extracts was determined using reverse phase-HPLC with pre-column phenylisothiocyanate (PITC) derivatization (Dhar *et al.* 2013). The reverse phase C18 column (5 µm, 250 × 4.6 mm, *LUNA Phenomenex*, USA)

with a C18 guard security pre-column (4 × 3 mm) was connected to *ÄKTA* purifier equipment (*GE Healthcare*, Uppsala, Sweden). 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; 50 µM) were prepared in distilled water or 0.1 M HCl in accordance with their solubility. A working standard mixture was prepared by diluting the intermediate stock standard solution to 2 µM concentration.

Calibration curves were done in the range 0.2 - 20 nM of each amino acid and repeated two times using two different working standard amino acid mixtures. The derivatization procedure was as follows: an equal volume of coupling reagent [methanol/water/triethylamine (TEA); 2:2:1, v/v] was added to each point of the curve and the solution was mixed and dried immediately under vacuum. After this, PITC reagent (methanol/TEA/water/PITC, 7:1:1:1, v/v) was added and allowed to stand at room temperature for 20 min before drying in vacuum. PITC derivatives were dissolved in 0.5 cm<sup>3</sup> of sodium acetate buffer (mobile phase A). For mobile phase A, 19 g of sodium acetate trihydrate was dissolved in 1 dm<sup>3</sup> of HPLC grade water. To this, 0.5 cm<sup>3</sup> of TEA was added and the content was mixed properly, adjusted to pH 6.4 with glacial acetic acid, and filtered. Acetonitrile (60 cm<sup>3</sup>) was added to the filtrate (940 cm<sup>3</sup>), mixed, and filtered through a 0.22 µm *Millipore* (Darmstadt, Germany) membrane.

The injection volume of the sample and standard was 0.1 cm<sup>3</sup>. Separation of amino acids was performed on reverse phase C18 column with sodium acetate buffer, pH 6.4 (mobile phase A) and acetonitrile/H<sub>2</sub>O (6:4, mobile phase B) with gradient mode of operation (Table 2 Suppl.), column temperature of 39 °C, and 150 kPa limit of pressure. The absorbance at 254 nm was recorded and used for calculation. Chromatogram resolution of the amino acids standards and calibration curves are shown in Figs 4 and 5 Suppl.

For analysis of free amino acids in tomato fruits, pieces of fruits (approx. 0.3 g) were processed using a mortar and pestle, and 1 cm<sup>3</sup> of 0.1 M HCl. After centrifugation at 14 000 g and 4 °C for 15 min, the supernatant was precipitated with 10 % (m/v) trichloroacetic acid and maintained on ice for 30 min. After centrifugation at 14 000 g and 4 °C for 15 min, 0.05 cm<sup>3</sup> of the supernatant was used for derivatization using the procedure described above. PITC derivatives were dissolved in 0.3 cm<sup>3</sup> of sodium acetate buffer (mobile phase A). All the volumes were documented and each amino acid was quantified using the calibration curve (Table 3 Suppl.).

**Statistical analysis:** Data from the qPCR experiments were tested using one-way analysis of variance (ANOVA). Continuous quantitative variables such as mass, firmness, and soluble solids were analyzed using two-way ANOVA.

Protein content was assessed taking in account variability between harvests, testing the three harvests pairwise alone using two-way ANOVA. When error normality assumption was not verified, logarithmic transformation was applied. The absence of interaction between variables was confirmed in all cases. Minimum

significance differences were calculated by the Bonferroni, Holm-Sidak, Dunnett, and Duncan tests ( $P = 0.05$ ) using the *Sigma Stat Package*. Also Spearman rank order correlation analysis was conducted with the *Sigma Stat Package*. Dehydration grade was analyzed using Score testing.

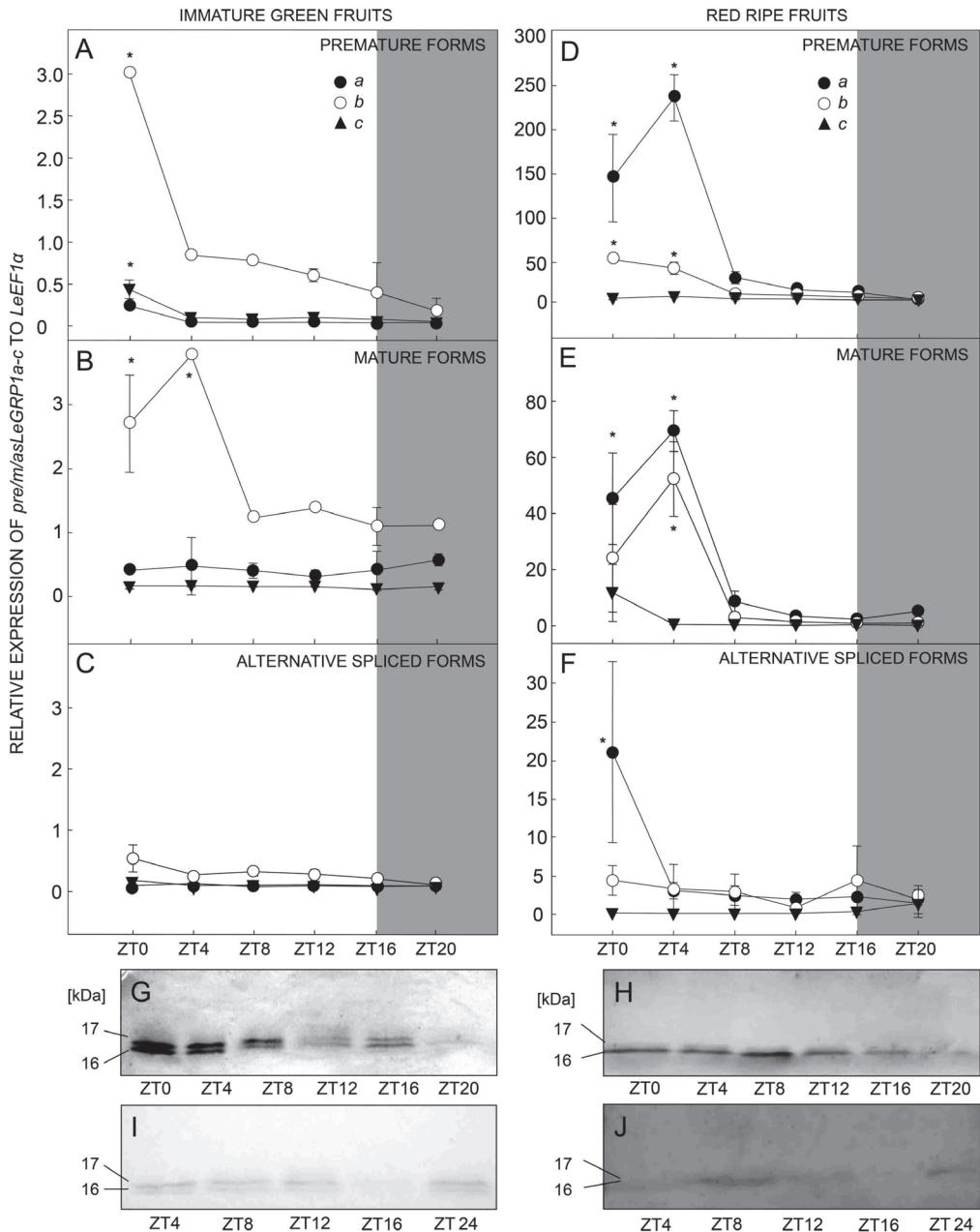


Fig. 1. *LeGRP1a-c* premature, mature, and alternative spliced mRNA (A-F) and *LeGRP1* protein content (G-J) in transgenic *PG::preLeGRP1a* fruits at the immature green (IG, *left panel*) and red ripe (RR, *right panel*) stages. Fruits of plants grown under a 16-h photoperiod were harvested at 4-h intervals. Means  $\pm$  SDs of the results obtained by real-time quantitative PCR, using two independent mRNAs as templates are shown. The y-axis refers to the fold difference in transcription relative to the *LeEF1α* level. Light and dark periods are represented by white and grey areas, respectively; and the Zeitgeber time (ZT) is indicated in the graph. For each transcript, asterisks indicate that the values are significantly different ( $P < 0.05$ ). Western blot using 25  $\mu$ g (G and I) and 10  $\mu$ g (H and J) of pericarp protein extracts were revealed with antibodies raised against *LeGRP1a*. Immunoreactive bands of 16 and 17 kDa are shown. Plants with IG (I) or RR (J) fruits were transferred to continuous irradiance for a 24 h and fruits were harvested at 4-h intervals. One representative image of three replicates is shown.

## Results

To increase the content of *LeGRP1a* protein in tomato fruits, we integrated the full-length sequence of the premature *LeGRP1a* cDNA (preLegrp1a, Solyc10g051390) under the control of tomato PG promoter (Gene Bank: FJ465170, which drives high expression in tomato fruits from the mature green stage), into the *S. lycopersicum* cv. Micro-Tom genome. Two independent *S. lycopersicum* PG::preLeGRP1a transgenic homozygous lines from the third generation (lines 1 and 2) containing the transgene were selected for further analysis.

Under normal growing conditions, no significant phenotypic changes were observed among WT and the two transgenic lines (Fig. 6 Suppl.); they were between 25 to 30 cm high, and they had similar flowering time.

Mature green (MG) and red ripe (RR) fruits were obtained at 36 - 38 and 45 - 48 DAA, respectively. The diameter of RR fruits was also similar (2 - 2.3 cm). Since the expression of *LeGRP1a* was directed to the fruits, we focused on the analysis of proteins in this organ at different developmental stages.

Time-course of all *LeGRP1a-c* transcriptional forms and LeGRP1 protein was analyzed over a 24-h period in fruits of PG::preLeGRP1a lines by real time qPCR and Western blot at two developmental stages: immature green (IG) and RR (Fig. 1).

Transgenic fruits displayed a similar pattern of time-course fluctuation of the premature forms of *LeGRP1*, *preLeGRP1a* and *c* at IG and *preLeGRP1a* and *b* at RR stage, with the greatest expression at the beginning of the

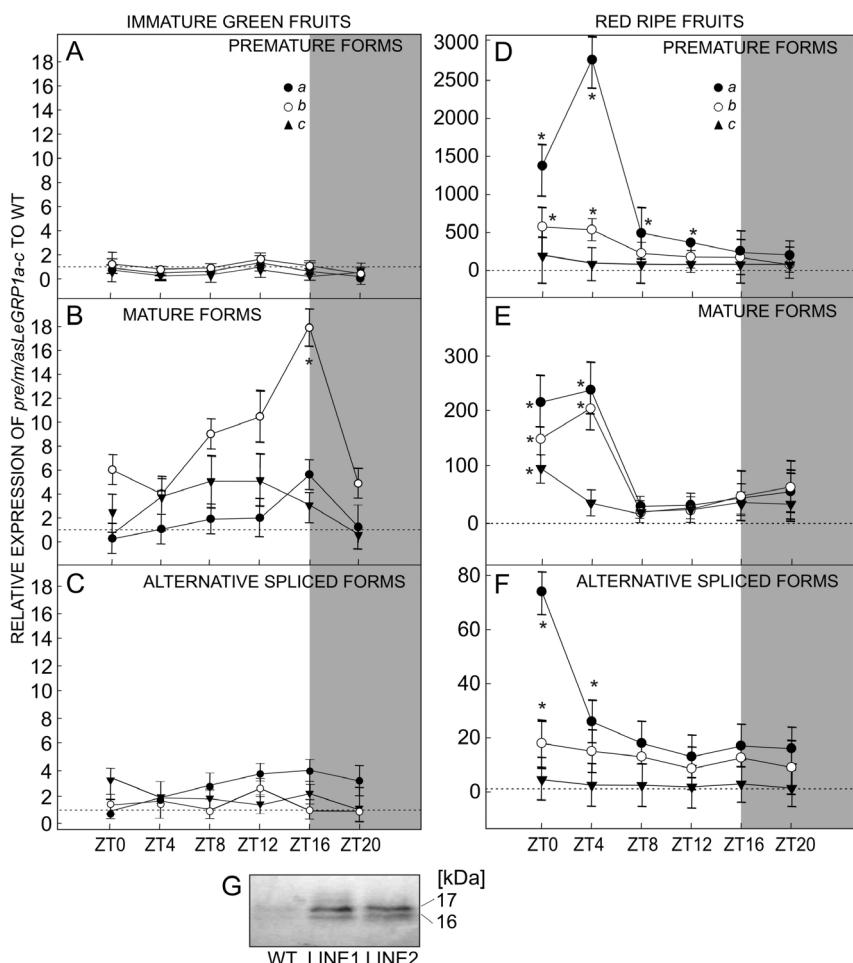


Fig. 2. *LeGRP1a-c* premature, mature, and alternative spliced mRNA content in PG::preLEGRP1a relative to WT fruits. Fruits of transgenic PG::preLEGRP1a plants were harvested at the immature green (IG, left panel) and red ripe (RR, right panel) stages from plants grown at a 16-h photoperiod at 4-h time intervals. Light and dark periods are represented by white and grey areas, respectively; the Zeitgeber time (ZT) is indicated on the x-axis. Means  $\pm$  SDs of the results obtained using two independent mRNAs as templates. The y-axis refers to the fold difference in a particular transcript level in PG::preLEGRP1a relative to its level in WT (dashed lines). For each transcript, asterisks indicate that the values are significantly different from WT ( $P < 0.05$ ). G - Western blot using 15  $\mu$ g of RR pericarp protein extracted from fruits at ZT0 was revealed with antibodies raised against LeGRP1a. Immunoreactive bands of 16 and 17 kDa are shown. One representative image of three replicates is shown.

day light (ZT0 - ZT4; Fig. 1A,D). In accordance, the mature forms, *mLeGRP1b* at IG and *mLeGRP1a* and *b* at RR stage, peaked at the first hours of irradiance (Fig. 1B,E). Regarding the alternatively spliced forms, *asLeGRP1a-c* exhibited little variation along the time at IG stage (Fig. 1C) but at the RR stage, *asLegrp1a* showed the highest content at ZT0 (Fig. 1F). The relative expression of each *LeGRP1* transcript in *PG::preLeGRP1a* lines with respect to the levels found in WT (Müller *et al.* 2014) is shown in Fig. 2. At IG stage, no significant modifications in transcription were detected in the *PG::preLeGRP1a* lines in comparison with the WT, albeit the increase of *mLeGRP1b* expression at ZT16 was found (Fig. 2). In contrast, at the RR stage drastic increases in expression were detected (Fig. 2), which agrees with the reported activity of the PG promoter. Particularly, the content of *preLeGRP1a* increased nearly 2 800 times at ZT4 in RR transgenic fruits with respect to that found in WT (Fig. 2D). In RR fruits, not only the *preLeGRP1a* content was increased, but also the content of its mature (*mLegrp1a*) and alternatively spliced (*asLeGRP1a*) forms, which increased at ZT0 nearly 200 and 80 times, respectively (Fig. 2E,F). Surprisingly, the amount of the transcriptional forms of *LeGRP1b* and *LeGRP1c* were also drastically increased in relation to WT fruits at RR: nearly 500 times for *preLeGRP1b* at ZT0 - 4, 180 times for *mLeGRP1b* at ZT4, 20 times for *asLeGRP1b* at ZT0 and 90 times for *mLeGRP1c* at ZT0 (Fig. 2E,F.). Accordingly to the content of the mature forms in transgenic RR fruits, the amount of the immunoreactive LeGRP1 bands increased with respect to WT (nearly 8 times, Fig. 2G). In transgenic *PG::preLeGRP1a*, at IG

stage the highest content of immunoreactive protein LeGRP1 occur concomitantly with the highest amount of the mature *LeGRP1b* form (Fig. 1G) and similarly to the profile found in WT fruits. In contrast, at RR, the highest content of immunoreactive LeGRP1 protein was observed at ZT8 (Fig. 1H). This result contrasts with the pattern of expression of the transcriptional mature forms, which peak earlier than ZT8 (Fig. 1E), but it agrees with the pattern detected in WT (Fig. 1H, Müller *et al.* 2014). Additionally, when transgenic plants with fruits at IG or RR stages, grown under a 16-h photoperiod, were transferred to continuous irradiance for 24 h, the patterns of accumulation of LeGRP1 protein remained practically the same when compared to fruits under a 16-h photoperiod (Fig. 1I,J).

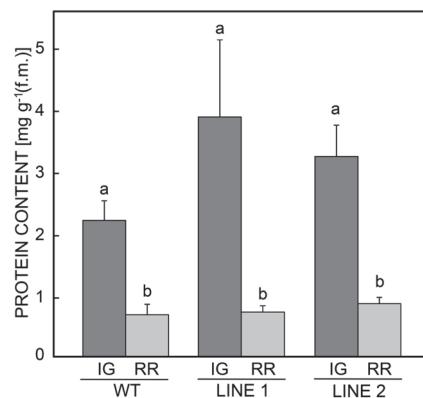


Fig. 3. Total protein content of WT and *PG::preLeGRP1a* fruits in IG and RR stages. Means  $\pm$  SDs,  $n = 30$ , bars with the same letters are not significantly different ( $P < 0.05$ ).

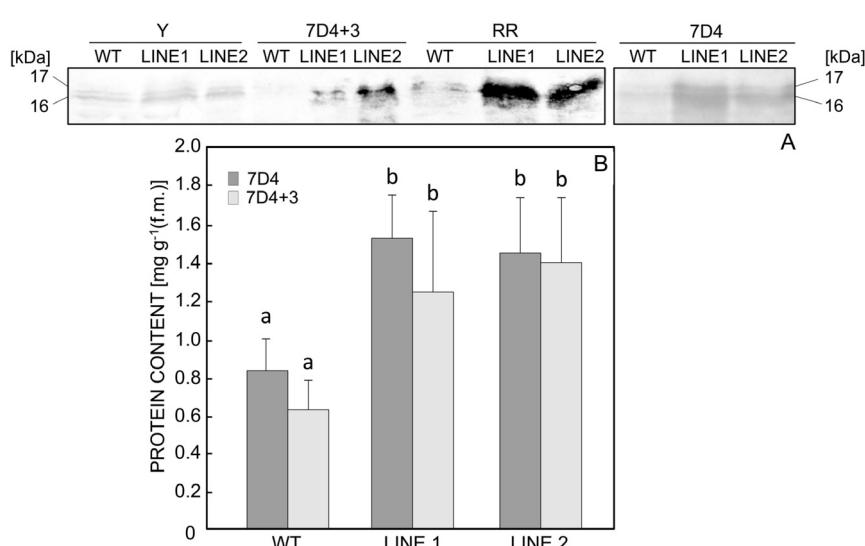


Fig. 4. Effects of cold treatments on the protein content of WT and *PG::preLeGRP1a* fruits. Fruits were harvested at green yellowish (Y) or RR stage. Y fruits were incubated at 4 °C for 7 d (7D4) and then transferred to 20 °C for another 3 d (7D4+3). A - Pericarp protein extracts (25 µg) were loaded in each lane and were revealed using antibodies against LeGRP1a. Immunoreactive bands of 16 and 17 kDa are shown. One representative image of at least three replicates is shown. B - Protein content of WT and *PG::preLeGRP1a* fruits after storage for 7 d at 4 °C (7D4) and after further ripening (3 d at 20 °C, 7D4+3). Means  $\pm$  SDs,  $n = 30$ . The experiment was repeated in three consecutive harvests. Bars with the same letters are not significantly different among the treatments ( $P < 0.05$ ).

Further, we tested whether the overexpression of *LeGRP1a* has an impact on the protein content in IG and RR fruits from transgenic lines. Independently of the genotype, the protein content was significantly higher in IG than in RR fruits (Fig. 3). However, no significant differences in total protein content were detected between fruits from WT and from transgenic lines at both IR and RR stages (Fig. 3).

In order to address the response of transgenic fruits to cold storage, fruits from *PG::preLeGRP1a* transgenic lines and WT were harvested at green yellowish (Y) stage and stored at 4 °C for 7 d (7D4) and then kept at 20 °C for 3 d to allow ripening (7D4+3, Fig. 2 Suppl.). Fruit

firmness, coloration, mass, and soluble solids of 7D4+3 WT and transgenic fruits are summarized in Table 1. No significant differences in these parameters were detected between WT and transgenic fruits. Quality parameters and visual inspection of the fruits indicate that the treatment explored in this work (7 days at 4 °C) does not affect the subsequent ripening of the fruits when transferred to 20 °C (Table 1 and Fig. 2 Suppl.). Accordingly, the content of pigments (chlorophylls and lycopenes) was similar in WT and *PG::preLeGRP1a* fruits (Fig. 7 Suppl.). In addition, no differences in visual dehydration were observed (Fig. 7 Suppl.).

Table 1. Fresh mass, firmness, total soluble solids, and coloration of WT and *PG::LeGRP1a* fruits (lines 1 and 2) after cold treatment at 4 °C for 7 d and subsequent storage at 20 °C for 3 d. Fruit colour was monitored using the CIE L\*a\*b\* (L: lightness, a: green-to-red scale, b: blue-to yellow scale). Firmness is expressed in Newton (N). Means ± SDs, n = 30. Values with an identical letter are not significantly different ( $P < 0.05$ ).

	Fresh mass [g]	Firmness [N]	Soluble solids [% of f.m.]	Colour		
				L	a*	b*
WT	1.8±0.2 <sup>a</sup>	63.4±4.0 <sup>a</sup>	5.0±0.4 <sup>a</sup>	53.9±1.5 <sup>a</sup>	27.5±2.1 <sup>a</sup>	44.1±1.9 <sup>a</sup>
Line 1	1.6±0.1 <sup>a</sup>	67.9±2.7 <sup>a</sup>	5.2±0.2 <sup>a</sup>	53.3±1.5 <sup>a</sup>	27.6±1.4 <sup>a</sup>	44.0±1.3 <sup>a</sup>
Line 2	1.7±0.1 <sup>a</sup>	69.4±2.8 <sup>a</sup>	5.2±0.2 <sup>a</sup>	55.2±1.1 <sup>a</sup>	25.4±1.4 <sup>a</sup>	46.7±1.3 <sup>a</sup>

Table 2. The content of free amino acids [ $\mu\text{mol g}^{-1}$ (f.m.)] in WT and transgenic fruits (nd - not detected). Means ± SDs, n = 6. Values with different letters are significantly different ( $P < 0.05$ ).

Amino acids	WT	Line 1	Line 2
Asp	1.90±0.30 <sup>a</sup>	0.90±0.40 <sup>a</sup>	1.31±0.30 <sup>a</sup>
Glu	0.31±0.01 <sup>a</sup>	0.27±0.08 <sup>a</sup>	0.40±0.10 <sup>a</sup>
Asn	0.40±0.20 <sup>a</sup>	0.50±0.10 <sup>a</sup>	0.33±0.07 <sup>a</sup>
Ser	0.40±0.20 <sup>a</sup>	0.15±0.10 <sup>a</sup>	0.33±0.07 <sup>a</sup>
Gln	0.60±0.20 <sup>a</sup>	0.40±0.20 <sup>a</sup>	0.50±0.10 <sup>a</sup>
Gly	nd	0.80±0.10 <sup>a</sup>	1.00±0.20 <sup>a</sup>
His	0.13±0.06 <sup>a</sup>	0.13±0.03 <sup>a</sup>	0.29±0.05 <sup>a</sup>
Citrulline	0.04±0.01 <sup>a</sup>	0.11±0.03 <sup>a</sup>	0.09±0.03 <sup>a</sup>
Arg	0.20±0.08 <sup>a</sup>	0.11±0.03 <sup>a</sup>	0.18±0.05 <sup>a</sup>
Ala	0.30±0.10 <sup>a</sup>	0.30±0.10 <sup>a</sup>	0.40±0.10 <sup>a</sup>
Pro	0.80±0.10 <sup>a</sup>	1.00±0.30 <sup>a</sup>	1.00±0.30 <sup>a</sup>
Tyr	0.01±0.05 <sup>a</sup>	0.06±0.03 <sup>a</sup>	0.10±0.30 <sup>a</sup>
Val	0.40±0.05 <sup>a</sup>	0.30±0.10 <sup>a</sup>	0.30±0.07 <sup>a</sup>
Cystine	0.16±0.02 <sup>a</sup>	0.16±0.03 <sup>a</sup>	0.19±0.03 <sup>a</sup>
Orn	0.62±0.05 <sup>a</sup>	0.36±0.05 <sup>b</sup>	0.20±0.04 <sup>b</sup>
Lys	nd	0.19±0.03 <sup>a</sup>	0.18±0.03 <sup>a</sup>

The content of LeGRP1 protein was higher in the transgenic *PG::preLeGRP1a* lines than in WT after the fruits were exposed to cold treatment and after subsequent ripening (7 times in average, Fig. 4A). However, these amounts were lower than when transgenic fruits ripened on the plant (2.7 times in average, RR fruits, Fig. 4A).

Total soluble protein content was analyzed in transgenic and WT fruits. Higher protein content in transgenic than in WT fruits (average 50 % higher) was determined after cold storage (7D4), and after subsequent ripening at 20 °C (7D4+3, Fig. 4B, Fig. 8 Suppl.). The overall pattern of protein bands, assessed by SDS-PAGE, was similar in transgenic and WT fruits (Fig. 8 Suppl.).

Considering the difference in protein content, free amino acids in fruits after cold treatment were also investigated (Table 2). The relative amounts of the majority of the amino acids (Asp, Glu, Asn, Citrulline, Val, Gln, His, Ser, Arg, and Cystine) did not change in the transgenic fruits in comparison to the WT. On the other hand, the content of Orn was higher in WT than in transgenic fruits. Notably, Lys and Gly were found in fruits from transgenic lines but not in those from WT plants (Table 2).

## Discussion

In agreement with high PG promoter activity at RR stage, fruits from *PG::preLeGRP1a* plants showed a high expression of *preLeGRP1a* and the highest one occurring

during the first hours of irradiance (Fig. 1D and Fig. 2D). In addition to the great increase in *preLeGRP1a* expression, *mLeGRP1a* expression was also higher in

transgenic than in WT plants (Fig. 2D-E), demonstrating that *preLeGRP1a* transcription was correctly processed in respective fruits. Interestingly, all transcript forms of *Legrp1b* gene were also increased in transgenic fruits with respect to WT fruits in RR stage (Fig. 2D-F). The increase in transcription occurred concomitantly with a significant increase in LeGRP1 protein content (Figs. 2 and 4). Although the increase of *Legrp1a* and *-b* expressions and LeGRP1 protein content in transgenic fruits with respect to WT was found, the circadian profile of LeGRP1 protein in fruits at RR stage was similar to that observed in WT, with maximum at ZT8 in RR (Fig. 1H; Müller *et al.* 2014). In accordance with the high expression of *mLeGRP1a-c* in transgenic *PG::preLeGRP1a* RR fruits (Figs. 1E and 2E), the content of LeGRP1 protein in RR *PG::preLeGRP1a* fruits was 8 times higher than in WT RR fruits (Fig. 2G).

Overall, the results obtained are in accord with a positive regulation of the different LeGRPs in tomato fruits (Fig. 9 Suppl.). The overexpression of *preLeGRP1a* under the control of PG promoter in RR fruits generated the accumulation of *preLeGRP1a*, which was processed

to the mature form (*mLeGRP1a*) that led to an increase in LeGRP1 protein. This protein would activate the expression of *Legrp1b-c* genes through an unknown mechanism. In turn, immature transcripts *preLeGRP1b* and *c* would be processed to their mature forms (*mLeGRP1b* and *c*, respectively) and finally, they could also be translated; contributing to the increase of LeGRP1 protein (Fig 2D-G and Fig. 4A). Moreover, these proteins could, in turn, regulate *Legrp1a-c* genes. This model, based on results obtained here, deeply differs from the one proposed for *A. thaliana* leaves, in which *AtGRP7* negatively regulates the expression of *AtGRP8* and vice versa (Schöning *et al.* 2007, 2008, Staiger *et al.* 2003). In the case of tomato fruits, the regulation would also be reciprocal, but in contrast to the *Arabidopsis* model, it would be positive since the increase of *LeGRP1a* promotes the increase of *LeGRP1b* and *c*. The model presented here is in accordance with the transcript correlation analysis proposed for tomato WT RR fruits, in which *preLeGRP1a-c* transcripts positively correlate with each other and with *mLeGRP1a* (Müller *et al.* 2014).

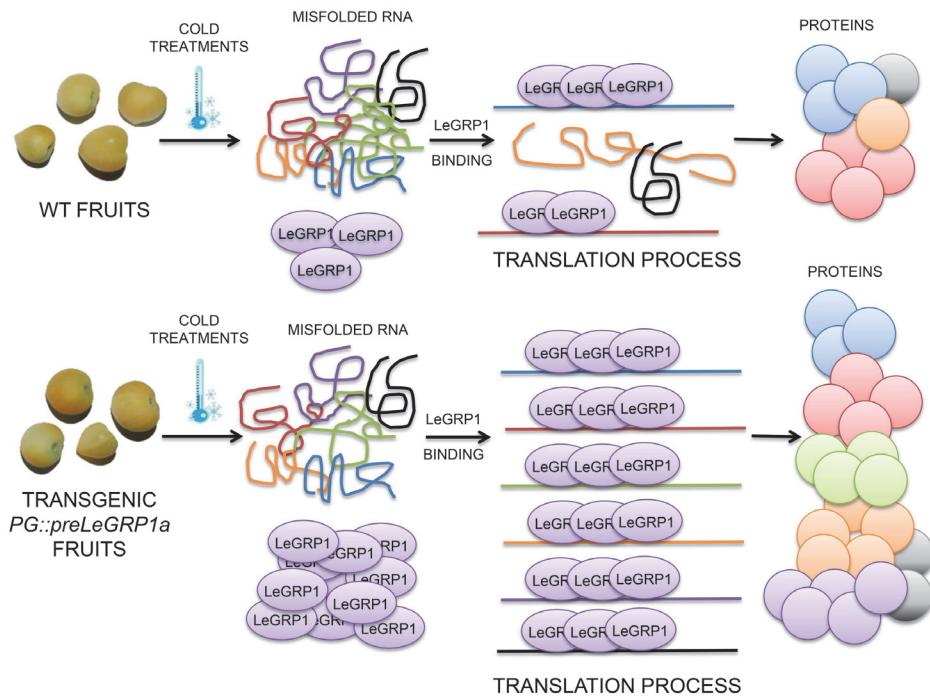


Fig. 5. A proposed model of LeGRP1-RNA complexes during cold treatments. When cold treatment is applied to fruits, processes such as protein synthesis, translation, and ripening are arrested. In this model, the increased LeGRP1 content in *PG::preLeGRP1a* fruits get importance in the structural mRNA rearrangements and/or stabilization of miss-folded RNA allowing protein translation.

In plants, cold shock domain (CSD) proteins play essential roles in freezing tolerance, and regulate embryo development, flowering time, and fruit development (Sasaki and Imai 2012). The fact that transgenic fruits had higher protein content than WT fruits after 7 d of cold treatment, but not when comparing non-treated fruits, reinforced the notion that LeGRP1 function as RNA chaperone in fruits during cold. We demonstrated in

our previous work (Müller *et al.* 2014) that LeGRP1 harbours *in vivo* RNA chaperone activity (*in vivo* transcription antitermination abilities assayed in *Escherichia coli* RL211 system) and so contributes to cold tolerance enhancement (by complementing *E. coli* BX04 mutant, which is highly sensitive to cold stress). Thus, it is likely that LeGRP1a facilitates translation by inducing structural rearrangement of mRNAs, which is

specially required for efficient translation under low temperatures. However, we cannot rule out that LeGRP1 could be stabilizing RNAs in a non-specific manner during cold, as it is demonstrated for other GR-RBPs in plants (Kim *et al.* 2008, Kwak *et al.* 2011, 2016, Khan *et al.* 2014). Overall, we postulated that, during ripening at ambient temperature, the overexpression of LeGRP1 in fruits did not lead to an increment in total protein content, since RNA is correctly folded and translation continues at normal rate (Fig. 5). However, under cold treatment, the increased LeGRP1 content in transgenic fruits induced structural rearrangements of mRNAs and/or stabilized miss-folded RNA allowing protein translation (Fig. 5). In addition, the formation of high molecular complexes of LeGRP1 with RNAs could be a plausible possibility, enabling RNA metabolism, as it was revealed for its homologue in *Nicotiana tabacum*, NtGR-RBP1, where intra-molecular interaction between the RNA-domain and the GR domain, as well as inter-molecular interaction between GR domains were demonstrated (Khan *et al.* 2014).

It is interesting to note that some amino acids like Gly and Lys were more abundant in transgenic fruits than in WT fruits after cold storage. These amino acids are precursors of polyamines, alkaloids, and compatible

solutes (Pratelli and Pilot 2014). Gly is a precursor of glycine-betaine, an osmoprotectant reported in tomato and other plants under stress conditions (Sakamoto and Murata 2002, Park *et al.* 2007). Probably, the overexpression of LeGRP1a could stabilize enzymes involved in the biosynthesis of these amino acids, whose transcripts may be particularly sensitive to cold. Future experiments are required to address these issues.

In conclusion, the data presented in this work revealed that the overexpression of *LeGRP1a* in tomato fruits led to a great induction of the other *LeGRP1* family members and so positive regulation among the *Legrp1* genes. Although *LeGRP1a* transcription and LeGRP1 protein content were increased, circadian profiles of LeGRP1 proteins were similar when comparing WT and transgenic fruits. Moreover, total protein content in chilled transgenic fruits was higher than in chilled WT fruits. Considering that *PG::preLeGRP1a* fruits do not exhibit detrimental changes in the organoleptic parameters neither under ripening at ambient conditions nor under cold storage, the overexpression of *LeGRP1a* in fruits emerges as a promising biotechnological tool to improve nutritional quality of tomatoes, by increasing total protein content and the content of precursors of some osmoprotectants.

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