

Temporal expression patterns of fruit-specific α -EXPANSINS during cell expansion in bell pepper (*Capsicum annuum* L.)

Andrés Mayorga-Gómez

University of Georgia

Savithri Nambesan (✉ sunamb@uga.edu)

University of Georgia

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Abstract

Background Expansins (EXP) facilitate non-enzymatic cell wall loosening during several phases of plant growth and development including fruit growth, internode expansion, pollen tube growth, leaf and root development, and during abiotic stress responses. In this study, the spatial and temporal expression patterns of *C. annuum* α -EXPANSINS (*CaEXPA*) genes were characterized. Additionally, fruit-specific *CaEXPA* expression was correlated with the rate of cell expansion during bell pepper fruit development.

Results Spatial expression patterns revealed that *CaEXPA13* was up-regulated in vegetative tissues and flowers, with the most abundant expression in mature leaves. Expression of *CaEXPA4* was associated with stems and roots. *CaEXPA3* was expressed abundantly in flower at anthesis suggesting a role for *CaEXPA3* in flower development. Temporal expression analysis revealed that 9 out of the 21 genes were highly expressed during fruit development. Of these, expression of six genes, *CaEXPA5*, *CaEXPA7*, *CaEXPA12*, *CaEXPA14*, *CaEXPA17* and *CaEXPA19* were abundant 7 to 21 days after anthesis (DAA), whereas *CaEXP6* was strongly expressed between 14 and 28 DAA. Further, this study revealed that fruit growth and cell expansion occur throughout bell pepper development until ripening, with highest rates of fruit growth and cell expansion occurring between 7 and 14 DAA. The expression of *CaEXPA14* and *CaEXPA19* positively correlated with the rate of cell expansion, suggesting their role in post-mitotic cell expansion-mediated growth of the bell pepper fruit. In this study, a ripening specific EXP transcript, *CaEXPA9* was identified, suggesting its role in cell wall disassembly during ripening.

Conclusion This is the first genome-wide study of *CaEXPA* expression during fruit growth and development. Identification of a fruit-specific EXPAs suggest their importance in facilitating cell expansion during growth and cell wall loosening during ripening in bell pepper. These *EXPA* genes could be important targets for future manipulation of fruit size and ripening characteristics.

Background

Expansins are proteins that mediate cell wall loosening during cell enlargement mediated growth in plants [1, 2]. Additionally they are involved in cell wall modification during fruit softening, root growth, pollen tube growth and in abiotic stress responses [2–7]. Expansins belong to a large superfamily of genes which are mainly divided into four subfamilies based on sequence analysis; α -EXPANSINS (*EXPA*), β -EXPANSINS (*EXPB*), EXPANSIN A-like (*EXPLA*) and EXPANSIN B-like (*EXPLB*) [8, 9]. Of these, *EXPA* constitutes the largest subfamily with well-documented roles in cell wall expansion [10] (Table 1). The *EXPB* subfamily members also demonstrate cell wall loosening activity and this subfamily includes group 1 grass pollen allergens which facilitate pollen tube invasion [9, 11, 12]. *EXLA* and *EXLB* proteins belong to smaller subfamilies and their biological function is not clearly understood [9].

EXPA have been indicated to play a role in hypocotyl extension in cucumber [13, 14] and leaf initiation in tomato [15]. Expression of both *EXPA* and *EXPB* has shown to be associated with internode elongation in deep-water rice [11, 16, 17]. Certain members of the *EXPA* subfamily regulate the initiation and elongation

of root hairs in Arabidopsis, rice and soybean [5, 18, 19]. The expression of *EXPA* genes during fruit development suggests a role in fruit expansion and ripening in several fruit crops such as tomato, pear and peach [3, 4, 20–23].

EXPA typically consists of 250-275 amino acids and mainly contains three domains: an N-terminal 20-30 amino acid signal peptide; Domain 1, made of the double-psi beta-barrel (DPBB) domain which is structurally similar to the glycosyl hydrolase family 45 (GH45); and Domain 2, which has a β -sandwich fold and is categorized as the carbohydrate binding module family 63 (CBM63) [9, 12]. In spite of the similarity to GH45 enzymes, EXPs do not exhibit hydrolytic activity. In fact, EXPA mediates non-enzymatic cell wall loosening in a pH dependent manner to enable cell expansion [10, 24]. Although the precise mechanism of action is not fully elucidated, EXPs are involved in disrupting noncovalent bonds between cellulose microfibrils and xyloglucan [9, 10].

Fruit development, in many species including pepper (*C. annuum*), can be mainly divided into four phases: fruit set, cell division, cell expansion and ripening [25]. Among these, fruit growth primarily occurs during the cell division and cell expansion phases, with the vast majority of growth occurring during the latter phase. In tomato, post-mitotic cell expansion results in an overall increase in cell volume by over 30,000 fold [26]. In pepper, however, nearly all cell division occurs pre-anthesis and only post-mitotic cell expansion is noted post-anthesis [27, 28]. The potential roles of specific EXPs in regulating post-mitotic cell expansion and fruit growth in bell pepper have not been evaluated.

In this study, EXPs were identified from bell pepper and spatial expression patterns of *CaEXP* transcripts in seedlings, root, stem, leaves and fruit were determined. In addition, temporal expression patterns of *CaEXP* transcripts were determined during fruit growth and development. Finally, patterns of *CaEXP* transcript abundance were associated with changes in the relative rate of cell expansion during fruit growth and development. This is the first genome-wide identification of *EXP* genes during fruit expansion and ripening in bell pepper.

Materials And Methods

Plant material

Capsicum annuum cv. Aristotle, a sweet type pepper (Seminis, St. Louis, MO, USA) was grown in the greenhouse from Dec 2017-May 2018 in Athens, GA. Initially, seeds were germinated in plug nursery trays in a low temperature incubator (Model 2015; VWR International, Randor, PA, USA) at 25 °C with 12 h of light and dark. Subsequently the seedlings were transplanted in Fafard 3B Mix Metro-Mix 830 (Sun Gro Horticulture, Agawam, MA, USA) in a 11 L plastic nursery container. During the experiment, the minimum and maximum temperature in the greenhouse was set at 15 °C and 26 °C respectively, with relative humidity at 66%.

Experimental design and tissue collection

A completely randomized design was used and plant tissue samples were harvested in four replicates. Tissues were harvested from seedlings, roots, stems, leaves, flowers, and fruit from five developmental stages. Seedlings (above ground tissue) were harvested 15 days after germination when approximately 4 true leaves were present. Roots, stems, and young and mature leaves were harvested separately from the same plant before flowering. Young leaves were defined as apical and expanding whereas mature leaves were basal and fully expanded. Stem tissue was harvested from the apical region by collecting approximately 3 internodes. Fully open flowers were harvested at anthesis. At anthesis, individual flowers were tagged, manually pollinated and fruit samples were collected at 7 days after anthesis (DAA), 14 DAA, 21 DAA, 28 DAA and at the ripe stage. Fruit was considered ripe when the fruit changed from green to completely red.

Identification and nomenclature of the *CaEXP* gene families

All *CaEXPA* sequences were obtained from National Center for Biotechnology Information (NCBI) and SolGenomics databases. All sequences were compared between the two databases and within each database to eliminate identical sequences. The sequences of *CaEXPB*, *CaEXPLA* and *CaEXPLB* were obtained from NCBI database and were compared using Clustal X (<http://www.clustal.org/>) to determine unique sequences within each gene family. In case of three *CaEXP* genes, *CaEXPA21*, *CaEXPB6*, and *CaEXLB6*, two transcripts variants were detected in NCBI (Table 2); the longer transcript variant X1 was used for all the subsequent analysis. Nomenclature for all the *CaEXP* gene sequences within a gene family were in the order of the most recent publication date followed by the chromosomal location information from NCBI. Since all the *EXP* sequences were from *C. annuum* cv. Zunla-1 [29], genes were ordered based on their respective chromosomal position (Table 2).

Phylogenetic analysis, protein domain identification and gene structure prediction.

The *CaEXP* sequences were aligned using Clustal X (<http://www.clustal.org/>). The alignment was verified using the Muscle option on MEGA 7 [30]. The phylogenetic tree was generated using the neighbor joining method on MEGA 7 using p-distance model, partial deletion for missing data treatment and 1000 bootstrap replicates. To identify protein domains, the location of signal peptide, double psi beta-barrel DPBB_1, and Pollen allergen regions in protein sequences were obtained from the software SMART (<http://smart.embl-heidelberg.de/>) along with PFAM (<https://pfam.xfam.org/>). For gene structure predictions, the positions of exons, introns, 5' UTR and 3' UTR for *CaEXPA* were obtained from the NCBI database. Subsequently, visualization of gene and protein structure was performed using GSDS 2.0 (<http://gsds.cbi.pku.edu.cn/>).

Primer design

Primers for *CaEXPA* and reference genes were designed using ApE- A Plasmid Editor (<http://jorgensen.biology.utah.edu/wayned/appe/>) software (Additional table 1). Three reference genes, *UBIQUITIN-CONJUGATING ENZYME (UBE2)*, NCBI accession: DQ924970), *GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (GAPDH)*, NCBI accession: XM_016722738.1), *18S RIBOSOMAL RNA (18S*

rRNA, NCBI accession: EF564281.1) were developed to normalize the expression of *CaEXPA* [31]. Of these, two reference genes *UBE2* and *GAPDH* were used for seedling, leaf, flower, and fruit tissues, and *GAPDH* and *18S rRNA* for root and stem tissues. *18S rRNA* was used since expression of *UBE2* was not detectable in root and stem tissues. All primer pairs were checked for their specificity using NCBI primer-blast (<https://www.ncbi.nlm.nih.gov/tools/primer-blast/>).

RNA extraction, cDNA synthesis, qRT-PCR and generation of heatmap.

For gene expression analyses, a total of four replicates were used for all tissues. For each replicate, to ensure sufficient material for RNA extraction, variable numbers of organs were collected. One replicate consisted of four seedlings, 10 flowers, 10 fruit from 7 DAA, and four fruit for 14 DAA, 21 DAA, 28 DAA and ripe stages. For a single replicate, four young and mature leaves, entire roots, and stem section containing approximately 3 internodes were harvested from a single plant as mentioned previously. All tissue samples were immediately frozen in liquid N₂ and stored at -80 °C until further analysis. RNA from root, stem and fruit tissues was extracted using the protocol described in [32]. However, this protocol did not yield RNA for seedling, leaf and flower and therefore RNA from these tissues was isolated using the E.Z.N.A. Total RNA Kit I (Omega Bio Tek, Norcross, GA) following the “difficult samples protocol” outlined in the manufacturer’s instructions. In the final step, RNA was resuspended in 30-40 µl of diethyl pyrocarbonate (DEPC) - treated water. RNA quality was evaluated using Nanodrop (Thermo Scientific Nanodrop 8000 Spectrophotometer, Waltham, MA) and the 260/280 absorbance was between 2.0 to 2.1 for all samples. The integrity of RNA was visualized on a 1.2% agarose gel with 0.5X Tris-Borate-EDTA (EMD Chemicals Inc., Gibbstown, NJ, USA) buffer. cDNA was prepared from 1 µg of RNA following the manufacturers protocol (Promega, Madison, WI, USA) and diluted to 100 µl [32].

Forward and reverse primers (0.2 mM) and cDNA (1 µl) were combined with PowerUP SYBR Green PCR Master Mix (Applied Biosystems, Foster City, CA, USA) for qRT-PCR reactions using Stratagene MX 3005P qRT-PCR System (Agilent Technologies, CA) following: 50 °C for 2 min, 95 °C for 5 min, followed by 95 °C for 15 sec, and 60 °C for 1 min repeated for 40 cycles. This was followed by a melting curve analysis, 95 °C for 1 min, 55 °C for 30 sec, 95 °C for 30 sec. LinRegPCR (v. 11.0) was used to determine PCR reaction efficiency. Relative gene expression was determined following efficiency correction according to [32]. To generate the heatmap, data were transformed using: $\text{Log}_2(X+0.001)$ where “X” was the fold-change value and 0.001 in the equation accounted for the genes that showed no expression in certain tissues or developmental time-points. Finally heatmap was created in R-3.5.3 using pheatmap-package v.1.0.12 [33]

Fruit growth measurements

Measurements were taken from fruit harvested for gene expression and microscopy analysis (see below). Samples were collected in four replicates, every replicate consisted of multiple fruit: 14 from 7 DAA, 8 from 14-28 DAA, and three from ripe fruit. Fruit diameter, height and weight were measured using digital micrometers and scale, respectively. Relative fruit growth was calculated using the formula: (see Formula

1 in the Supplemental Files) where w_2 =final fruit weight, w_1 =initial fruit weight, t_2 = final time in days and t_1 = initial time in days.

Microscopy analyses

For microscopy analyses, for each replicate, two flowers and two fruit from each of the developmental stages described above (7-28 DAA) and ripe fruit were used. A total of four replicates were used for each stage of sample collected. Flower and fruit tissue at various developmental stages were harvested into a fixative solution consisting of chromic acid (0.3%), acetic acid (2%) and formaldehyde (10%) (CRAF III) for subsequent microscope analysis. For flower and fruit at 7 DAA, fixed tissues were embedded in the optimum cutting temperature (OCT) compound and sections around 20-30 μm of thickness were prepared using a cryostat microtome (Leica Jung Frigocut 2800N). Fruit at 14 DAA, 21 DAA and 28 DAA were first cut into $\sim 0.5 \text{ cm}^2$ sections. Subsequently, sections of around 60 to 120 μm thickness were obtained using a Vibratome 3000 Plus Sectioning System (TED PELLA, INC, Redding, CA, USA). All the sections were stained with 0.1% toluidine blue and images were captured with a BX51 microscope (Olympus, Shinjuku, Tokyo, Japan). The images were analyzed using ImageJ software to measure average cell area from 30 cells per section. Relative cell expansion rate was calculated with the formula: where a_2 =final cell area, a_1 =initial cell area, t_2 =final time in days and t_1 =initial time in days.

Statistical and Correlation analysis

Statistical analysis (one-way analysis of variance for a completely randomized design) was performed using JMP Pro 14 (SAS Institute, Cary, NC, USA). Means were separated using Tukey's honestly significant difference (HSD) test ($\alpha = 0.05$). Correlations between cell expansion rate and *EXP* gene transcript abundance in fruit were determined using pairwise correlations using JMP Pro 14 (SAS Institute, Cary, NC, USA).

Results

Characterization of *CaEXP* gene family

A total of 40 *CaEXP* genes were identified from the *C. annuum* cv. Zunla-1 genome and sequences were retrieved from NCBI database [29] (Table 2). The length of the predicted protein sequences ranged from 239 to 298 amino acids (Table 2). Each EXP family has a characteristic sequence of conserved cysteine and tryptophan residues, and EXPA and EXPB also contain the conserved HFD motif [12]. Based on the conserved amino acids characteristic of a particular EXP family, 21 *CaEXPA*, 7 *CaEXPB*, 1 *CaEXLA* and 9 *CaEXLB* genes were identified (Table 2; Additional Fig. 1). All the conserved amino acids previously identified and described were present in CaEXPs with a few exceptions [12]. The characteristic HFD motif in EXPA and EXPB families was HFV in case of CaEXPA5 and CaEXPA10 and HLV in case of CaEXPB3 (Additional Fig. 1). While majority of the tryptophan residues were conserved in EXPA, they were not completely conserved in EXPB (Additional Fig. 1). Next, phylogenetic analysis was performed, which indicated that members were more closely related within subfamilies than between subfamilies (Fig. 1A).

All the three domains, an N-terminal signal peptide domain, the double-psi beta-barrel (DPBB) domain and the CBM63 domain (homologous to group-2 pollen allergens in grass) were present in all the CaEXPs with the exception that the signal peptide was absent in CaEXPA4, CaEXPA9, CaEXPB5 and CaEXLB3 (Fig. 1B). Gene structure analysis indicated that *CaEXPs* had 1-5 introns (Fig. 1C). Most of the *CaEXPA* family members contained 1-2 introns with a few exceptions; *CaEXPA15* and *CaEXPA5* had 3 introns and *CaEXPA14* had 4 introns (Fig. 1C). All *CaEXPB* contained 3 introns except *CaEXPB2* and *CaEXPB7* which had 2 introns each. *CaEXLA1* had 4 introns and *CaEXLB* introns were variable ranging from 2 to 5 (Fig. 1C).

Spatial and temporal transcript abundance patterns of *CaEXPA* genes

The transcript abundance patterns of 21 *CaEXPA* genes was determined in seedlings, young and mature leaves, flowers at anthesis, and fruits at 7, 14, 21, 28 DAA and ripe stage (Fig. 2A). Of the 21 *CaEXPA* genes, 19 displayed expression in the tissues analyzed. The transcripts of *CaEXPA1* and *CaEXP11* were not detectable. Among the 19 detectable transcripts, *CaEXPA13* showed highest expression in mature leaves and was generally higher in vegetative tissues and flowers in comparison to the fruit (Fig. 2A). *CaEXPA3*, *CaEXP13*, *CaEXPA18* and *CaEXPA21* displayed highest transcript abundance in the flowers when compared to other tissues (Fig. 2A). In the case of fruit tissues for example, *CaEXPA17*, *CaEXPA19*, *CaEXPA12*, *CaEXPA7*, and *CaEXPA10* showed higher transcript abundance from 7 to 28 DAA and reduced abundance in ripe fruit (Fig. 2A). On the other hand, *CaEXPA9* and *CaEXP4* transcript abundance was highest at the ripe fruit stage (Fig. 2A). Only 4 of the 21 *CaEXPA* genes, *CaEXPA3*, *CaEXPA4*, *CaEXPA10* and *CaEXPA17* were expressed in root and stem tissues (Fig. 2B). Of these, *CaEXPA4* showed a substantially higher expression compared to the other genes (Fig. 2B).

Temporal transcript abundance patterns of *CaEXPA* during fruit growth and development

To identify the abundantly expressed *CaEXPA* transcripts within the fruit samples, transcript abundance levels of all *CaEXPA* in flower and fruit tissues was normalized to that of *CaEXPA21* at 7 DAA (Fig. 3). Initially, clustering of the transcript abundance data separated *CaEXPA* genes into 2 groups, one set with nine genes showing higher expression compared to the other set, with 10 genes displaying lower expression during fruit development (Fig. 3). Of the latter 10 genes, *CaEXPA3* was highly expressed at anthesis (Fig. 3; Additional Fig. 2). Of the remaining nine highly abundant transcripts, several patterns of *EXP* expression were evident during fruit development. The expression of *CaEXPA5*, *CaEXPA7*, *CaEXPA12*, *CaEXPA14* and *CaEXPA17* increased significantly from anthesis to 7 DAA and remained high until 21 DAA after which it gradually decreased; the expression of these five genes were positively correlated to each other (Figs. 3 and 4; Table 3). The expression of *CaEXPA19* similarly increased significantly from anthesis to 7 DAA, however the peak expression was at 14 DAA after which it gradually decreased and positively correlated with *CaEXP12*, *CaEXP14* and *CaEXP17*. *CaEXPA6* expression was high from 14-28 DAA (Figs. 3 and 4; Table 3). *CaEXPA9* transcript abundance was only high in ripe fruit and increased by 13.2-fold in ripe fruit as compared with previous stages (anthesis until 28 DAA; Fig. 4). *CaEXPA4* as such was not substantially altered during early fruit development, however, its transcript abundance increased

by 3.8-fold from 28 DAA until ripening and was negatively correlated with that of *CaEXP5*, *CaEXP12*, *CaEXP14* and *CaEXP17* (Fig. 4; Table 3).

Fruit growth patterns in bell pepper

Fruit height increased by 3.3-fold between 7 and 14 DAA. It subsequently increased by 1.4-, 1.2- and 1.2-fold between 14-21 DAA, 21-28 DAA and 28 DAA-ripe, respectively (Fig. 5A). Increase in fruit diameter was 2.4-fold between 7-14 DAA and fold-changes across other developmental time-points were similar to that in fruit height (Fig. 5B). Fruit weight increased by 14.7-fold between 7-14 DAA. Subsequently, it increased by 2.7-, 2- and 2.1-fold between 14-21 DAA, 21-28 DAA and 28 DAA-ripe, respectively (Fig. 5C). Relative fruit growth was the highest between 7-14 DAA; it was almost 1.5-fold higher in comparison to that between 21-28 DAA and 4.8-fold higher than that compared to 28 DAA and the ripe stage (Fig. 5D).

Cell expansion rate during fruit development and correlation with *CaEXP* transcript abundance

Cell area increased gradually during fruit development, particularly between 7 and 28 DAA. Over the course of development, fruit pericarp cell area increased by around 60-fold (Fig. 6A). The relative cell expansion rate was highest between 7-14 DAA and subsequently declined over the rest of fruit development (Fig. 6B).

Correlations between the transcript abundance and the relative cell expansion rate during fruit growth were performed. Among the highly expressed *EXPA* genes in the fruit, only the transcript abundance of *CaEXPA14* and *CaEXPA19* significantly correlated with the relative cell expansion rate (Table 4).

Discussion

The *CaEXPA* sub-family was the most abundant among the *EXPs* in bell pepper, similar to that observed in other *Solanaceae* crops such as tobacco (36 *EXPA*s) [34], tomato (25 *EXPA*s; Additional fig. 3) [23], and potato (24 *EXPA*s) [35]. This is also true for other species including Arabidopsis, grape, apple, soybean, poplar and rice in which the largest number of *EXP* genes belong to the *EXPA* family (Table 1) [36–41]. *CaEXPs* contained 239 to 298 amino acid residues, similar to what was observed in tobacco and tomato [23, 34]. Classification of the *CaEXP* family was based on identification of conserved amino acids and characteristic domains within each family [12]. Further, the grouping of *CaEXP* families was confirmed in the phylogenetic analysis. The inconsistencies in the occurrence of the conserved tryptophan residues in *CaEXPB* and lack of conservation of the HDF motif in *CaEXPA* in bell pepper were also noted in *EXP* gene families from tomato, potato and grape [23, 37, 42]. The differences in conserved amino acid residues may suggest differences in substrate specificity and cell wall loosening activity [23]. The protein domains and exon-intron structure of *CaEXP* family were similar to other species such as sugarcane [43] and tobacco [34].

The spatial transcript abundance patterns revealed that *CaEXPA13* is the most highly expressed *EXPA* in vegetative tissues such as seedlings, young and mature leaves compared with fruit, suggesting a role in

leaf development. Indeed, a transgenic approach has shown that certain EXPA genes play a role during leaf initiation and development in *Arabidopsis* [44] and tobacco [45]. In this study, in comparison with *CaEXPA13*, *CaEXPA18* and *CaEXPA21*, the transcript abundance of *CaEXPA3* was greater in flowers compared to the other tissues and therefore *CaEXPA3* may play a role in flower development. In several other studies, expression of *EXP* has been associated with pollen, stigma, and ovary where it may facilitate pollen tube growth by loosening of stigma cell walls [2, 46, 47]. Further *EXPs* have also been shown to regulate petal development in petunia and rose [48, 49]. However, since the entire flower tissue was pooled together in this study, floral organ-specific expression patterns of *CaEXPA3* could not be determined. In this study, only 4 out of 21 *EXPA* genes were expressed in the stem and root tissues, among which *CaEXPA4* showed significantly higher expression. Hence it is likely that *CaEXPA4* is associated with stem elongation and root growth. The role of certain members of *EXP* in stem elongation has been well established in rice [11] and root development in *Arabidopsis* [5].

Fruit growth is one of the longest phases of development. In tomato, although fruit growth does not increase significantly after the mature green stage of development, cell expansion within the pericarp tissue may continue until ripening [50, 51]. The highest rate in cell expansion occurred at 4 DAA in tomato [50]. Our results indicated that in bell pepper, fruit growth and cell expansion occur throughout fruit development until ripening. More frequent sampling during later stages of fruit development is necessary to confirm if these processes continue during ripening. The highest rates of fruit growth and cell expansion occurred during early fruit growth, particularly between 7 and 14 DAA, as clearly evident from the analysis of relative rates of fruit growth and cell expansion. These data suggest that increase in fruit growth during this period is largely facilitated by cell expansion.

Post-mitotic cell expansion-mediated growth is largely driven by the cell turgor pressure, associated with water-uptake, often into the cell vacuoles. During turgor-mediated growth, cell wall stress relaxation occurs which results in cell wall loosening [52]. Expansins have been shown to induce cell wall loosening to promote cell wall enlargement by disrupting noncovalent bonds between cellulose microfibrils and xyloglucan [9, 10]. In this study, analysis of temporal transcript abundance patterns revealed higher expression of nine *CaEXPA* genes in the fruit. These genes displayed varying patterns associated with distinct fruit developmental stages. Although the expression of six genes, *CaEXPA5*, *CaEXPA7*, *CaEXPA12*, *CaEXPA14*, *CaEXPA17* and *CaEXPA19* increased during early stages of fruit growth, only the transcript abundance of *CaEXPA14* and *CaEXPA19* were significantly and positively correlated with the relative rate of cell expansion. These data indicate that at least *CaEXPA14* and *CaEXPA19* are associated with post-mitotic cell expansion-mediated growth of the bell pepper fruit. In addition, the transcript abundance patterns of *CaEXPA14* and *CaEXPA19* were strongly and significantly correlated with *CaEXPA5*, *CaEXPA7*, *CaEXPA12* and *CaEXPA17*, all of which are upregulated during early stages of fruit growth suggesting they may as well be associated with cell expansion during fruit growth. The transcript abundance of *CaEXP6* was highest between 14 and 28 DAA and therefore *CaEXP6* may facilitate cell expansion during later stages of fruit development. These data indicate that several *EXPA*s may be important in mediating cell expansion during bell pepper fruit growth. Similarly, the expression of several *EXP* genes were associated with the expansion of immature fruit in tomato and tubers in potato [20, 23, 35, 42].

Ripening is the final stage of fruit development where multiple textural changes and fruit softening occur, mediated in part by EXPs [20, 25]. Ripening-specific *EXPs* have been identified in several fruits such as tomato, banana, pear and strawberry [3, 22, 53, 54]. Among the *EXPA*s analyzed in this study, *CaEXPA4* and *CaEXPA9* displayed high transcript abundance during late stages of fruit development in bell pepper. These genes did not appear to have substantial changes in transcript abundance during early fruit development; *CaEXPA4* increased by 3.8-fold and *CaEXPA9* displayed a dramatic rise by over 12-fold from 21 DAA until ripening. Thus it is likely that *CaEXPA9* plays a predominant role in fruit softening during ripening in bell pepper.

Conclusions

This study presents the first genome-wide report of the spatio-temporal expression patterns of *EXPA* genes in bell pepper. Expression of seven *CaEXP* genes, *CaEXPA5*, *CaEXPA6*, *CaEXPA7*, *CaEXPA12*, *CaEXPA14*, *CaEXPA17* and *CaEXPA19* was associated with cell expansion and fruit growth. These results suggest the role of specific *CaEXP* genes in facilitating cell expansion during fruit growth. The phase of cell expansion during fruit development is important in contributing to final fruit size in bell pepper. Further, physiological disorders such as blossom-end rot, are initiated during the period of cell expansion, with higher cell expansion rates resulting in potentially greater susceptibility. Functional characterization of these *CaEXP* genes may help evaluate their direct roles in regulation of fruit growth and blossom-end rot incidence. This study also revealed *CaEXPA9* to be a fruit ripening specific gene which may play a role in ripening associated fruit softening in bell pepper. Thus, *CaEXA9* could be a potential target for slowing down cell wall disassembly during ripening and postharvest storage.

List Of Abbreviations

18S Rrna: 18S RIBOSOMAL RNA

C. annuum: *Capsicum annuum*

CBM63: carbohydrate binding module family 63

CRAF III: chromic acid (0.3%), acetic acid (2%) and formaldehyde (10%)

DAA: days after anthesis

DEPC: diethyl pyrocarbonate

DPBB: double-psi beta-barrel

EXP: Expansins

EXPLA: *EXPANSIN A-like*

EXPLB: EXPANSIN B-like

GAPDH: GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE

GH45: glycosyl hydrolase family 45

NCBI: National Center for Biotechnology Information

OCT: optimum cutting temperature

UBE2: UBIQUITIN-CONJUGATING ENZYME

EXPA: α - EXPANSINS

EXPB: β - EXPANSINS

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and materials

Datasets used in the current study are available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests.

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Author contribution

AM-G and SUN conceived the study and designed the experiments. AM-G was involved in data collection and processing of samples for microscopy and gene expression. AM-G and SUN were involved in data analysis, preparation of figures and preparation of the manuscript.

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Footnotes

Not applicable

References

1. Cosgrove DJ, Li LC, Cho HT, Hoffmann-Benning S, Moore RC, Blecker D. The growing world of expansins. *Plant Cell Physiol.* 2002;43:1436–44.
2. Marowa P, Ding A, Kong Y. Expansins: roles in plant growth and potential applications in crop improvement. *Plant Cell Rep.* 2016;35:949–65.
3. Rose JKC, Lee HH, Bennett AB. Expression of a divergent expansin gene is fruit-specific and ripening-regulated. *Proc Natl Acad Sci U S A.* 1997;94:5955–60.
4. Brummell DA, Harpster MH, Civello PM, Palys JM, Bennett AB, Dunsmuir P. Modification of expansin protein abundance in tomato fruit alters softening and cell wall polymer metabolism during ripening. *Plant Cell.* 1999;11:2203–16.
5. Cho HT, Cosgrove DJ. Regulation of root hair initiation and expansin gene expression in *Arabidopsis*. *Plant Cell.* 2002;14:3237–53.
6. Li F, Xing S, Guo Q, Zhao M, Zhang J, Gao Q, et al. Drought tolerance through over-expression of the expansin gene *TaEXPB23* in transgenic tobacco. *J Plant Physiol.* 2011;168:960–6.
7. Valdivia ER, Stephenson AG, Durachko DM, Cosgrove D. Class B β -expansins are needed for pollen separation and stigma penetration. *Sex Plant Reprod.* 2009;22:141–52.
8. Kende H, Bradford KJ, Brummell DA, Cho HT, Cosgrove DJ, Fleming AJ, et al. Nomenclature for members of the expansin superfamily of genes and proteins. *Plant Mol Biol.* 2004;55:311–4.
9. Cosgrove DJ. Plant expansins: Diversity and interactions with plant cell walls. *Curr Opin Plant Biol.* 2015;25:162–72.
10. Sampedro J, Cosgrove DJ. The expansin superfamily. *Genome Biol.* 2005;6:1–11.
11. Lee Y, Kende H. Expression of β -Expansins is correlated with internodal elongation in deepwater rice. *Plant Physiol.* 2001;127:645–54.
12. Choi D, Kim JH, Lee Y. Expansins in plant development. *Adv Bot Res.* 2008;47:47–97.
13. McQueen-Mason S, Durachko DM, Cosgrove DJ. Two endogenous proteins that induce cell wall extension in plants. *Plant Cell.* 1992;4:1425–33.
14. Cosgrove DJ, Durachko DM. Autolysis and extension of isolated walls from growing cucumber hypocotyls. *J Exp Bot.* 1994;45:1711–9.
15. Fleming AJ, McQueen-Mason S, Mandel T, Kuhlemeier C. Induction of leaf primordia by the cell wall protein Expansin. *Science* 1997;276:1415–8.

16. Cho HT, Kende H. Expression of expansin genes is correlated with growth in deepwater rice. *Plant Cell*. 1997;9:1661–71.
17. Lee Y, Kende H. Expression of α -Expansin and Expansin-Like genes in deepwater rice. *Plant Physiol*. 2002;130:1396–405.
18. Lee DK, Ahn JH, Song SK, Choi Y Do, Lee JS. Expression of an expansin gene is correlated with root elongation in soybean. *Plant Physiol*. 2003;131:985–97.
19. Yu Z, Kang B, He X, Lv S, Bai Y, Ding W, et al. Root hair-specific expansins modulate root hair elongation in rice. *Plant J*. 2011;66:725–34.
20. Brummell DA, Harpster MH, Dunsmuir P. Differential expression of expansin gene family members during growth and ripening of tomato fruit. *Plant Mol Biol*. 1999;39:161–9.
21. Hayama H, Shimada T, Haji T, Ito A, Kashimura Y, Yoshioka H. Molecular cloning of a ripening-related expansin cDNA in peach: Evidence for no relationship between expansin accumulation and change in fruit firmness during storage. *J Plant Physiol*. 2000;157:567–73.
22. Hiwasa K, Rose JKC, Nakano R, Inaba A, Kubo Y. Differential expression of seven α -expansin genes during growth and ripening of pear fruit. *Physiol Plant*. 2003;117:564–72.
23. Lu Y, Liu L, Wang X, Han Z, Ouyang B, Zhang J, et al. Genome-wide identification and expression analysis of the expansin gene family in tomato. *Mol Genet Genomics*. 2016;291:597–608.
24. Cosgrove DJ. Cell wall loosening by Expansins. *Plant Physiol*. 1998;333–9.
25. Gillaspay G, Ben-David H, Gruissem W. Fruits: A Developmental Perspective. *Plant Cell*. 1993;5:1439.
26. Chevalier C, Bourdon M, Pirrello J, Cheniclet C, Gévaudant F, Frangne N. Endoreduplication and fruit growth in tomato: Evidence in favour of the karyoplasmic ratio theory. *J Exp Bot*. 2014;65:2731–46.
27. Munting AJ. Development of flower and fruit of *Capsicum annuum* L. *Acta Bot Neerl*. 1974;23:415–32.
28. Bosland P, Votava E. Peppers: Vegetable and Spice Capsicums. 2nd edition. CAB International, Oxfordshire, U.K; 2012.
29. Qin C, Yu C, Shen Y, Fang X, Chen L, Min J, et al. Whole-genome sequencing of cultivated and wild peppers provides insights into *Capsicum* domestication and specialization. *Proc Natl Acad Sci U S A*. 2014;111:5135–40.
30. Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. *Mol Biol Evol*. 2016;33:1870–4.
31. Cheng Y, Pang X, Wan H, Ahammed GJ, Yu J, Yao Z, et al. Identification of optimal reference genes for normalization of qPCR analysis during pepper fruit development. *Front Plant Sci*. 2017;8:1–14.
32. Vashisth T, Johnson LK, Malladi A. An efficient RNA isolation procedure and identification of reference genes for normalization of gene expression in blueberry. *Plant Cell Rep*. 2011;30:2167–76.
33. Kolde R. Package ‘pheatmap.’ 2019;1–8.
34. Ding A, Marowa P, Kong Y. Genome-wide identification of the expansin gene family in tobacco (*Nicotiana tabacum*). *Mol Genet Genomics*. 2016;291:1891–907.

35. Chen Y, Zhang B, Li C, Lei C, Kong C, Yang Y, et al. A comprehensive expression analysis of the expansin gene family in potato (*Solanum tuberosum*) discloses stress-responsive expansin-like B genes for drought and heat tolerances. *PLoS One*. 2019;14:1–21.
36. Lee Y, Choi D, Kende H. Expansins: ever-expanding numbers and functions. *Curr Opin Plant Biol*. 2001;4:527–32.
37. Dal Santo S, Vannozzi A, Tornielli GB, Fasoli M, Venturini L, Pezzotti M, et al. Genome-wide analysis of the Expansin gene superfamily reveals grapevine-specific structural and functional characteristics. *PLoS One*. 2013;8.
38. Zhang S, Xu R, Gao Z, Chen C, Jiang Z, Shu H. A genome-wide analysis of the expansin genes in *Malus × Domestica*. *Mol Genet Genomics*. 2014;289:225–36.
39. Zhu Y, Wu N, Song W, Yin G, Qin Y, Yan Y, et al. Soybean (*Glycine max*) expansin gene superfamily origins: Segmental and tandem duplication events followed by divergent selection among subfamilies. *BMC Plant Biol*. 2014;14:1–19.
40. Sampedro J, Carey RE, Cosgrove DJ. Genome histories clarify evolution of the expansin superfamily: New insights from the poplar genome and pine ESTs. *J Plant Res*. 2006;119:11–21.
41. Sampedro J, Lee Y, Carey RE, DePamphilis C, Cosgrove DJ. Use of genomic history to improve phylogeny and understanding of births and deaths in a gene family. *Plant J*. 2005;44:409–19.
42. Jung J, O'Donoghue EM, Dijkwel PP, Brummell DA. Expression of multiple expansin genes is associated with cell expansion in potato organs. *Plant Sci*. 2010;179:77–85.
43. Santiago TR, Pereira VM, de Souza WR, Steindorff AS, Cunha BADB, Gaspar M, et al. Genome-wide identification, characterization and expression profile analysis of expansins gene family in sugarcane (*Saccharum spp.*). *PLoS One*. 2018;13:1–18.
44. Cho HT, Cosgrove DJ. Altered expression of expansin modulates leaf growth and pedicel abscission in *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A*. 2000;97:9783–8.
45. Kuluev BR, Safiullina MG, Knyazev A V., Chemeris A V. Effect of ectopic expression of *NtEXPA5* gene on cell size and growth of organs of transgenic tobacco plants. *Russ J Dev Biol*. 2013;44:28–34.
46. Mollet JC, Leroux C, Dardelle F, Lehner A. Cell wall composition, biosynthesis and remodeling during pollen tube growth. *Plants*. 2013;2:107–47.
47. Cosgrove DJ, Bedinger P, Durachko DM. Group I allergens of grass pollen as cell wall-loosening agents. *Proc Natl Acad Sci U S A*. 1997;94:6559–64.
48. Zenoni S, Reale L, Tornielli GB, Lanfaloni L, Porceddu A, Ferrarini A, et al. Downregulation of the *Petunia hybrida* α -Expansin gene *PhEXP1* reduces the amount of crystalline cellulose in cell walls and leads to phenotypic changes in petal limbs. *Plant Cell*. 2004;16:295–308.
49. Dai F, Zhang C, Jiang X, Kang M, Yin X, Lü P, et al. *RhNAC2* and *RhEXPA4* are involved in the regulation of dehydration tolerance during the expansion of rose petals. *Plant Physiol*. 2012;160:2064–82.

50. Renaudin JP, Deluche C, Cheniclet C, Chevalier C, Frangne N. Cell layer-specific patterns of cell division and cell expansion during fruit set and fruit growth in tomato pericarp. *J Exp Bot.* 2017;68:1613–23.
51. Cheniclet C, Rong WY, Causse M, Frangne N, Bolling L, Carde JP, et al. Cell expansion and endoreduplication show a large genetic variability in pericarp and contribute strongly to tomato fruit growth. *Plant Physiol.* 2005;139:1984–94.
52. Cosgrove DJ. Diffuse growth of plant cell walls. *Plant Physiol.* 2018;176:16–27.
53. Civello PM, Powell ALT, Sabehat A, Bennett AB. An expansin gene expressed in ripening strawberry fruit. *Plant Physiol.* 1999;121:1273–9.
54. Trivedi PK, Nath P. MaExp1, an ethylene-induced expansin from ripening banana fruit. *Plant Sci.* 2004;167:1351–8.

Tables

Table 1: Classification and number of EXPANSINS in various species

Species	EXPA	EXPB	EXPLA	EXPLB	Total	Reference
<i>Capsicum annuum</i>	21	7	1	9	38	
<i>Nicotiana tabacum</i>	36	6	3	7	52	[34]
<i>Solanum lycopersicum</i>	25	8	1	4	38	[23]
<i>Solanum tuberosum</i>	24	5	1	6	36	[35]
<i>Arabidopsis thaliana</i>	26	6	3	1	36	[36]; TAIR
<i>Vitis vinifera</i>	20	4	1	4	29	[37]
<i>Malus × domestica</i>	34	1	2	4	41	[38]
<i>Glycine max</i>	49	9	2	15	75	[39]
<i>Populus trichocarpa</i>	27	3	2	4	36	[40]
<i>Oryza sativa</i>	33	18	4	1	56	[41]

Table 2. Nomenclature of *CaEXP* with chromosomal position and amino acid length

NCBI Reference	Start position	End position	Length of aa	Chromosome	Gene Name
XM_016697484.1	6719269	6721107	265	1	CaEXPA1
XM_016698864.1	34381193	34384169	259	1	CaEXPA2
XM_016725129.1	128210443	128229587	241	1	CaEXPA3
XM_016704650.1	141996220	141999652	298	2	CaEXPA4
XM_016704699.1	142745201	142754239	266	2	CaEXPA5
NM_001324793.1	159594986	159597115	239	2	CaEXPA6
XM_016707763.1	12037829	12040394	249	3	CaEXPA7
XM_016707805.1	12599557	12601253	254	3	CaEXPA8
NM_001324929.1	1850043	1853156	256	4	CaEXPA9
XM_016714938.1	205362103	205365240	256	4	CaEXPA10
XM_016719265.1	198682908	198687183	258	5	CaEXPA11
XM_016722288.1	6039531	6042076	259	6	CaEXPA12
XM_016721684.1	138349371	138352444	258	6	CaEXPA13
XM_016720362.1	194769127	194772961	257	6	CaEXPA14
XM_016724770.1	105746513	105750286	258	7	CaEXPA15
XM_016724051.1	216012510	216015368	257	7	CaEXPA16
XM_016686945.1	210752505	210757330	259	9	CaEXPA17
XM_016687787.1	173800676	173802860	258	10	CaEXPA18
XM_016692780.1	197808765	197811908	249	11	CaEXPA19
XM_016694169.1	14028294	14030798	257	12	CaEXPA20
XM_016697490.1/ XM_016697491.1	3209	7051	266	Unplaced	CaEXPA21
XM_016702157.1	229210413	229212116	275	1	CaEXPB1
XM_016702797.1	128353249	128354680	262	2	CaEXPB2
XM_016702801.1	128491704	128498302	269	2	CaEXPB3
XM_016719262.1	197346396	197348955	264	5	CaEXPB4
XM_016725274.1	196431721	196438912	269	7	CaEXPB5
XM_016689117.1 / XR_001666564.1	10571649	10577821	259	10	CaEXPB6
XM_016689293.1	172669446	172671192	257	10	CaEXPB7
XM_016684533.1	152306708	152308564	261	8	CaEXLA1
XM_016715121.1	14318386	14321060	255	1	CaEXLB1
XM_016698173.1	14323996	14327102	250	1	CaEXLB2
XM_016715143.1	14381013	14383514	251	1	CaEXLB3
XM_016698182.1	14393234	14395650	250	1	CaEXLB4
XM_016715155.1	14401512	14404354	252	1	CaEXLB5
XM_016698223.1 / XM_016698230.1	15548055	15549963	255	1	CaEXLB6
XM_016695791.1	298511555	298516534	252	1	CaEXLB7
XM_016721597.1	40422100	40426589	250	4	CaEXLB8
XM_016719579.1	40488989	40494318	249	4	CaEXLB9

Table 3. Correlation among abundantly expressed fruit *CaEXPA* genes. Shown above the diagonal are correlations, significant positive correlation (blue) and significant negative correlation (yellow). Shown below the diagonal are *P* values, ns denotes not significant.

	CaEXPA4	CaEXPA5	CaEXPA6	CaEXPA7	CaEXPA9	CaEXPA12	CaEXPA14	CaEXPA17	CaEXPA19
CaEXPA4		0.037	ns	ns	ns	0.007	0.032	0.035	ns
CaEXPA5	-0.90		ns	0.002	ns	0.017	0.028	0.007	ns
CaEXPA6	-0.55	0.20		ns	ns	ns	ns	ns	ns
CaEXPA7	-0.83	0.99	0.09		ns	0.035	0.035	0.010	ns
CaEXPA9	0.86	-0.74	-0.70	-0.64		ns	ns	ns	ns
CaEXPA12	-0.97	0.94	0.44	0.90	-0.76		0.004	0.007	0.017
CaEXPA14	-0.91	0.92	0.44	0.90	-0.72	0.98		0.002	0.009
CaEXPA17	-0.91	0.97	0.35	0.96	-0.75	0.97	0.98		0.038
CaEXPA19	-0.88	0.79	0.55	0.77	-0.64	0.94	0.96	0.90	

Table 4. Correlation among abundantly expressed fruit *CaEXPA* genes and cell expansion rate. Significant positive correlations are in bold and ns denotes not significant.

<i>CaEXP</i>	Correlation to cell expansion rate	<i>P</i> value
CaEXPA4	-0.74	ns
CaEXPA5	0.72	ns
CaEXPA6	0.44	ns
CaEXPA7	0.74	ns
CaEXPA9	-0.49	ns
CaEXPA12	0.86	ns
CaEXPA14	0.93	0.023
CaEXPA17	0.86	ns
CaEXPA19	0.97	0.008

Additional Table

Additional Table 1. Primers for *CaEXPA* and reference genes

Gene	Primers	Amplicon (bp)
<i>CaEXPA1</i>	F 5' CCAAGCATTTCGCAACTCTTTCAGGCC 3' R 5' GACCCGACTAATCCGCTTTAGCCTATG 3'	192
<i>CaEXPA2</i>	F 5' GGTGCAATCCAGGCCAAGTCATAAC 3' R 5' CAACTCCGGCTTTGTACTTGGCAATC 3'	156
<i>CaEXPA3</i>	F 5' GC AATGCAGTGGTGGACTCTTT CAC 3' R 5' CCACATGTCCGTTGCTCATTACTGC 3'	171
<i>CaEXPA4</i>	F 5' GATCACAAATGTGGCCGGTGCAG 3' R 5' GAAGTAGAAGTGCGATGGTCACTGCC 3'	174
<i>CaEXPA5</i>	F 5' GGCCAAACCTTTGAAGGC AAGCAG 3' R 5' CAACACAATCGCAGAGCTTTGCTCAG 3'	184
<i>CaEXPA6</i>	F 5' CAAGGGTTCAAGAAGTCAAGTGGCAAC 3' R 5' GGCCAAAGGACCAAGAAGTGGAGC 3'	164
<i>CaEXPA7</i>	F 5' GTGGGAGGTT CAGGAGATGTC AATGC 3' R 5' GTGCGGCCATCACCTGTAGTAACC 3'	155
<i>CaEXPA8</i>	F 5' CTCTTCATGGTTACCCATGCAGCG 3' R 5' GACCAACTTGCCAGTTAGCAGGAAC 3'	152
<i>CaEXPA9</i>	F 5' GGTGGCATTGTACCTGTCCTCTACC 3' R 5' GACGCGCATTGGATTGCCAATTGG 3'	214
<i>CaEXPA10</i>	F 5' CGCGATCGAGTAGTGAAGCTTGAAGC 3' R 5' GTCAGCAACACTGGTCTATGTGCAAC 3'	174
<i>CaEXPA11</i>	F 5' GGT AATAATGGAGGGTGGCAAAGTGC 3' R 5' GAGCTGGTAACAAGCACCATGTC 3'	183
<i>CaEXPA12</i>	F 5' GCCTCAAAGGTTCAAAGACTGGTTGG 3' R 5' CCAAGTGTGCAGGTGCAATATTCCATG 3'	158
<i>CaEXPA13</i>	F 5' CACCAGCTAACTGGCGATTTGGAC 3' R 5' CACAAACTGACAGGTGAAAGCCTCTC 3'	137
<i>CaEXPA14</i>	F 5' CCATCCCACTGGCAATTTGGTCAGAC 3' R 5' GCCGCTTCAGCTCATATACGTACACC 3'	186
<i>CaEXPA15</i>	F 5' GCTGTGGCGCTTGTTCGAGATT AAG 3' R 5' GAGGAACATAGGCATGGCAAGGTC 3'	182
<i>CaEXPA16</i>	F 5' GGACAAGCATGTGGTGTCTTGCTACAG 3' R 5' GCGAAGGAAAAGCAGGCATGGACATG 3'	180
<i>CaEXPA17</i>	F 5' CATACCATTACCACTGACCAGAGGC 3' R 5' CCGGTAACCCATAACTTTCGTCCGG 3'	183
<i>CaEXPA18</i>	F 5' GCTGGCATCGTCCCTGTTACCTATC 3' R 5' CAGCACCTGCCACGTTGGTAACTATG 3'	121
<i>CaEXPA19</i>	F 5' GATCGAGAAGTGGTTGGCAACC AATG 3' R 5' CCAAATGACC AATGAGCAGGAGCAAC 3'	156
<i>CaEXPA20</i>	F 5' CAGCAGATTCTGGATGGACAAGTGC 3' R 5' GCATTGGCCACATGATCCTCCATC 3'	173
<i>CaEXPA21</i>	F 5' GTTCCTGTTTCGTATCGCAGGGTACC 3' R 5' GCTTGGCCACTTAGTGTTGCAAATGC 3'	218
<i>Ubiquitin-conjugating enzyme</i>	F 5' CACGACGCAGCTGCTGTATTGAGAG 3' R 5' CCGAATGCGTAGCAGAAAGACCACTG 3'	223
<i>Glyceraldehyde-3-phosphate</i>	F 5' CAGTTCCGAGCACGATGTGTCCTTAG 3' R 5' CCAACAGTAAACAGACGGCCACTC 3'	132
<i>18S ribosomal RNA</i>	F 5' CGGGTGACGGAGAATTAGGGTTCG 3' R 5' CCAATTACCAGACTCATTGAGCCCG 3'	156

Figures

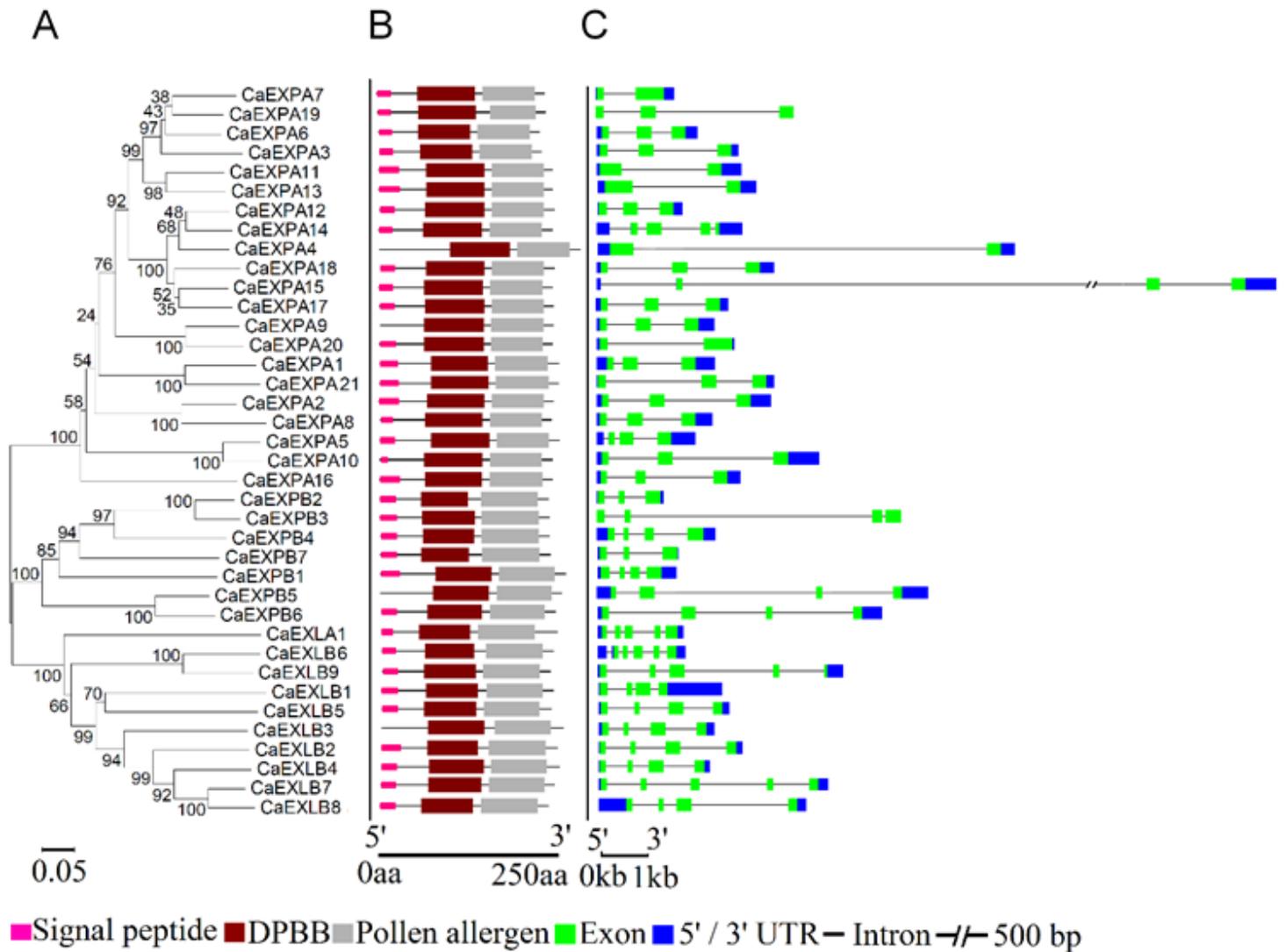


Figure 1

Phylogenetic analysis (A), schematic visualization of protein (B), and gene structure (C) of EXPANSINS in *C. annuum*. A. Phylogenetic tree performed using the neighbor joining method in MEGA 7.0 with 1000 bootstraps with p-distance model. B. Protein structure showing the signal peptide (pink), double-psi beta-barrel (DPBB; burgundy) and pollen allergen (grey) domains. Scale, 250 amino acids. C. Gene structure with exons in green, introns as a solid line and 5' and 3' UTR in blue. Break in second intron of CaEXPA15 is 500 bp.

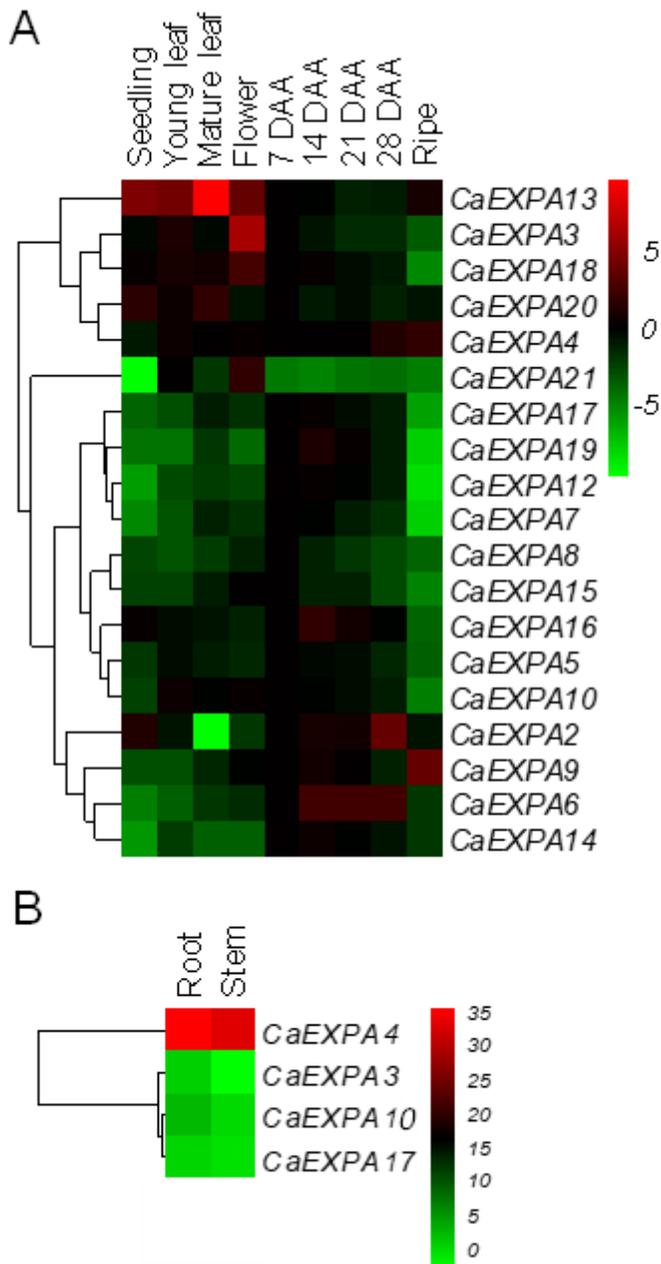


Figure 2

Spatio-temporal expression patterns of CaEXPA. A. Expression patterns of 19 of the 21 CaEXPA genes. Transcript abundance of each CaEXPA gene in every tissue and fruit developmental time-point was normalized to its expression at 7 DAA, except CaEXPA21, which was normalized to its expression in young leaf. Transcripts of CaEXPA1 and CaEXP11 were not detectable by qRT-PCR. B. Expression patterns of CaEXPA in root and stem. Only four out of the 21 CaEXPA genes were expressed in root and stem tissue. Transcript abundance of all 4 genes were normalized to that of CaEXPA10 in root. Tissues are displayed vertically and CaEXP genes horizontally. Color scale from green to red indicates lower and higher transcript abundance, respectively. Expression is presented in a Log₂ scale.

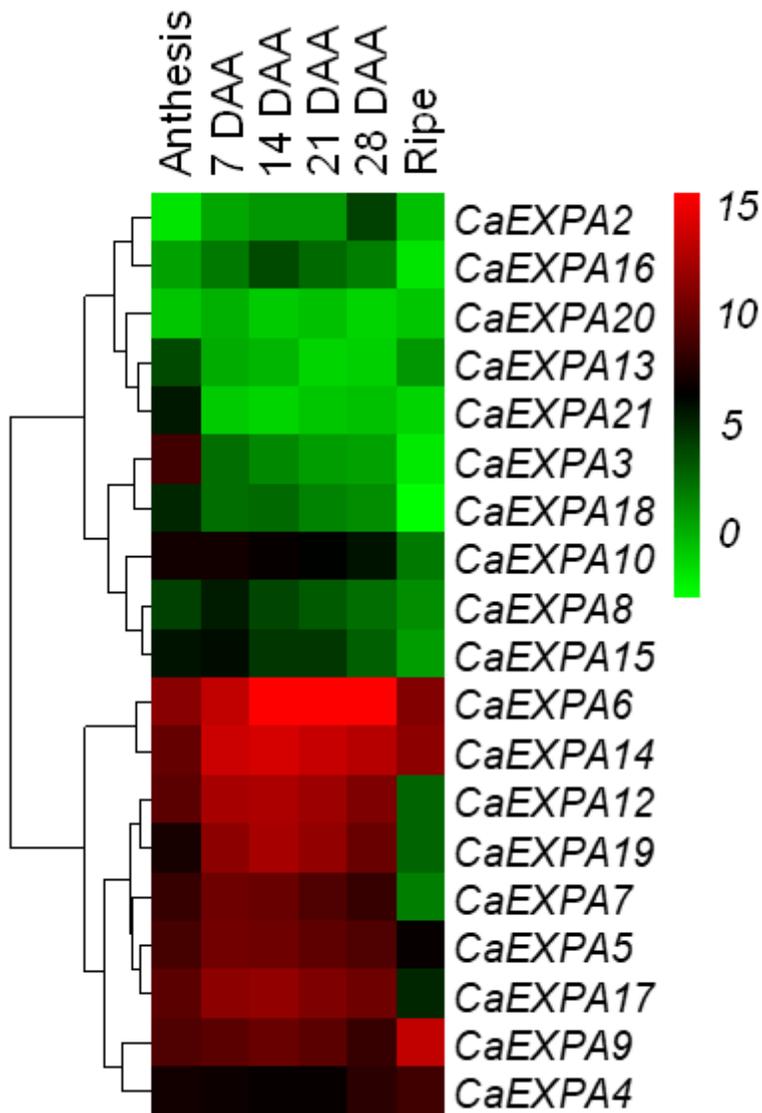


Figure 3

Temporal expression patterns of CaEXPA during flower and fruit development. Transcript abundance of all CaEXPA genes was normalized to that of CaEXP21 at 7 DAA. Tissues are displayed vertically and CaEXPA genes horizontally. Color scale from green to red indicates lower and higher transcript abundance, respectively. Expression is presented in a Log₂ scale.

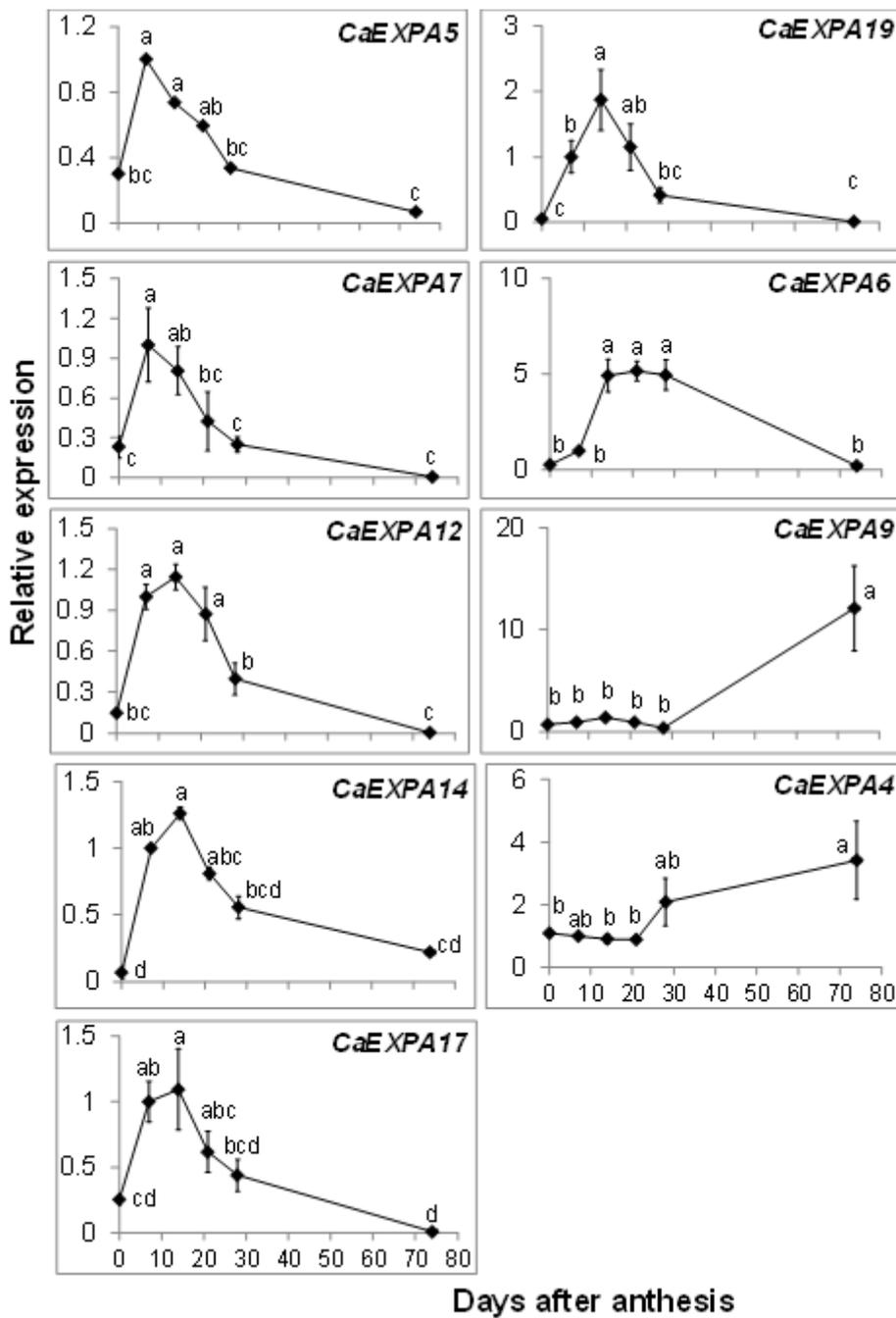


Figure 4

Relative transcript abundance of nine CaEXP genes in flower and fruit development. These nine CaEXP genes displayed relatively higher transcript abundance in Fig. 3. Values are means and standard errors of at least three replicates. Means separation was performed using Tukey's HSD following test of significance using ANOVA ($\alpha = 0.05$). Means followed by a different letter are significantly different.

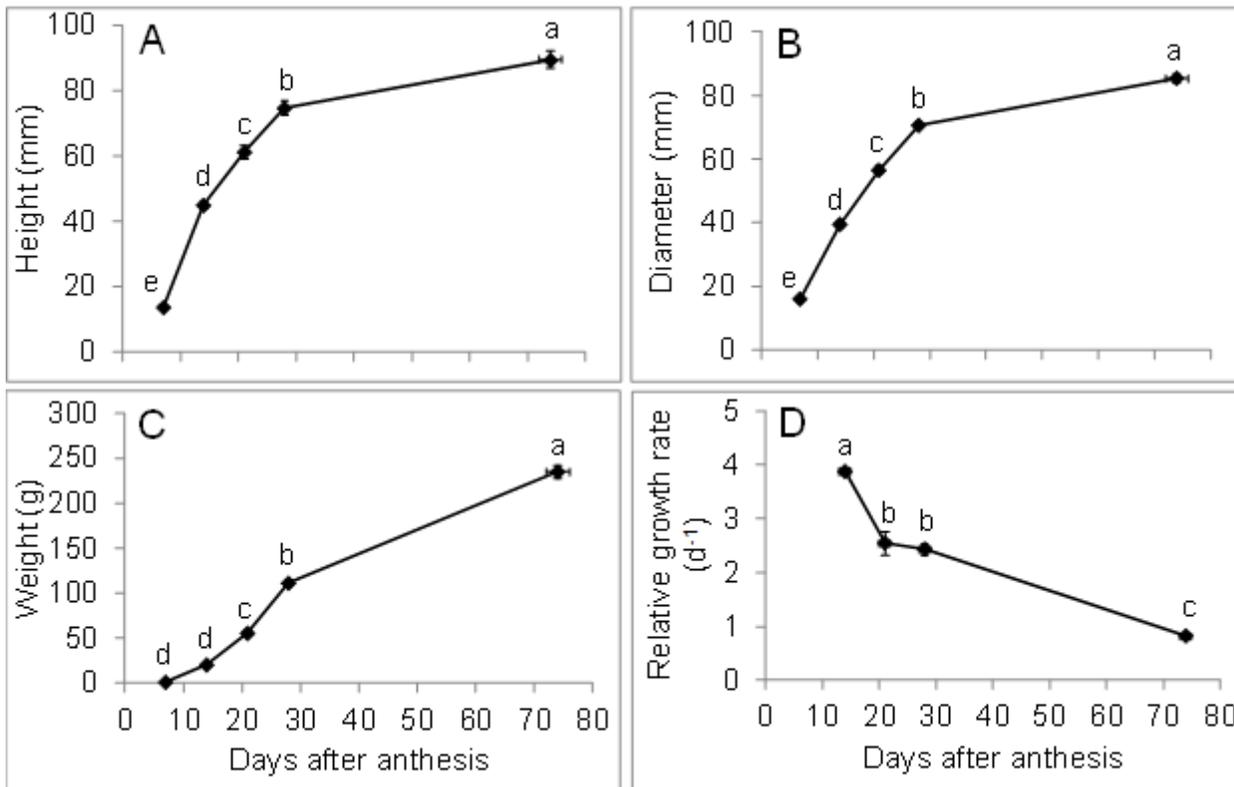


Figure 5

A. Fruit height, B. Fruit diameter, C. Fruit weight at five time-points during fruit development at various days after anthesis (DAA): 7, 14, 21, 28 DAA and ripening. D. Relative growth rate calculated using fruit weight (d^{-1}) at four different intervals during fruit growth and development; from 7–14 DAA, 14–21 DAA, 21–28 DAA and 28 DAA to the ripe stage. Means separation was performed using Tukey's HSD following test of significance using ANOVA ($\alpha = 0.05$). Means followed by a different letter are significantly different.

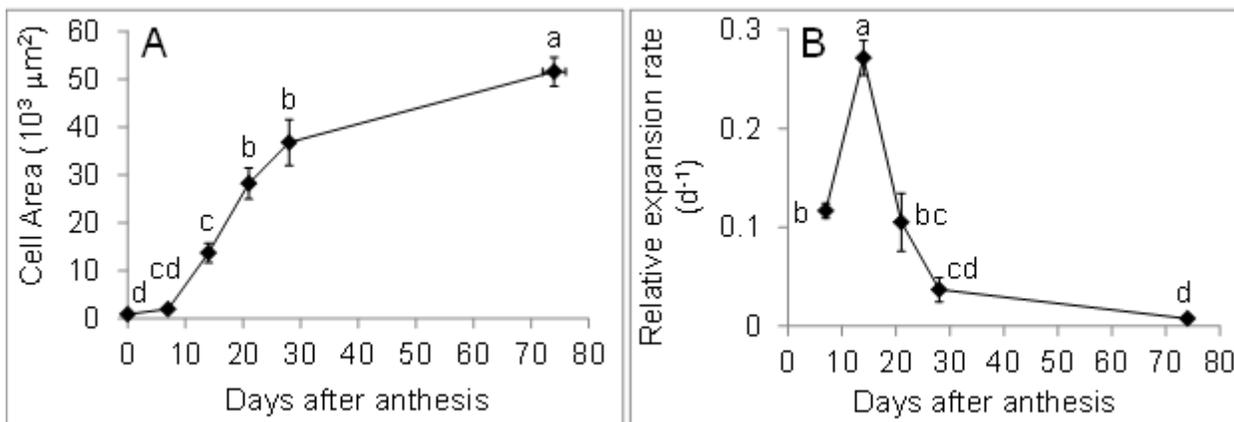


Figure 6

A. Fruit cell area ($\times 10^3 \mu m^2$) at various stages during fruit development: 0, 7, 14, 21, 28 DAA and ripening. B. Relative fruit cell expansion rate (d^{-1}) from 0–7 DAA, 7–14 DAA, 14–21 DAA, 21–28 DAA and 28

DAA to the ripe stage. Means separation was performed using Tukey's HSD following test of significance using ANOVA ($\alpha = 0.05$). Means followed by a different letter are significantly different.

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