

Isolation and study of a ubiquitously expressed tomato pectin methylesterase regulatory region

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Pectin methylesterase (PME) is an enzyme located in the plant cell wall of higher plants whose physiological role is largely unknown. We had isolated a PME gene from a tomato genomic library, including 2.59 kb of 5' flanking region and the coding region. Both coding and promoter region were sequenced and computer analyzed. Tobacco transgenic plants were created harboring constructs in which 2.596 Kb, 1.306 Kb and 0.267 Kb sizes of the promoter were driving the expression of β -Glucuronidase gene (GUS). GUS activity was studied by histochemical and fluorometric assays. Two introns of 106 and 1039 bp were found in the coding region and phylogenetic analysis placed this PME gene closer to genes from *Citrus sinensis* and *Arabidopsis thaliana* than tomato fruit-specific PME genes. In the promoter, it was found direct repeats, perfect inverted repeats and light responsive elements. GUS histochemical analysis showed activity in all plant tissues with the exception of pollen. The reduction in the promoter size induced a reduction in GUS activity in root, stem and leaf. Furthermore, root and leaf showed the highest and lowest activity, respectively. We had isolated a tomato PME gene with novel characteristics as compared with other known PME genes from tomato.

Pectin methylesterase (PME) is an enzyme that have been found in every plant tissue analyzed (Lineweaver and Jansen, 1951; Rexova-Benkova and Markovic, 1976), several fungi (Christgau, et al. 1996; Mendgen, et al. 1996), bacteria (Plastow, 1988; Barras et al. 1994) and even insects (Ma et al. 1990; Shen et al. 1999). In higher plants, it is known to be a cell wall associated protein and several of the PME cDNA available in the literature, are known to have toward the N-terminal sequence, a characteristic signal peptide which is thought to help in targeting the protein to the plant cell wall (Gaffe et al. 1997 and references therein). PME catalyzes the deesterification of galactosyluronate methylesters of pectins, releasing protons and methanol into the media (Frenkel et al. 1998). Despite the biochemical mode of action of PME is well known, it have been difficult to demonstrate any role for PME in the physiology of plants. However, several hypothesis had been proposed: pollen germination and/or tube growth (Mu et al. 1994), abscission (Sexton and Roberts, 1982), regulation of cell enlargement through changes in the plant cell wall Donnan potential (Ricard and Noat, 1986), fruit softening during postharvest fruit ripening (Zeng et al. 1996) and plant defense (Chamberland et al. 1991; Wietholter et al. 2003). Furthermore, strong experimental evidences had

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been provided to suggest that a PME role in the release of cells from the root cap (Stephenson and Hawes, 1994; Wen et al. 1999), plant pathogenesis (Collmer and Keen, 1986; Mendgen, et al. 1996; Nun et al. 1996; Valette-Collet et al. 2003), plant systemic infection by tobacco mosaic virus (Chen and Citovsky, 2003) and maintenance of the tomato fruit tissue integrity during postharvest shelf life (Tieman and Handa, 1994). However, the actual physiological role of PME is still matter of controversy.

Four papers to our knowledge had been published in which the cloning of regulatory sequences of PME from higher plants was described. However, in all of them DNA comparison by computer was the only tool used to prove that the gene located downstream was indeed encoding a pectin methylesterase. Albani et al (1991) reported the finding of a genomic clone from *Brassica napus* which contains the PME gene and its 5' upstream regulatory region. Studies were conducted using a piece of the gene located downstream as a probe. This gene was found to be expressed mainly during pollen development. Two putative PME promoter regions were cloned from *Brassica campestris* (Kim et al. 1997). Study of their sequence found them to have high homology with the previously reported promoter PME from *Brassica napus* (Albani et al. 1991). Further, a sequence motif similar to the one known to exist in two tomato pollen-specific promoter was located. Tobacco transgenic plants with constructs containing two different promoter sizes from one of those two promoter available were made. Expression of the GUS gene was only detected during developing and mature pollen grains germinated in vitro. Recently, the cloning of two 5' upstream region of PME from *Citrus sinensis* was published. Northern blot analysis showed that both DNA regulatory region are active in most of vegetative tissues (Nairn et al. 1998).

In our laboratory, we have cloned a 13.7 kb. genomic DNA from tomato containing a 2.59 kb. of DNA 5' flanking region, along with all the PME genomic clone. Identification of the protein encoded by the gene downstream was made by creating tobacco transgenic plants over expressing the PME cDNA (Gaffe et al. 1997) and comparing the sequences of the genomic and cDNA regions. In this work, we describe the study of a 5' flanking region of a PME gene called pmeu1 (which stands for PME ubiquitous one) using computer tools and tobacco transgenic plants.

MATERIALS AND METHODS

Cloning of the genomic fragment

The plaque lift technique was used to screen 810,000 clones of a tomato cv 'Cherry' genomic library made in EMBL3A λ phage with a radiolabeled small piece of PME; cloned by RT-PCR from tomato roots poly-A⁺ mRNA (Gaffe et al. 1995). We found several hybridizing, putatively positives, plaques. From every plate, we made two lifts and only that

plaques producing signal in both lifts were chose to continue. After four rounds of purification and screening, one plaque turns out to be positive. Elimination of the bacteria present in the agar was made by using chloroform-containing SM buffer. For phage amplification, *E. coli* strain LE 392 was infected with the phage after cultured in LB media. DNA isolation from the phage was made through a phenol chloroform protocol (Ausubel et al. 1988). Digested DNA with several restriction enzyme was separated by electrophoresis and blotted into nylon membranes. These DNA blots were probed with the PME cDNA complete sequence available to locate the phage DNA region encoding the genomic PME gene and the region 5' upstream. Sal I and EcoR I digested DNA fragments were subcloned into pBSKS (+/-) vector (STRATAGENE CLONING SYSTEMS. La Jolla, CA).

The EMBL3A λ phage library screened was created using the Sal I restriction site. Because of this, digested DNA fragments using Sal I were used to calculate the size of the tomato DNA inserted into the phage isolated, found to be 13.7 kb. All the procedure above mentioned was performed essentially as described (Sambrook et al. 1989) unless otherwise indicated.

DNA sequencing of the promoter and the genomic coding region

Nested unidirectional deletions of the 5' upstream DNA Sal I fragment were made by following the recommendations of the company (Erase-a-Base[®] System, Promega Corporation, Madison, WI). Deleted clones with about 250 bp of size difference were used for DNA sequencing using the T₃ universal primer by the Sanger dideoxy chain termination technique following the recommendations (Sequenase Kit, United States Biochemical Corporation, Cleveland, Ohio). Second strand sequencing was determined by the DNA sequencing facility of IOWA State University by using primers designed at proper positions in the sequence (Iowa State University, Ames, Iowa).

Creation of the constructs

Three chimeric constructs driving the β -glucuronidase gene (*uidA*) under different sizes (2.596 Kb, 1.306 Kb and 0.267 Kb) of the promoter region were created by transcription fusion through the insertion of two stop codons in between the ATG of the pmeu1 gene and the ATG of the *uidA* gene. Every chimeric construct was ligated into the promoterless binary vector pBI101.3 (Bevan, 1984). This plasmid includes the neomycin phosphotransferase gene (NPTII) which confers resistance to kanamycin to be used as selectable marker. Furthermore, in this plasmid the DNA introduced is located between the right and left borders of the T-DNA, which allows the transference into the plant genome by *Agrobacterium* infection (Hooykaas, 1989; Zupan and Zambryski, 1995; Nester et al. 1996). Proper insertion of the different promoter sequences into the plasmid was confirmed by DNA digestion using suitable

restriction enzymes and PCR using primers designed against sequences in the PME promoter and *uidA* gene.

Every chimeric construct created included 150 bp in between the ATG of the *pmeu1* gene and the ATG of the *uidA* gene, containing sequences from the *pmeu1* gene and pBSKS(+/-) phagemid and pBI101.3 binary vector. Sequencing between the two ATG's was used to verify the presence of two stop codons and to corroborate the transcription fusion of the two ATG.

Tobacco transgenic plants

Mobilization of the pBI101.3 plasmid into *Agrobacterium* LBA4404 was performed by triparental mating using the broad-host helper plasmid pRK2013 (Ditta, 1981). *Agrobacterium* transconjugants were screened on plates containing a mixture of kanamycin and rifampicin antibiotics in YEP media (Sambrook et al. 1989). Verification of the mobilization of the constructs was made by purification DNA from *Agrobacterium* following the recommendations (Wizard Minipreps, Promega Corporation, Madison, WI) and digestion with proper restriction enzymes. Tobacco (*Nicotiana tabacum* W38) young leaves were infected with *Agrobacterium* by using the leaf disk technique (Mathis and Hichee, 1994) and selection for transformants was done by using kanamycin in the media.

GUS activity measurement

After induction of roots, about 50 primary independent transformant plants growing *in vitro* harboring every of the three constructs were selected at random to measure GUS activity in leaf. This was done using the fluorometric technique (Jefferson et al. 1987) with a Perkin Elmer LS5 fluorometer. Quantification of reaction product was done by using a 4-methylumbelliferone standard curve. Also, six independent transgenic plants were used to measure GUS in root, stem and leaf tissues. Every GUS measurement was done at least three times. For enzymatic specific activity, protein determination was made using Bradford (1976) with bovine serum albumin as standard.

In order to examine the GUS presence in different tissues, at least 20 primary transgenic plants harboring the different constructs, were vacuum infiltrated with a 1.9 μ M solution of 5-Bromo-4-Chloro-3-Indolyl-Glucuronide (Jefferson et al. 1987) as described (Mandel et al. 1995).

Pollen germination *in vitro*

Tobacco flowers in anthesis were collected from plants growing in the greenhouse and transported immediately to the laboratory. Anthers were cut and only that pollen released by a gently shaking was used for germination studies. Pollen was germinated using the Brewbaker and Kwack solution as described (Brewbaker and Kwack, 1963). Histochemical GUS staining was performed after four hours of pollen germination. Germination solution was

changed by the GUS staining solution and left at 37°C for at least 18 hrs before examination for GUS staining.

Computer analysis

DNA sequence from the different *pmeu1* 5' flanking region deletions were joined together using DNAsis (Hitachi Software Engineering Co., LTD., 1991). Comparison between the *pmeu1* cDNA and *pmeu1* genomic clone was performed using Harr plot analysis with DNAsis software. Presence of known cis-acting elements was determined using the programs MathInspector ver. 2.2 (Quandt et al. 1995), TFSEARCH ver. 1.3 (Parallel Application, Tsukuba Laboratory, RWCP, Japan), Signal Scan ver. 4.05 (Prestridge, 1991) and Pattern Search (Wingender et al. 1996; Wingender et al. 1997). Percent of identity among the different PME promoters and PME transcribed regions were determined using Align (Myers and Miller, 1988). Alignment of deduced amino acid sequences was performed using GCG's Pileup Program (Genetics Computer Group, Madison, WI). Multiple sequence alignment was performed using CLUSTAL W (Thompson et al. 1994). DNA direct repeats for the tomato PMEU1 promoter were determined using Proscan ver 1.7 and repeats from GCG software ver. 9.0 (Genetics Computer Group, 1995). Perfect inverted repeats (mirror repeats) were located using Palindrome from GCG software ver 9.0 (Genetics Computer Group, 1995). Putative TATA box was located by Signal Scan ver. 4.05. Phylogenetic analysis were done using the phylogeny inference package (Felsenstein, 1989; Felsenstein, 1993).

Statistical analysis

Comparison of leaf GUS activities for the three constructs and for the different tissues was made by variance analysis using a completely randomized design for unbalanced number of repetitions. Tukey test was used when needed to find differences among means. Because it is known that the GUS enzymatic activity in populations of first-generation transgenic plants does not follow a normal distribution (Nap et al. 1993), we performed a Box-Cox transformation before variance analysis. From here, we learned that a square root was a suitable transformation to bring the GUS activity parameter into normality. Statistics reported in this paper represents the back transformation of the square root transformed data. All statistical analysis were performed using the SAS software (SAS Institute Inc. Cary, N.C.).

RESULTS

Isolation and characterization of PMEU1 gene

The cloning and characterization of the entire PMEU1 tomato cDNA has been previously reported (Gaffe et al. 1996; Gaffe et al. 1997). The next step lead us to the isolation and characterization of the genomic fragment

containing the PMEU1 gene. An EMBL3A phage of a tomato genomic library (VNTF cherry) was screened using 300 bp cDNA fragment corresponding to the conserved PME domain in PMEU1 (Gaffe et al. 1996; Gaffe et al. 1997). Four rounds of phage amplification allowed us to purify a single positive clone.

Subcloning, analysis by restriction mapping and DNA blot of the tomato genomic DNA fragment contained in the EMBL3A phage indicated that the size of the inserted tomato genomic DNA is 13.7 kb and the PMEU1 gene was found to be located toward the 5' region, spanning 5.28 kb.

In [Figure 1](#), is presented the organization of the EMBL3A clone containing the PMEU1 gene. This region includes 2.59 kb of DNA regulatory region and 2.89 kb of DNA transcribed region, shown as white and black areas. In the figure it is also shown the location of the right and left lambda phage arms and the main restriction sites.

DNA sequence of the transcribed region of PMEU1 gene

In [Figure 2](#), it is shown the sequence of the PMEU1 genomic clone (GenBank Accession Number: AY046596). In italics, it is presented the 5' untranslated region (Gaffe et al. 1997) and the partial 3' untranslated region. In bold, it is shown the sequence of the two introns present. Underlined, it is presented the translation start site and stop codon (TAA). Double underlined it is shown the putative polyadenylation signal and polyadenylation site (GT).

The polyadenylation signal was found to follow the plant consensus sequence AAUAAA (Li and Hunt, 1995). The two introns present are of 106 and 1039 bp in length. Both of them showed a significantly higher composition of U's with respect to the flanking exon sequences. This is a characteristic known to be present in many plant genes (Ko et al. 1998).

Intron-exon organization of PMEU1 and other PME genomic clones

The intron-exon structure of the PME genomic sequences available has been analyzed. The splice junction of all the clones conform to the GT/AG boundary rule for the 5' donor and 3' acceptor site (Liu and Filipowicz, 1996). The intron size range from 72 to 1577 bp and the exon from 117 to 1353 bp. The average value for intron and exon size is 109 and 519, respectively.

Seventeen clones have only one or two introns. Three putative PME genomic sequences from *Arabidopsis* contains four introns and show a level of similarity with PMEU1 of around 50%. Further, AtPME7 with five introns is more closely related to PMEU1 (64.9% of similarity). These observations suggest that there is not a simple relationship between the phylogenetic distance and intron number in the different PME genomic clones.

The position of one intron, relative to the deduced amino acid sequence, is conserved in 19 out of the 22 plant PME genomic sequences. This intron is located 17 amino acid residues upstream of the PME signature sequence GPXKHQAVLR; observed in the rice genomic clone as well ([Figure 3](#)). This observation suggests that monocots and dicots share a common ancestor. The other three clones (AtPME8, AtPME9 and AtPME10) are clustered together in one group by the phylogenetic analysis ([Figure 4](#)) which agrees with the lack of the intron located at the same distance from the signature sequence and the common characteristic of the presence of four introns.

Phylogeny analysis among PMEU1 and other plant PME genes

Deduced amino acid sequences of 22 plant PME genes as well as PMEB from *Erwinia chrysanthemi* were included in our study. The plant PME genes were chosen based in published data providing experimental evidences or presence of the full genomic sequence from the *Arabidopsis thaliana* genome project from which some of the PME genes were included. One of the pectin methylesterase genes from *Oriza sativa* was included to be able to compare with a PME from monocots. Furthermore, the gene from *E. chrysanthemi* was chosen in order to compare PME from plants with a distantly related PME and also to have a control in the phylogenetic analysis. The PMEU1 gene includes 2900 bp and a theoretically deduced open reading frame of 583 amino acids ([Figure 3](#)). Several sequences shorter than 400 bp like PECS-1-2 from *Citrus sinensis*, are known to be partial. However, PPE1 sequence from *Petunia inflata* is shorter than 400 bp and still encodes a full polypeptide.

Sequence alignment of these different encoded polypeptides indicate that the N-terminal half of these clones is loosely conserved compared with the C-terminal half, involved perhaps in the PME catalytic activity ([Figure 3](#)). Because of this, a final alignment, edited to represent only the phylogenetically relevant fraction of the sequences was used to derive a phylogenetic tree ([Figure 4](#)).

Based on this phylogenetic analysis, we organized up to 18 genomic clones in five groups. Five PME genomic clones from various origins can not be associated with any of these groups. The lack of association of PME from *Erwinia chrysanthemi* with other plant PME's was something expected, however, it is interesting that the clone PECS-2.1 from *Citrus sinensis* is distantly related with the two clones PECS-1.1 and PECS-1.2 from the same source that clustered together with the PMEU1 clone.

This phylogenetic analysis indicates that PMEU1 belong to a group containing two *Citrus sinensis* PME genes, PECS-1.1 and PECS-1.2 and two *Arabidopsis thaliana* genes, AtPME2 and AtPME3; however, it is distant from the three tomato PME genes expressed only in tomato fruit tissues: LePME1, LePME2 and LePME3 (Harriman et al. 1992),

suggesting the PMEU1 is a gene evolved to have a different and novel function. However, due to the limited amount of information concerning the expression of these genes, we can not establish a clear relationship between these groups of PME genes and their possible function.

Structure of PMEU1 promoter

In [Figure 5](#) it is shown the 2.59 kb. PMEU1 promoter sequence (GenBank Accession Number AY050764). Computer study of this sequence showed several features commonly present in DNA regulatory sequences. The largest direct repeats within the promoter sequence, are shown underlined and numbered. Mirror repeats are shown with arrows in opposite directions. Putative cis-acting elements are shown boxed and roman numbered. The putative TATA box is shown double underlined. In bold, it is shown the transcription start site.

Study of the 5' region of this sequence did not indicate the presence of elements commonly present in the 3' region of genes, suggesting that the PMEU1 promoter region could be larger than 2.59 kb.

The number of direct repeats located by computer in the PMEU1 promoter varied with the size of the fragment, in such a way that it was found only one for repeats consisting of 17 and 26 bp, four for repeats with 12 bp, three for repeats with 11 bp and greater than 1000 for repeats with 5 bp (data not shown). However, the significance of this repeats within the PMEU1 promoter remains to be elucidated.

We also locate in the promoter sequence several perfect inverted repeats or mirror repeats, depicted in [Figure 5](#) as arrows pointing in opposite directions. It is interesting that the longest inverted repeats is contained within the longest direct repeats. As in the case of the direct repeats, the function of these inverted repeats, if any, is unknown.

Short sequences with resemblance to known cis-acting elements present in other ADN regulatory regions were located in the PMEU1 promoter sequence. In [Figure 6](#) are included only the ones with the highest degree of similarity. Two copies of the sequence GAAAGA shown to confer responsiveness to red light in the phytochrome A3 promoter (Bruce et al. 1991) are present in PMEU1 promoter (box I). Also, one copy similar to the sequence GTGAGGTAATAT, known to be regulated by light (Fluhr and Dankekar, 1986; Green et al. 1987) was found (box II). Furthermore, we found regions similar to a G-box (box III), shown to be light inducible (Schindler et al. 1992). Also, it was located a sequence similar to an abscisic acid responsive element (box IV) (Guiltinan et al. 1990). As can be seen from above, three of the four putative cis-acting elements located are known to be regulated by light. Experiments to show whether PMEU1 promoter is regulated by light deserves further attention. However, still the function of this cis-acting elements within the PMEU1

promoter is largely theoretical and experimental evidences to confirm any function of these sequences remains to be provided.

We were able to locate a putative TATA box 44 bp upstream of the transcription start site ([Figure 5](#)). However, as mentioned for the other elements above described, the confirmation of this region as actual TATA box still need to be experimentally probed. We did not find the presence of a CAAT box, although it had been shown to be present in several promoter of plant genes (Joshi, 1987).

Paired comparisons among the DNA sequence of the PMEU1 promoter with sequences of PME promoters from *Brassica campestris* (GBAN215-6 and GBAN215-12), *Brassica napus* (Bp 19), *Citrus sinensis* (CsPME1 and CsPME3) and *Arabidopsis thaliana* (AtPME1) did not showed any special pattern or similarity with any of the promoters included in the analysis. Indeed, all the pair comparisons showed around 50% of identity. Further, analysis by multiple sequences alignment among all PME promoters failed to locate an homologous region in common to all of them (data not shown).

Transgenic tobacco plants

With the goal to test whether the 2.59 kb. DNA region located in the 5' flanking region of the PMEU1 genomic coding region represent an active promoter, we created several tobacco transgenic plants expressing chimeric constructs in which 2.59, 1.3 and 0.267 kb of promoter sequence is driving the expression of the reporter gene *uidA* encoding the β -glucuronidase enzyme.

In [Figure 6](#) it is shown the three constructs made along with the average of leaf GUS activity for about 50 independently tobacco transformed plants growing *in vitro* and expressing the corresponding construct. From the graph, it is clear the trend: the bigger the piece of the promoter, the higher the activity of the *uidA* gene. Statistical analysis of root squared-transformed data found differences among all of them ($p < 0.05$).

Histochemical staining of many independent primary tobacco transgenic seedlings showed activity in leaf, stem and roots of the plants. We also found activity in petals and sepals. However, no activity was detected in pollen grain or *in vitro* germinated pollen (data not shown).

In [Figure 7](#), it is shown the average values of GUS activity for root, stem and leaf of six independent tobacco plants harboring every of the three constructs. The effect of reducing the size in the PMEU1 promoter for the different tissues analyzed followed the pattern already observed in leaf. The decrease in the size of the PMEU1 promoter region reduce its transcriptional activity in all differentiated tissue analyzed.

Statistical analysis found significant differences ($p < 0.05$)

among the root tissues from plants harboring the different sizes of the promoter. For stem tissues, significant differences were found only between plants with 0.267 kb and 2.59 kb of promoter size. This result is most likely due to the few independent transformants used in the analysis. However, the trend is clear and similar in all plant differentiated tissues analyzed.

DISCUSSION

We have cloned and analyzed a genomic DNA region containing an almost complete and novel PME gene. Several tools were used to probe that this region encodes the genomic sequence of a PME gene. Comparison of the sequences of PMEU1 genomic coding region with the PMEU1 cDNA already cloned showed that both are identical with the exception of the intron sequences located in the genomic clone. Further, analysis of the cDNA sequence using BLAST resulted in high similarity with several DNA regions encoding PME genes. Also, transgenic plant overexpressing the PMEU1 cDNA under the control of the cauliflower mosaic virus showed higher levels of PME activity as compared with control plants. It was also shown that this high level of PME activity correlated with the presence of a band hybridizing with a PMEU1 specific probe (Gaffe et al. 1997).

The PMEU1 gene is presented in the tomato genome as a single copy (Gaffe et al. 1997), in contrast with other PME genes published which had been shown to form clusters (Richard et al. 1996; Turner et al. 1996).

We perform several experiments to find another copy of the gene, like increasing the number of plaques screened and using probes from the 5' end of the gene with unsuccessful results. Also, DNA blot analysis of the 8.4 kb of the 3' end of the DNA inserted in the phage did not show any hybridization with PMEU1 probe even under low stringency conditions (data not shown). Further, DNA blot analysis of the tomato genome using EcoR I as restriction enzyme showed one band hybridizing to a 6.0 kb band, which correspond precisely with the fragment released from the DNA phage and shown to hybridize with the PMEU1 specific probe (data not shown). Taken together, these evidences support that the PMEU1 gene is presented as a single copy in the tomato genome and that it is part of the DNA contained by the isolated phage from the genomic library.

Comparison of the PMEU1 genomic coding region with the PMEU1 cDNA sequence showed the presence of two introns with 106 and 1039 bp in size (Figure 2). We compared the structure of genomic regions encoding PME genes in regard to the number and size of introns. The analysis did not show any clear pattern of structure since there is a high variability in both the size and the number of introns present. However, when we compared the amino acid sequence of 23 PME genes from higher plants and a PME gene from *E. chrysanthemi* (Figure 3), the analysis highlighted a large region in common for most of the plant

PME genes: GPXKHQAVALLR. Also, we noted that it is located most of the time at the same place with respect to the presence of the first intron. Experiments of site directed mutagenesis with a PME gene from *Aspergillus niger* strain 5344 had shown that there is an histidine residue essential for PME activity within the amino acid sequence HQAVA (Duwe and Khanh, 1996). From Figure 3, we can see that most of the PME enzymes from higher plants has the sequence HQAVA as well. This seems to suggest that this histidine residue can be playing an important role in the catalytic activity of the enzyme. Multiple sequence alignment failed to locate the sequence of HQAVA of *Erwinia chrysanthemi* PME A or PME B at the same location as plant PME's. However, pair comparison between PMEU1 and PME A or PME B from *Erwinia chrysanthemi* correctly aligned the sequence HQAVA at the same position.

Studies of the three-dimensional structure of *Erwinia chrysanthemi* pectin methylesterase (PME-A) support the presence of two aspartate and one arginine residues in the active site of the enzyme (Jenkins et al. 2001) and not an histidine. However, some of the PME isoenzymes show an aspartate residue instead of histidine in the same site (Figure 3).

We believe that the study of the possible involvement of either an histidine or an aspartate residues in the catalytic activity of PME from higher plants deserves further attention.

Computer analysis of the PMEU1 genomic region showed that this sequence follows several features commonly present in other genes from higher eukaryotic organisms, as mentioned above. The phylogenetic analysis (Figure 4) had shown that this PME gene is not related with other PME genes isolated from the tomato genome (Harriman et al. 1991). Rather, from Figure 4, we can see that PMEU1 is more related to two genes from *Arabidopsis thaliana* (AtPME2 and AtPME3) and two genes from *Citrus sinensis* (PECS-1.1 and PECS-1.2). Efforts to find a correlation between relatedness of the PME genes and pattern of expression were not successful. However, the finding just mentioned further support that the cloned PME gene described in this work belong to a entirely novel type of PME gene from tomato.

Experiments carried out in our lab with tobacco transgenic plants overexpressing the PMEU1 gene and tomato plant with lower levels of this gene did not produce a change in the plant phenotype that could be give us an insight as to what is the physiological role of the PMEU1 gene. Therefore, we decided to computer analyzed the PMEU1 promoter sequence to look for DNA boxes or elements with known function, in search for insights as to what can be the physiological role of this PMEU1 gene.

In Figure 5, it is presented the sequence of the DNA regulatory region of the PMEU1 gene. We are not sure of

having the complete genomic sequence of the PMEUI gene for two reasons: the DNA segment of the PMEUI gene was located toward the 5' end of the tomato genomic DNA carried by the isolated phage (Figure 1). Further, computer analysis of the PMEUI promoter 5' end region failed to find elements known to exist toward the 3' end of the gene coding regions. However, considering the size of the largest sequence of a PME regulatory region published to date, 2.3 kb (Albani et al. 1991), it is quite possible that we almost had the entire PMEUI regulatory region. Our efforts to isolate from the tomato genomic library the remaining segment of the PMEUI regulatory region were largely unsuccessful.

The computer analysis of the PMEUI regulatory region showed the presence of both direct repeats and perfect inverted repeats. In Figure 5, only the largest ones are shown. It is interesting that repeats 1 and 2, which are only separated by one base pairs appears to come from only one repeat in which a mutation took place, splitting this long repeats into two shorter ones. Also, some of the largest perfect inverted repeats are present inside of the largest direct repeats. It can be interested to test whether this repeats belong to the PMEUI promoter or they are part of the intergenic region of the plant genome which is known to contain repeat sequences. However, the possible role if any of these repeats remains to be elucidated.

We also located two sequences identical to cis-acting elements found in the phytochrome A3 promoter (Bruce et al. 1991). Also, it showed two more sequences similar to known cis-acting elements regulated by light. From here, the possible regulation of this PMEUI gene by light deserves further attention. We also located a sequence similar to a known abscisic acid responsive element, close to the transcription start site (Figure 5). The phytohormone ABA had been related to the abscission phenomena in plants (Label et al. 1994; Aneju et al. 1999) and to the plant responses to abiotic stress in plant (Zhu, 2001). One of the genes encoding a pectin methylesterase isolated from *Citrus sinensis* was shown to be up-regulated in abscission zones of leaves (Nairn et al. 1998). Currently, experiments in our laboratory are being carried out to test the possible role of the gene PMEUI in the plant responses to light, abscission and abiotic stress, however, a possible function for the PMEUI gene in these phenomena is still matter of controversy.

With the goal to demonstrate that the 5' flanking region of the PMEUI genomic clone correspond with an active regulatory region, and to find the smallest size of the region able to direct transcription, we created transgenic tobacco plants expressing different constructs in which the *uidA* gene, encoding the enzyme β -glucuronidase, is being regulated by different regions of the PMEUI promoter.

In Figure 6, it is shown the results of analyzing the β -glucuronidase activity of around 50 independent transformed tobacco plants. From the figure, it is clear that

by reducing the size of the promoter, its transcriptional activity is also reduced. As can be seen, even 267 bp of the PMEUI regulatory region is transcriptionally active. This means that we did not reach the lower limit where the promoter loose completely its transcriptional activity, although a large reduction was accomplished. In contrast, it was reported that a truncated piece of 440 bp of a flax PME promoter (Lupme3) lost completely the ability to drive transcription of a reporter gene (Roger et al. 2001). The results of GUS activity in leaf tissue are supported by the histochemical staining analysis in which the transgenic plants showed weaker activity in the parenchyma tissue surrounding the leaf vascular tissue with decrease in the promoter size (data not shown).

The change in transcriptional activity among the different sizes of promoter is of 6 fold when comparing the 0.267 kb. with the 1.306 kb. and 4 fold when comparing the 1.306 kb. with the 2.59 kb. There is a difference of 1.03 kb between 0.267 kb and 1.306 kb and 1.29 kb between 1.306 kb and 2.59 kb. The differences in sizes are similar and still the variation in activity is higher between the 0.267 Kb. and 1.306 kb which means that perhaps there are stronger enhancer element(s) in the promoter region closest to the ATG. Overall, we obtained up to 95% in reduction of PMEUI promoter transcriptional activity with the construct including 0.267 kb of PMEUI promoter. Reduction of the promoter size which brings an associated reduction in promoter activity as measured with a reporter gene had been found in deletion studies of other promoters (Darasiela et al. 1996; Royo et al. 1996), however, sometimes smaller pieces are able to drive higher levels of reporter gene activity in general (Canevascini et al. 1996) or at some specific tissues (Royo et al. 1996).

The standard deviation of the parameter is indicating a very high variability which is most likely due to the presence of multiple copies in the genome of the different transformants (not determined), dissimilarities in the physiological status among the leaf tissues used and to the position effect (Wilson et al. 1990). This result is alike with studies reported earlier, in which a high variability among independent transformants was also found in liquid cell cultures expressing the GUS gene under the manopine synthase (Peach and Velten, 1991). Also, tobacco cells stably transformed with a chimeric construct in which the CaMV35S was driving the expression of GUS, showed a standard deviation three times higher than average for the GUS specific activity parameter (Allen et al. 1993).

The average of GUS activity in tobacco leaf for the construct harboring the 2.59 kb of promoter size was 324.334 pMoles of MU/min/mg protein (Figure 7). This activity is similar to the one reported earlier for tobacco (*Nicotiana tabacum* var Samsun) leaf of about the same size used in this work, harboring GUS (*uidA* gene) under the control of the cauliflower mosaic virus 35S promoter: 321 pMoles/min/mg protein (Jefferson et al. 1987). This result suggest that PMEUI promoter is as strong as the

CaMV35S which in turn indicates its usefulness in overexpressing proteins in plants.

We also studied the expression of the three constructs in the three main plant tissues: root, stem and leaf of six independent transformants (Figure 7). It is clear from the graph that the three constructs showed the same pattern already observed for leaf tissue. However, we recorded 1.7 and 8 fold PMEUI transcriptional activity for stem and root, respectively. This suggest a difference in the strength of the enhancer elements present in the PMEUI promoter depending upon the type of plant tissue. These results also suggest that the enhancer element(s) are active en several differentiated tissues and are not specific for leaf tissue. These results are supported by the GUS histochemical staining in which the transgenic plants harboring the construct including the smallest promoter region showed weaker activity in the parenchyma tissue surrounding the vascular tissue as compared with tissues of transgenic plants expressing the construct with the highest promoter region (data not shown).

These findings are in contrast with deletion studies of other promoter in which it was found that for specific tissues, smaller pieces of the regulatory regions are able to direct higher values of reporter gene enzymatic activity (Royo et al. 1996).

Deletion studies of the PMEUI promoter could be of significant insight to locate this putative enhancer elements. However, stronger experimental evidences are needed to probe their presence in the PMEUI promoter region.

In summary, we had isolated an entirely new gene encoding a pectin methylesterase isozyme from the tomato genome which is represented by a single copy. It shows an ubiquitous pattern of expression, in contrast with the tissue specific gene isolated earlier from tomato. Analysis of its promoter region suggest several potential function for this gene and we believe that further analysis of this gene will bring new insights to understand better the physiological role of the pectin methylesterase enzyme.

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APPENDIX Figures

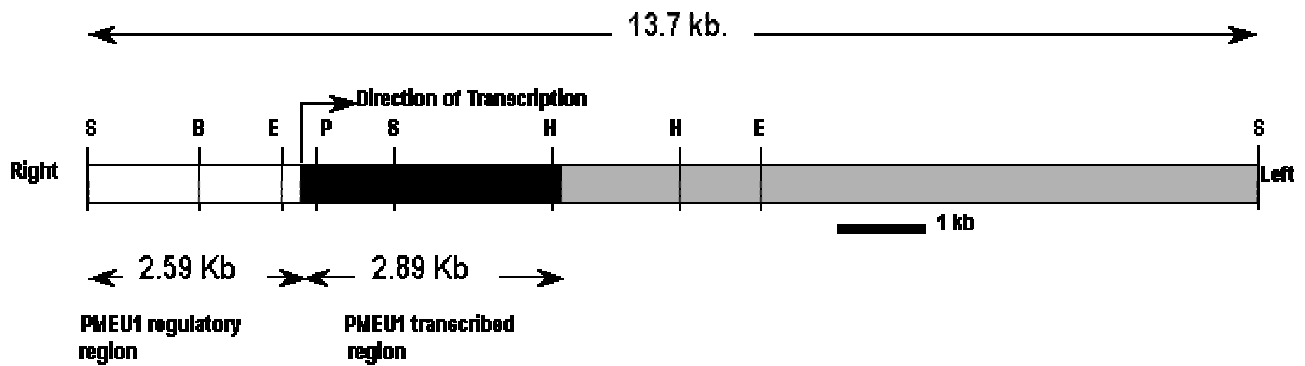


Figure 1. Partial restriction map of the λ phage and location of the PMEU1 genomic sequence. Open box, black box and gray box represent the PMEU1 promoter, genomic DNA coding region, and the phage DNA region flanking the 3' end of *pmeu1* gene. Right and left represent the right (8.8 kb) and left (19.9 kb) lambda arms. Abbreviations: B, E, H,P, and S indicate BamHI, EcoR I, Hind III, Pst I and Sal I restriction sites. Sal I sites at the left and right borders are from the λ EMBL3A.

-79 GGACCAATGT CACGGATATA AAACCCCCAC CAATCCGATC CAATTTCTCC
 -31 ACAACTCTCC CTTAAATTTT TCATCCAAA ATGACACGTG TTGAAGATTT
 21 TTTCAGCAA CAATCGATT TTTGTAAGA GAAGAAAAAA ATCTACTTGG
 71 CCATTGTTGC CTCAGTCTTG CTGGTTGCTG CAGTAATCGG AGTAGTCGCC
 121 GGAGTAAAAT CTCATTGAA AACTCCGAC GATCATGCAG ACATAATGGC
 171 CATTTGCTCT TCAGCCCATG CTATTGTAAA ATCTGCGTGT AGCAACACTC
 221 TACACCCCGA ACTGTGTTAC TCTGCGATTG TCAATGTTTC TGATTTCTCA
 271 AAAAAAGTAA CAAGCCAAA AGATGTGATT GAATTGTCTT TGAATATCAC
 321 TGTCAAAGCC GTTCGACGCA ACTACTATGC AGTCAAGGAA CTCATCAAAA
 371 CTAGAAAAGG TACTTGRCRC GTTARCTTA ATACTCCATT GTABBBATGT
 421 TBSAAGTCT CTTCCTCTT TATTGAAAT ATAGTTGGTT TAICTCACTA
 471 TTTTATTTTT CATAGGTTTA ACCCCACGAG AAAAGGTTGC GCTGCATGAC
 521 TGCTGGAGA CGATGGACGA GAACTCGAC GAGCTCCACA CTGCTGTAGA
 571 AGATCTGGAG CTATATCCCA AAAAAAATC ATTGAAAGAA CACGTGGAAG
 621 ACCGAAAAC TCTAATAAGT TCCGCAATTA CAAACCAGGA AACTTCCCTC
 671 GACGGTTTCT CTCACGATGA GCGCGATAAA AAGGTACGCA AGTTTTTGT
 721 GAAAGGCCAA AAGCACGTGG AAAAAATGTG CAGCAATGCT TTAGCTATGA
 771 TCTGTAACAT GACCGATACC GACATTGCAA ATGAGATGAA ATTATCGGCC
 821 CCCGCCAATA ATAGGAAGTT AGTAGAGGAT AACGGCGAGT GCGCGAGT
 871 GTTGTCCGCC GCGACAGGA GGTATTGCA GTCGTCGACG GTGACGCGAG
 921 ATGTGGTTGT GCGCGCCGAC GGAAGCGGAG ATTACAAAAC GGTCAGAG
 971 GCGGTACGAA AAGCGCCAGA GAAGAGTAGC AAGAGGTATG TGATTAGGAT
 1021 AAAAGCTGGT GTTACAGGG AAAACGTGGA TGTCCAAAAG AAGAAGACGA
 1071 ATATTATGTT TATGGGAGAT GCAAAAAGCA ATACAATAAT CACAGCAAGT
 1121 AGGAATGTGC AAGATGATG CACTACCTTC CACTCTGCTA CAGTTGGTBA
 1171 GTTATTATTA TTATCTTAT CAACCAATTG CCTAATTG CAGCTAECTA
 1221 CTTATACAG GTAGAGTTA ATTTAATTTG GTAGCGAGT GATBATTIT
 1271 TGTATCACAT GTTAATGTA TACTAATTTT TTACTTTANT ACTTTATGTA
 1321 TAGTCAAGG ACAGTAAAG TGAAACCAAT AACACACTT CATTCCCGTG
 1371 CTAGATAGT GAGCAATA AACACACTTC ACTTAATGT TTGTCAAGT
 1421 GGTAGCATT TAGGTTGATC TATTCTCCT GTTAAATAA ABAAGTCTC
 1471 TATTTACCT TTAAGGAG AAAGATAT TAAATTAGC TTGACCAAG
 1521 AGTTCGAGTA CTAAATAGT TCAGTAATAG ACTATTCTG TTGGTAGTA
 1571 GTTAGAGGA ATTAAGAGC TTTTGTACT ACAATAGTC GTATAATTAA
 1621 AAGTAAAGT TATCTCTTA TTGTACTACA AATGAGAGTA AATAATTTCA
 1671 CTTATACCA AAACCAATGT ACATCTCTT GTTTTTTAA TCTGAGGTT
 1721 ATTATCCCTT AACCAATCAA CCAACAGTT AATGTTATTG GTGAGGCTG
 1771 GCTTATACTC AATATGACTA TATATAACGA ATCCACGTC TGTAAGGTT
 1821 GGATAAAGG CATATCTTAT GGACGAGG ATATAGATTI GTCAGCCCT
 1871 TTTTGTAGT GGTGTATCTA TCGCTTGTG ATATAGATC TGCTTTCCG
 1921 CTGGGGTAGC GCTCCCTTTC CTTGABTAA TCGTAAATG ACTTCTTCT
 1971 TGTATAATA TTTTFACTA CATATAATTT TCGTACCAG GGTCCGTTT
 2021 CTTTGCAGCG GCCTATAATA ATCGTGTCTT TTGATAAGGA CAGCTCAGGG
 2071 GTACTTCTT AGCTGACAT AATAGAGCA CCGTCCCTT TAGTCCGCTG
 2121 GATATTTATT CAARATTTA AATGTATCA TGACATTTT TATGAGTTG
 2171 TCCAAATAG AATGACATA ACTAATTTGA TCGGTCCGC GTGGCAGGAA
 2221 AAGTTCTTGC CCGGATATA ACCTTCCAAA ACACAGCAGG AGCCTCGAAG
 2271 CATCAAGCCG TGCACTCTG CGTGGCTCT GATTTGTCCG CATTTATAG
 2321 ATGTGACATG TFGCTTATC AGGACACCCT CTACGTCCAC TCTAATCGTC
 2371 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

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AtPME9      1 -----
AtPME10     1 -----
AtPME8      1 -----
ATPME4      1 -----MIGKVVVSVASILLVGVVAIGVVAFINKN
BP19        1 -----MAVGKIVISVASMLLVGVVAIGVVTFVNKG
PER         1 -----MGGTRYNGGHDOSKRFALVGVSSILLVAVVATVADAQQ--
PEF1        1 -----MGGNDNNGGQGGQKKHALLVGSCILLVAVVGVVAVSLTKG
PPE1        1 -----
AtPME6      1 -----MGSDGDKKKKIVAGSVSGFIVIMVVSVAUVTSKH
ATPME2      1 -----EFISKFSDFKNNKKLILSSAAIALLLLASTVGGIAATTTNQNKNOK
ATPME3      1 -----MAPSMKEIFSKDNFKNNKKLVLLSAAVALFVAAVAGISAGASKANEKR-
PECS-1.1    1 -MTHIKEFFTKLSESSSNQINISNIPKKKKKFLALFATLLVVAAVVIGVAGVNSRKNSGD
PECS-1.2    1 -----
PMEU1       1 -----MTRVEDFFSKQIDFCRKKKKIYLAIVASVLLVAAVVGVVAGVKSHSKNSD
PECS-2.1    1 -----MALRILITVSLVLFSLSHTSPGYSP
LEPME1      1 -----
LEPME2      1 -----MATPQQPLLTKHKQNSIISFKILTFVVTDFVALFLVVFLVAPY
LEPME3      1 -----MATPLQPFLTRKHKQNP IIGFNILTFVVTDFVALFLVVFLVAPY
RCPME1      1 -----MAIQETLIDPKKSPKPTFWLLLSLAAVIGSSALIVSHLNKPI
AtPME7      1 -----
OsPME       1 MAHATLGSPEPAAPRLCADGRHRRRLIVVLCIVGVAVAVAVAVLGRSRMTSS
ATPME1      1 ---MDSVNSFKGYGKVDEAQLALKKKTRKRLLLSISVVVLIAMVIAAVVAVTVVHKVKN
PMEB        1 -----

AtPME9      1 -----
AtPME10     1 -----
AtPME8      1 -----
ATPME4      30 GDAN---LSPQMKAVQGIQSTSDKASCVKTEPEVKSE---DPNKLKAFMLATKDE
BP19        31 GGAGGDKTLNSHQKAVESLCASATDKGSCAKTIDPVKSD---DPSKLKAFMLATKDA
PER         39 -----GQPNVQILCESTQYQQTCHQSLAKAPAETAGVKDLIKAAFSAT---SE
PEF1        41 GDGEQKAHISNSQKNVDMLCQSTKFKETCHKTEKASFS--NMKNRIKGAIGAT---EE
PPE1        1 -----
AtPME6      36 SPRDDENHIRKTTKAVQAVCAPTDFKDTCVNSLIMGASPDSDDPVDLKLGFVKT----IK
ATPME2      46 ----ITTLFSTSHAILKSVCSSTLYPELCFSAVAATGGK--ELTSOKEVIEASLNLTTKA
ATPME3      50 -----TLSPSSHAVLRSSCSSTRYPCLCISAVVTAGAC--ELTSQKDVIEASVNLTTA
PECS-1.1    60 -----NGNEPHHAILKSSCSSTRYPDLCFSAVAAVPEASKKVTSQKDVIEMSLNITTTA
PECS-1.2    1 -----
PMEU1       51 DHADIMAISSSAHAIDKSAACSNLHPELCVSAIVNVVSDFSKKVTSQKDVIELSLNITVKA
PECS-2.1    27 -----EVKSWCGKTPNPQPCFYFLTQKTQDVT---SIKQDIDFYKISLQLAL
LEPME1      1 -----
LEPME2      45 Q-----FEIKHSN--LCKTAQDSQLCLSYVSDLMS-NEIVTTSDGSLILMKFLVNY
LEPME3      45 Q-----FEIKHSN--LCKTAQDSQLCLSYVS-----EIVTTSDGVTVLKFLVKY
RCPME1      44 S-----FFPLSSAPNLCEHAVDTKSLCTHSEVVOGQALANTRDKHKLSTLISLLTKS
AtPME7      1 -----
OsPME       61 SGGGRAPRGRAPTEAARTCGVTLYPELCVGEIMAFPGAAG--AGDAELVPMSLNATHRR
ATPME1      58 ESTPSPPELTPSTSKAICSVTRFPESCISSESKLPSS---NTTDPETLFLKLSLKI
PMEB        1 -----

AtPME9      1 -----
AtPME10     1 -----
AtPME8      1 -----
ATPME4      81 LTKSSNFTGQTEVNMGSSISPNNKAVLDYCKRVFMYALDDIATIIEEMG-----EDL
BP19        86 VTKSTNFTASTEEMGRNINATSKAVLDYCKRVLMYALDDIETIIEEMG-----EDL
PER         84 ELLKHINSS--LIQELQDKMTKQAEVQNEVLDYAVDGHKSGAVD-----KFDI
PEF1        95 ELRKHINNSA--LYOELATDSMTKQAEICNEVLDYAVDGHKSGVGLD-----QDFD
PPE1        1 -----
AtPME6      92 SINESLEKASGDIKAKADKNPEAKGAFELCEKLMIDAIDDKKCDHNG-----FSV
ATPME2      100 VKHN-YFAVKKLIAKRGLTPREVTALHDCLDTEIDETLDELHVAVEDLHQY----PKQ-
ATPME3      102 VEHN-YFTVKKLIKRRGLTPREKTAALHDCLDTEIDETLDELHETVEDLHLY----PTK-
PECS-1.1    114 VEHN-YFGIQKLLKRTN-LTKREKVALHDCLDTEIDETLDELHKAQEDLEEY----PNK-
PECS-1.2    1 -----
PMEU1       111 VRRN-YYAVKELIKTRKGLTPREKVALHDCLDTEIDETLDELHTAVEDLELY----PNK-
PECS-2.1    70 ERAT-TAQSRTYTLGSKCRNEEKAQWEDCRELYELTVLKNQTSN-----
LEPME1      1 -----NDIRQHGALTDCLDQLDQSVDLASDSIAATD-----
LEPME2      94 VHQMNAIPVVKMKMNQINDIQEGALTDCLDQLDQSVDLASDSIAATD-----
LEPME3      89 VHQMNAIPVVRKIKNQINDIQOQALTDCLDQLDQSVDLASDSIAATD-----
RCPME1      96 TSHIQKAMETANVIKRRVNSPKETALNDCEQLMDLSEDRVWDSQLTET-----
AtPME7      1 -----MKERKCFADPFGDRRLQNAVSDCLDQLDQSVSEETWASASENP-----KGGK
OsPME       119 VVDALYNATALGGAALLAGARSGAAYGDCVEMLDAAEELIARSUGATAAPPPPDSDA
ATPME1      113 IDELDSISDLPEKLSKETEDERIKSALRVCGDLIEDALDRNDTQSAIDDE----EKKK
PMEB        1 -----MSLTHYSGLAAAAMSLSLITACGGQTPNSARFQPVFPGTVSRP-----VL

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Isolation and study of a ubiquitously expressed tomato pectin methylesterase regulatory region

AtPME9 1 ---MGYISLALVALLVFFASPVVLAADDITPIPADRAQIPQWFMANVFPFSQRRGTDPPEL
 AtPME10 1 ---MGYISMSVVAFLVVFASPVVLAATDIPENRAQIPQWFKTNVFPYSQRRGTDPAL
 AtPME8 1 -----MVFADDLTPPEGKPVVQVFNTHVGPLAQKRGIDPAL
 ATPME4 133 SQIGSKIDQLKQNLIGVYNYQTDCLDDIEEDDLRKAIGEGIANSKILTTNAIDIFHTVVS
 BP19 138 QQSGSKMDQLKQNLIGVYNYQTDCLDDIEESELKRVMGEGIAHSKILLSNAIDIFHALTT
 PER 135 NKIHEYSYDLKRWLIGLSSHQQTCLDGFANTTTKAGETMARALNTS IQLSSNAIDVVDVAV
 PEF1 146 HKLSEYAFDIKRWLIGLSSHQQTCLDGFVNTKTHAGETMAKVLKTSMESSNAIDVMDVV
 PPE1 1 -----MVKLLNSTEELSINALSMLNSF
 AtPME6 143 DQIEVFDLRYWLSGSIAFQQTCDMSFGEIKSNLMQDMLKIFKTSSELSNSLAVVTRI
 ATPME2 153 KSLRKHADDLKTLISSAINTQQTCLDGFSDADRVRKALLKGOVEVEHMCSNAIAMIK
 ATPME3 155 KTLREHAGDLKTLISSAINTQQTCLDGFSDADKQVRKALLKGOVEVEHMCSNAIAMIK
 PECS-1.1 166 KLSLQHADDLKTLMSSAANTNQQTCLDGFSDADANKHVRDALSDGOVEVEKMCSNAIAMIK
 PECS-1.2 1 -----IK
 PMEU1 164 KSLKEHVEDLKTLLISSAINTQQTCLDGFSDADKVRKALLKGOVEVEKMCSNAIAMIK
 PECS-2.1 115 SSPGCTKVDKQITLSTALTNLETCRASLEDLGVPEYVLPPLSN-----EAKVALAMLASITTT
 LEPME1 32 KRSRSEHAMSESWLSGVLTNHVTCIDELDSFTKAMINGTNLEELISEAKVALAMLASITTT
 LEPME2 143 KRTHSEHAMASWLSGVLTNHVTCIDELDSFTKAMINGTNLEELISEAKVALAMLASVTT
 LEPME3 138 KRSRSEHAMASWLSGVLTNHVTCIDELTSFSLSTRNGTVLDELITSEAKVALAMLASVTT
 RCPME1 145 KMNIDSQDAHTWLSGVLTNHATCLNGLEGTSRVVMES-DLQDLISEARSSLAVALSVLP
 AtPME7 50 NGTGDVGSDFRITWLSAALSNOQTCEMGFDGTSGLVKSLSVAGSLDQLYSMLRELLPVPQPE
 OsPME 179 DTAGRDDDDIMTWSAALTSHTCDMSLQEVGAGGDDGDDGGRIKQMLGYLGNMGEHL
 ATPME1 168 TLSSSKIEDLKTWLSAALTSHTCDMSLQEVGAGGDDGDDGGRIKQMLGYLGNMGEHL
 PMEB 46 SAQEAGRFTPOHFFAHGGEYAKPVADGWTPTPIDTSRVTAAYVVGPRAGVAGATHTSIQQ

AtPME9 58 EAAEAS-----
 AtPME10 58 EAAEAA-----
 AtPME8 39 VAAEAA-----
 ATPME4 193 AMAKINNKVDDLKMNMTGGIPTPGAPPVVDESVPADPDGPARRLLEDIDETGIFPTWVSGAD
 BP19 198 AMSQMNKVVDDMK-----KGNLGETPAPDRDLLEDLDQKGLPKMHSDDKD
 PER 195 YDLTN-----AKRLLSLDNG-----YPLWVSEGG
 PEF1 206 SRILKGFHPSQYGVSRLLSDG-----IPSWVSDGH
 PPE1 23 GDMVAQATG---LNRKLLTTDS-----SDATA
 AtPME6 203 STLIPNSMLTAKYARKLLSTEDS-----IPTWVSGPEA
 ATPME2 213 NMTETDIANFELRDKFFNLHQQQQRK-----LKEVTG-----DLSDGQWPKMISVGD
 ATPME3 215 NMTDTDIANFEQKAKITSNRRLKEENQETTVAVDIAGAG-----ELDSEGEPTWVSGD
 PECS-1.1 226 NMTDTDMMIMRTSNRRLTEETSTVDG-----WPAWVSPGD
 PECS-1.2 3 NMTDTDMMIMRTSNRRLIEETSTVDG-----WPAWVSTGD
 PMEU1 224 NMTDTDIANEMKLSAPANNRKLVEDNGE-----WPEWVSGD
 PECS-2.1 158 -NVTKLISNTLSLNKVPYNEPSYKDG-----FETWVSPGD
 LEPME1 92 QDED---VFMTGLGKMP-----SWVSSMD
 LEPME2 203 PNDD---VLRPGLGKMP-----SWVSSRD
 LEPME3 198 PNDE---VLRQGLGKMP-----YVWSSRD
 RCPME1 204 AKSMDGFIDESLNGEFP-----SWVTSKD
 AtPME7 110 QKPKAVSKPGPIAKGPKAPPGRKLRDTE-----EDESLOFPDWRPDD
 OsPME 239 SNSLAIFAARGRPGGELSDVPVHNLHR-----RLLTIDDDDDDDGSPFRWRHMD
 ATPME1 228 SLAIVSKILSALSDLGPIIHRRRRLMS-----HHHQQSVDFEKWAR
 PMEB 106 AVNAALRQHPGQTR-----VYIKLLP

AtPME9 64 -----RRVITVWVQNGGDFKTIINAATKSIPLANKNEV
 AtPME10 64 -----RQIITVWVQNGGDFKTIINAATKSIPTGNKNEV
 AtPME8 45 -----PRIINWVNPKGG-EFKTLTDATKSVFAGNTRRV
 ATPME4 253 RRLMAKAGR-----GRRGGRRGGARVRTNFVVAKDGGGQFKTVQQAADACPENNRGRC
 BP19 242 RRLMAQAGRPGAPADEGIGEGGGGGKIKPTEVVAKDGGGQFKTISEAVKAKCEKKNPGRG
 PER 220 RRLLAEAT-----VKPFWVVAQDGGGQFKTLTDATKTVFANNAQNF
 PEF1 238 RRLLAGGN-----VKNANVVAQDGGGQFKTLTDALKTVPPTNAAPF
 PPE1 47 RRLQIISN-----AKPNAIVVAQDGGGQFKTIKALDAVPEKKNTEPF
 AtPME6 235 RRLMAAQGGG-----PGPVRANVVAQDGTGQFKTITDALNAVPEKGNKVPF
 ATPME2 260 RRLQGS-----TIKADATVADGGGDFDNGSAVAAAPEKSNRRF
 ATPME3 270 RRLQGS-----GVRDATVADGGGDFKTVAAVAAAAPENSRRY
 PECS-1.1 262 RRLQSS-----SWTPMAVVAADGGGDFKTVAAVAAAAPQGGTRRY
 PECS-1.2 39 RRLQSS-----SWTPMVAVVAADGGGDFKTVAAVAAAAPQGGTRRY
 PMEU1 261 RRLQSS-----TWTPDVVAADGGGDFKTVSAVVRKAPEKSSRRY
 PECS-2.1 192 RRLQQT-----TPRANVVAQDGGGDFKTVAAVAAAAPSRAGGSRY
 LEPME1 113 RRLMESSGK-----DIIANRVVAQDGTGKYFTLAEAVAAAAPNRSKRY
 LEPME2 224 RRLMESSGK-----DIIANRVVAQDGTGKYFTLAEAVAAAAPDKNKTRY
 LEPME3 219 RRLMESSGK-----DIIANRVVAQDGTGDTLAEAVAAAAPDKNKTRY
 RCPME1 228 RRLLESTVG-----DIKANVVAQDGGGDFKTVAAVAAAAPDNGKARY
 AtPME7 153 RRLLESN-----GRTYDVSVALDGTGNTKIMDAIKKAPDYSSTRF
 OsPME 290 RRLQAAAA-----ETIADMVVAQDGTGTHKIRDAIKKAPHSRRV
 ATPME1 269 RRLQQTAG-----LKPDTVVAQDGTGDLTVNEAVAKVKKSLKMF
 PMEB 127 GTYTGTVYVP-----EGAPPITLFGAGDRPEQVWVSLALDSMMSPADY

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AtPME9      96  IIKLAPGTYHERKVTVDVGRPYVTLIGKPGAETMLTYGTAAKYG---TVESATLIWVWATN
AtPME10     96  IIKLAPGVYNEKVTIDLARPFITLLGQPGAETVLYHGTAAQYG---TVESATLIWVWEY
AtPME8      76  IIKMAHCEYREKVTIDEMKPFITLHGQPNAMPVITYDCTAAKYG---TVDSASLIILSDY
ATPME4     306  IYIKAGLYREOVIIIPKKKNNIFMFGDGRKTVISYNSVALSRGTTTSLS--ATVESEG
BP19       302  IYIKAGVYREOVITPKKVMNVMFMDGATQTIITPDRSWGLSPGTTTSLSGTVQVSEEG
PER        261  VIYVKEGVYREIVMWPDMAFVTLIGDPAKTRFTGSLMYADG--LLPMTATLGVNGEN
PEF1       279  VIYVKEGVYREIVMWAREMNYVTVIGDGPTRTKFTGSLMYADG--INTYKTAIFGVNGAN
PPE1       88  IYIKAGVYKEYIDIPRSMTNVLIGGPTKTRITGMSVVKDG--PTTFHTITVGVNGAN
AtPME6     281  IIRIKAGIYREKVTIVKPKMPTVTFIGDGNPNTLITGSLNMFGLGK-VKPTPLTATITLEGDH
ATPME2     301  VIHIRKAGVYRENVEVTKKKNIMFLGDGRKTLITGSRNVVDG--STTFHSATVAAVGER
ATPME3     311  VIHIRKAGVYRENVEVAKKKKNIMFMDGGRTRTLITGSRNVVDG--STTFHSATVAAVGER
PECS-1.1   303  IIRIKAGVYRENVEVTKKHKNIIMFMDGGRTRTLITGSRNVVDG--STTFKSATVAAVGEG
PECS-1.2    80  IIRIKAGVYRENVEVTKKHKNIIMFMDGGRTRTLITGSRNVVDG--STTFKSATVGGT---
PMEU1     302  VIKRAGVYRENVDVPPKKTNIIMFMDGKSNITLITSRNVVDG--STTFHSATVVRVCKK
PECS-2.1   232  VIYIKAGTYRENLEVKLKN--IMFVGDGIGRTLITGSRNVVGG--ATTFKSATVAAVGDN
LEPME1     156  VIYVKEGVYRENVEVSSNKNMLMIVGDGMVATITGSLNVVDG--STTFRSATLAAVGCG
LEPME2     267  VIYVKEGVYRENVEVSSKMKMLMIVGDGMHATLITGNLNVVDG--STTFHSATLAAVGKG
LEPME3     262  VIYVKEGVYRENVEVTKKKNMLMIVGDGMNATLITGSLNVVDG--STTFPSNLAAVGCG
RCPME1     271  VIYVKEGVYREIVKIKKKNVMLVGDGMDATLITGNLNFIDG--TTTFHSATVAAVGDL
AtPME7     194  VIYIKRGLYLENVEVTKKKNIVMLGDGIDVTVISGNESFIDG--WTTFRSATFAVSGRG
OsPME      333  VIYVKEGVYREIVMVKIGSKKTNMLVGDGAGTVVVGYSVHDM--YTTFHTATLAVAGAG
ATPME1     310  VIYVKSCTYRENVEVDSKKNVMIMVGDGKGRTLITGSRNVVDG--PTTYETATFAVCGKG
PMEB      170  RARVNPHGQY@PADPAWYMYNACATKAGATINTTCS@VWWSQS---NDFQLKNITVWNAL

AtPME9     212  YIEGTVDYDFIFGRGASLYLMTQLHAVGDGLRVIAAHNR@STTE----QNGYSFVHCKRVTG-
AtPME10    212  YIEGTVDYDFIFGRGASLYLMTQLHAVGDGLRVITAQGR@CSATE----QNGYTFVHCKRVTG-
AtPME8     193  YVEGTVDYDFIFGSGTSMYLGTOHVHVVDGIRVIAAHACKSAEE----KSGYSFVHCKRVTG-
ATPME4     419  VVSGTVDFIFGKSAITVIONTLIVVRKSGKQYNTVTD@CNELGLGNKIGIVLNCRI@VFD
BP19       417  VVSGTVDFIFGKSAITVIONSLILCRGSPGCTN@HVTAD@CNEKGAVKIGIVLHNCRI@MAD
PER        374  SISGTTDMI@GDAFAV@ONCKLIVRKP@LEEQQCFV@ADGR@K-S@SSSGFV@F@SC@HFT@GE
PEF1       392  AISGTTDFVFGDAF@V@ONCKLIC@V@AKG@KCLV@TAG@RDK-QNS@SABALV@L@SS@HFT@GE
PPE1       201  TITGTVDFIFG@G@E@AVL@ONCKYIVR@KPA@N@CS@M@V@TA@Q@GR@E-F@CKGAIVL@N@C@H@K@P
AtPME6     395  TVSGTVDFIFGDAK@C@H@ONCKYIVR@KPN@K@G@C@M@V@TA@Q@GR@M-VRE@STGLV@L@H@G@C@H@T@G
ATPME2     414  HITGTVDFIFGMAA@AVL@Q@C@D@H@ARR@P@NS@G@K@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@V@I@Q@N@C@R@I@G@T
ATPME3     424  LIAGTVDFIFGMAA@AVL@Q@C@D@H@ARR@P@NS@G@K@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@V@I@Q@K@R@I@G@T
PECS-1.1   416  LIAGTVDFIFGMAA@AVL@Q@N@C@D@H@ARR@P@NS@G@K@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@V@I@Q@K@R@I@G@T
PECS-1.2   135  -----AAV@L@N@C@D@H@ARR@P@NS@G@K@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@V@I@Q@K@R@I@G@T
PMEU1     415  LVAGTVDFIFGMAA@AVT@Q@C@D@H@ARR@P@NS@G@K@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@V@I@Q@K@R@I@G@T
PECS-2.1   343  DIYGTVDYDFIFGMAA@AVV@L@Q@N@C@I@F@ARK@P-P@N@R@I@N@L@T@A@Q@GR@D-P@N@Q@T@G@I@H@H@N@C@R@V@T@A
LEPME1     269  YVTGTVDFIFGMAA@AVV@L@Q@K@C@L@V@ARK@P@G@K@Y@Q@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@S@I@Q@F@C@H@I@A@S
LEPME2     380  YVTGTVDFIFGMAA@AVV@L@Q@K@C@L@V@ARK@P@G@K@Y@Q@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@S@I@Q@F@C@H@I@A@S
LEPME3     374  YVTGTVDFIFGMAA@AVV@L@Q@K@C@L@V@ARK@P@K@R@K@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@S@I@Q@F@C@H@I@A@S
RCPME1     384  FITGTVDFIFGMA@AVV@L@Q@K@S@L@V@ARK@P@M@S@N@O@R@N@M@V@TA@Q@GR@D-P@N@Q@T@G@I@S@I@Q@F@C@H@I@A@S
AtPME7     307  TITGTVDFIFG@D@G@T@V@F@Q@N@C@I@L@K@E@L@P@N@C@K@N@I@T@A@Q@GR@K@D-V@N@C@P@S@G@F@S@I@Q@F@C@H@I@A@S
OsPME      446  DVAGTVDFIFGMAA@AVV@L@Q@N@C@I@L@W@ARR@L@P@G@C@E@N@I@V@TA@Q@GR@D-P@N@Q@T@G@I@S@V@H@G@C@R@L@L@P@S
ATPME1     423  DVTGTVDFIFGSA@AVV@L@Q@G@K@I@P@E@Q@L@S@N@O@F@N@I@T@A@Q@GR@K@D-P@N@C@S@G@S@I@Q@F@C@H@I@A@S
PMEB      286  YIEGDVDYDFGRATAY@D@R@V@R@F@H@T@V@S@S@R@G@S@K@E@A@Y@V@F@A@P@D@S@I@P--S@V@K@Y@G@L@V@I@N@S@C@I@T@G

AtPME9     267  -----VGTGTYLGRANM@SHP@V@V@Y@S@Y@E@M@S@S@V@M@P@S@G@M@C@E@N@R@V@R---A@H@D@K@I@V@F
AtPME10    267  -----TGTGTYLGRANM@SHP@V@V@Y@A@F@E@M@T@S@V@M@P@S@G@M@C@E@N@L@N@R---G@Y@D@K@I@V@F
AtPME8     248  -----TGGGTYLGRANM@SHP@V@V@Y@A@T@E@M@T@S@V@M@P@T@G@M@C@E@N@K@P---A@H@D@K@I@V@F
ATPME4     479  RKL@I@P@E----RLTVATY@L@GR@P@W@K@K@F@S@T@V@I@M@S@E@M@G@D@I@R@E@G@M@K@I@M@D@G@E---S@F@H@K@S@C@R
BP19       477  K@E@L@E@A@D----RLTVK@S@Y@L@GR@P@W@K@P@F@A@T@A@V@I@G@E@I@G@D@L@I@C@P@T@G@M@E@M@Q@G@E---K@F@H@L@I@A@T
PER        433  P@E@V@A@K@I----D@P-KI@A@Y@L@GR@P@W@K@S@Y@S@V@V@I@M@D@S@I@D@D@I@F@D@E@G@Y@M@P@M@M@G@S---A@F@K@D@I@C@T
PEF1       451  P@A@L@T@S@V----T@P-KL@S@Y@L@GR@P@W@K@L@Y@S@V@V@I@M@D@S@I@D@A@F@A@P@E@G@Y@M@P@M@V@G@G---A@F@K@D@I@C@T
PPE1       260  T@Y@F@S@L----S@P@S@R@T@Y@L@GR@P@W@K@E@Y@S@R@T@I@M@Q@S@Y@I@D@K@F@E@P@E@G@A@F@M@I@T@N--F@G@R@D@T@S@Y
AtPME6     454  P@A@Y@I@P@M----K@S@V@N@K@A@Y@L@GR@P@W@K@E@F@S@R@T@I@M@K@T@I@D@D@V@I@D@P@A@G@L@P@W@S@G@D---F@A@L@K@T@L@Y
ATPME2     473  S@D@L@L@A@V----K@G@T@F@P@T@Y@L@GR@P@W@K@E@Y@S@R@T@V@I@M@Q@S@I@D@S@V@I@R@E@G@M@E@M@S@G---S@F@A@L@D@T@L@T
ATPME3     483  S@D@L@Q@S@V----K@C@S@F@P@T@Y@L@GR@P@W@K@E@Y@S@R@T@V@I@M@Q@S@A@I@S@D@V@I@R@E@G@M@E@S@E@W@T@G---T@F@A@L@N@T@L@T
PECS-1.1   475  S@D@L@K@P@V----Q@G@S@F@P@T@Y@L@GR@P@W@K@E@Y@S@R@T@V@I@M@Q@S@I@T@D@L@I@H@P@A@G@M@E@W@D@G---N@F@A@L@N@T@L@F
PECS-1.2   181  S@D@L@K@P@V----Q@G@S@F@P@T@Y@L@GR@P@W@K@E@Y@S@R@T@V@I@M@Q@S@I@T@D@V@I@H@P@A@G@M@E@W@D@G---N@F@A@L@N@T@L@F
PMEU1     474  S@D@L@R@P@V----Q@K@S@F@P@T@Y@L@GR@P@W@K@E@Y@S@R@T@V@I@M@Q@S@I@T@D@V@I@Q@P@A@G@M@E@W@N@G---N@F@A@L@D@T@L@F
PECS-2.1   401  S@D@L@K@P@V----Q@S@S@V@R@T@L@G@R@P@W@K@O@Y@S@R@T@V@I@K@I@F@I@D@S@L@I@H@P@A@G@M@E@W@S@G---D@F@A@L@N@T@L@Y
LEPME1     328  S@D@L@E@P@V----L@K@E@F@P@T@Y@L@GR@P@W@K@E@Y@S@R@T@V@V@M@E@S@Y@L@G@L@I@H@P@A@G@M@E@W@D@G---D@F@A@L@K@T@L@Y
LEPME2     439  S@D@L@E@P@V----L@K@E@F@P@T@Y@L@GR@P@W@K@Y@S@R@T@V@V@M@E@S@Y@L@G@L@I@H@P@A@G@M@E@W@D@G---D@F@A@L@K@T@L@Y
LEPME3     433  P@D@L@E@P@V----M@N@E@Y@T@Y@L@GR@P@W@K@H@S@R@T@V@V@M@Q@S@Y@L@D@G@H@I@D@S@G@M@E@W@R@G---D@F@A@L@K@T@L@Y
RCPME1     443  S@D@L@K@P@V----Q@G@S@I@R@T@Y@L@GR@P@W@K@Y@S@R@T@V@V@L@Q@S@V@D@S@H@I@D@P@A@G@M@E@W@D@R@A-S@K@D@F@L@Q@T@L@Y
AtPME7     366  A@D@L@V@P@Y----L@N@T@T@R@T@Y@L@GR@P@W@K@L@Y@S@R@T@V@F@I@R@N@M@S@D@V@R@E@G@L@E@W@N@A---D@F@A@L@D@T@L@F
OsPME      505  P@E@L@E@L@A@A@R@R@G@R@A@T@Y@L@GR@P@W@K@P@Y@S@R@V@Y@M@S@Y@D@A@G@H@A@A@G@L@A@D@A@S@G--R@A@P@D@I@L@Y
ATPME1     482  G@N@V@I@A@P-----T@Y@L@G@R@P@W@K@E@F@S@T@V@I@M@E@V@I@G@A@V@R@E@S@G@M@S@W@V@S@G--V@D@P@P@A@S@I@V
PMEB      344  N@G@Y@R@G@A-----Q@K@A@R@L@G@R@A@D@Q@G@A@Q@T@G@Y@L@P@G@K@T@A@N@G@Q@L@V@I@R@D@S@T@I@D@S-----S

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Isolation and study of a ubiquitously expressed tomato pectin methylesterase regulatory region

AtPME9	313	YGEYMC	TGPG	SHKAKR	VAH---	TQDIDN	KEASQ	FLTLG	VTKG	----	SKULL	PPPPAY	---																																
AtPME10	313	YGEYKCF	GPGE	SHLEKRV	PY---	TQDIDN	KEVTP	FLTLG	VTKG	----	STULL	PPPKY	---																																
AtPME8	294	YGEYKCS	GPGE	SHKAKR	VPPF---	TQDIDD	KEANCF	LSLG	VIQG	----	SKULL	PPPAL	---																																
ATPME4	532	YVEYNNR	RGPCAF	ANRRV	MMAKVARS	AAEVN	GF	TAANWL	GFIN	-----	WIQE	ANVP	VTI																																
BP19	530	YVEYNNR	RGPCAM	TAAARV	PMAKMAKS	AAEVE	RF	TVANWL	TPAN	-----	WIQE	ANVP	VQL																																
PER	485	FVEYNNK	GGAD	TNLRV	KWHGV	LVLT	SNVAA	EYTP	GGKFE	IVN	ATARD	WLVK	GVVSL																																
PEF1	503	FVEYNNK	GGAD	TNLRV	KWHGV	LVLT	SNVAA	EYTP	GGKFE	IVN	ATARD	WLVK	GVVSL																																
PPE1	314	YREYQNR	GP	GAALDR	ITTKGF	QKGF	TGEAA	QKFT	AGV	IMN	----	DENUL	QKANVP	MEA																															
AtPME6	507	YAEHMT	TGPG	ENQAQR	VKMPG	IKKLT	P-	QDALL	V	TGDR	FLRG	----	DTULP	QTP	WTA																														
ATPME2	526	YREYLMR	GGGAG	TANRV	KKGYR	VITSD	TEA	QPF	TAG	CF	IGG	----	GGUL	AST	GF	P																													
ATPME3	536	YREYSMT	GAGAG	TANRV	KKGYR	VITAA	EA	QKFT	AG	CF	IGG	----	GGUL	SST	GF	P																													
PECS-1.1	528	YGEHONS	GAGAG	TSGRV	KKGYR	VIT	SATE	AQAF	TP	GSF	IAG	----	SSUL	GST	GF	P																													
PECS-1.2	234	YGEHONS	GAGAG	TSGRV	KKGYR	VIT	SATE	AQAF	TP	GSF	IAG	----	SSUL	GST	GF	P																													
PMEU1	527	YGEYANT	GAGAPT	SGRV	KKGYR	VIT	SSTE	AQAF	TP	GRF	IAG	----	GSUL	SST	GF	P																													
PECS-2.1	454	YREYMT	TGPG	ESTAN	RVKR	GYH	VLT	SPS	QVS	QF	TV	EMF	IAG	----	NSUL	PAT	NP	P																											
LEPME1	381	YGEFMN	NGPG	AGT	SRV	KKGYR	VIT	DP	AK	MPF	TV	AKL	IQG	----	GSUL	RST	GW	AVD																											
LEPME2	492	YGEFMN	NGPG	AGT	SRV	KKGYR	VIT	DP	AK	MPF	TV	AKL	IQG	----	GSUL	RST	GW	AVD																											
LEPME3	486	YGEFMN	NGPG	AGT	SRV	KKGYR	VIT	DP	AK	MPF	TV	AKL	IQG	----	GSUL	NST	GW	AV																											
RCPME1	498	YGEYLS	CGAG	AGT	SRV	TP	GYH	IKT	AA	ES	RFT	V	TQL	IQG	----	NVUL	KNT	GW	AV																										
AtPME7	419	YGEFMNY	GPGE	GLSS	RVK	MPG	YH	VFN	NSD	Q	ANNF	TV	SQ	IKG	----	NLUL	PST	GW	AV																										
OsPME	563	YGEYRNS	GP	GA	AVG	RV	PP	GH	V	IKL	PE	AME	F	TV	GRF	IGG	----	YSUL	PPT	GW	AV																								
ATPME1	531	YGEYKNT	TGPG	EDVT	CRV	KAGY	KP	MSD	AE	AA	KFT	V	ATL	LHG	----	ADUL	PAT	GV	IN																										
PMEB	388	YDLANP	WGA	ALMT	TD	RP	FF	EG	-----	NIS	PQR	LD	DI	H	NRL	----	WE	YMT	Q	LL																									
AtPME9		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
AtPME10		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
AtPME8		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
ATPME4	585	GL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
BP19	583	GL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
PER	545	ALD	ATS	NQ	GAT	PG	Q	GT	V	T	G	G	A	E	G	P	A	P	A	E	G	P	A	S	A	G	R	S	S	G	L	V	N	K	G	K	V	K	D	N	T	H	N	F	G
PEF1	563	CPM	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
PPE1	370	GMMKV	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
AtPME6	561	KV	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
ATPME2	581	SL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
ATPME3	591	GL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
PECS-1.1	583	GL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
PECS-1.2	289	GL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
PMEU1	582	GL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
PECS-2.1	509	GL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
LEPME1	436	GLYD	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
LEPME2	547	GLYD	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
LEPME3	541	GLVE	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
RCPME1	553	GL	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
AtPME7	474	GLYI	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
OsPME	618	GLTV	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
ATPME1	586	S	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																
PMEB	434	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----																																

Figure 3. Aminoacid Alignment of 22 Plant PME's and *Erwinia chrysanthemi* PME. PMEU1 (U49330), LEPME1 (U70677), LEPME2 (U70675) and LEPME3 (U70676) are from *Lycopersicon esculentum*; AtPME1 (NP_175787), AtPME2 (PC4168), AtPME3 (NP_188048), AtPME4 (AF077855), AtPME6 (AAF63815), AtPME7 (T05202), AtPME8 (NP_568181), AtPME9 (NP_196359) and AtPME10 (NP_196360) are from *Arabidopsis thaliana*; PER (AJ249611) and PEF1 (AJ249611) are from *Medicago truncatula*; PECS-1.1 (U82973), PECS-1.2 (U82974) and PECS-2.1 (U82975) are from *Citrus sinensis*; Bp19 (X56195) is from *Brassica napus*, PpE1 (L27101) is from *Petunia inflata*, RCPME1 (AF081457) is from *Pisum sativum*, OsPME1 (BAA96597) is from *Oriza sativa* and PME B (X84665) is from *Erwinia chysanthemi*. Alignment of deduced aminoacid was done using GCG's Pileup Program (Genetics Computer Group, Madison, WI).

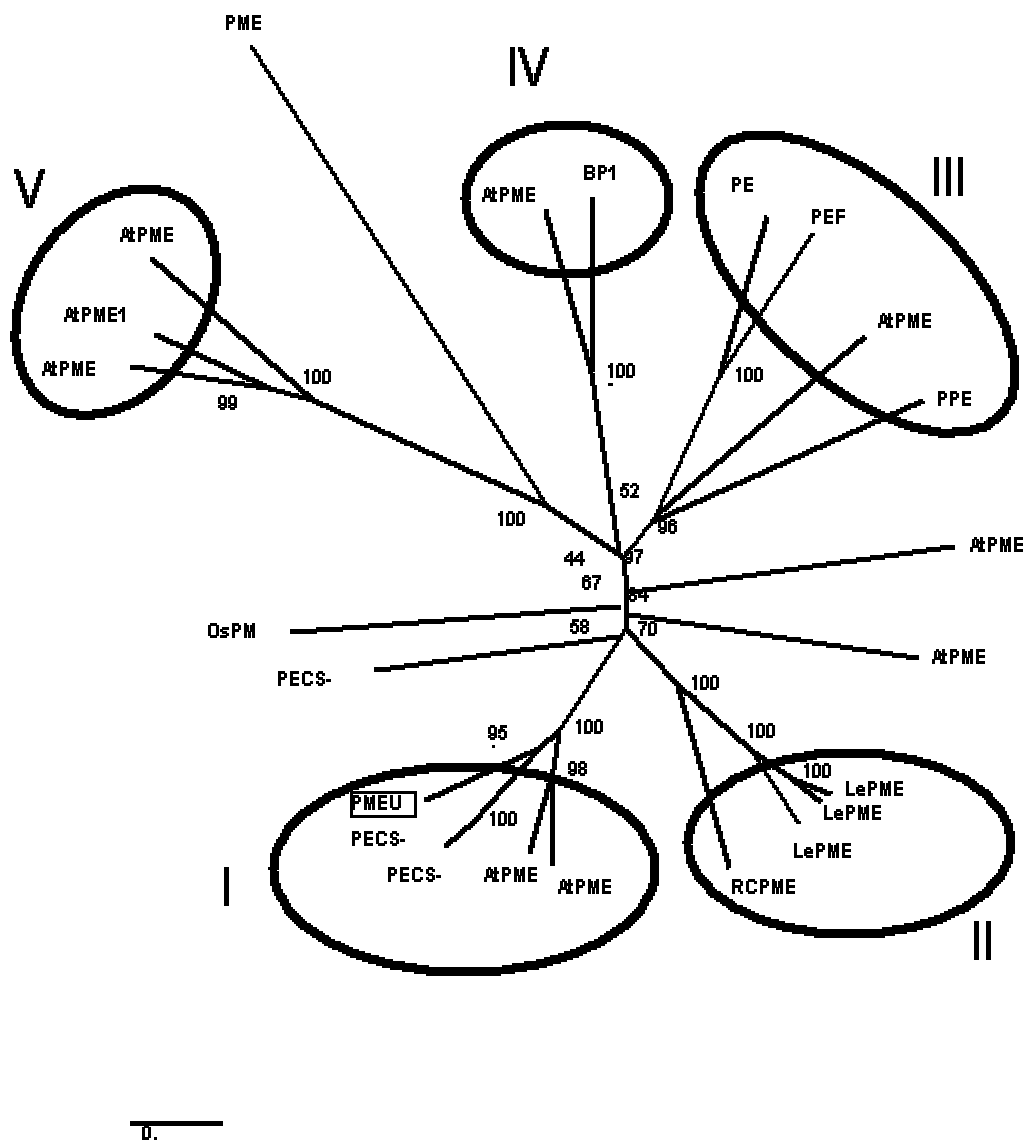


Figure 4. Phylogenetic Analysis of 22 Plant PME's and *Erwinia chrysanthemi* PME. PMEU1 (U49330), LePME1 (U70677), LePME2 (U70675) and LePME3 (U70676) are from *Lycopersicon esculentum*; AtPME1 (NP_175787), AtPME2 (PC4168), AtPME3 (NP_188048), AtPME4 (AF077855), AtPME6 (AAF63815), AtPME7 (T05202), AtPME8 (NP_568181), AtPME9 (NP_196359) and AtPME10 (NP_196360) are from *Arabidopsis thaliana*; PER (AJ249611) and PEF1 (AJ249611) are from *Medicago truncatula*; PECS-1.1 (U82973), PECS-1.2 (U82974) and PECS-2.1 (U82975) are from *Citrus sinensis*; Bp19 (X56195) is from *Brassica napus*, PpE1 (L27101) is from *Petunia inflata*, RCPME1 (AF081457) is from *Pisum sativum*, OsPME1 (BAA96597) is from *Oriza sativa* and PME1 (X84665) is from *Erwinia chrysanthemi*. Numbers are the bootstrap values. Phylogenetic analysis were done using PHYLIP (phylogeny inference package) ver 3.5c.


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-847 TTAGATATTTAGTTTGTATCATAGATTCTCAATTTTTGAAGAAAAGTAGCCGCT
-794 CGTCTCCGGTTCTTGAAGAACTTTACTTATAGCTAATTTAGAGAGCTTTACGT
-741 AAGATATGAGGTTCTGCTCCTCCAAGGTTCCAAAGTCCACCCTTACATATATC
-688 GATTTTATAGATAGATTAAATGGGAAATAATACCACAAAAGAAGTAAACAATTG
-635 GATTCTTGTAATTTAGCCTACACACTAAACTACTCCATAATTAGCAGTTCAT
-582 TAAAACACTTAATTAGGCCAAAAACAAGAAAGCTAGTTAACGAACATCTGCCAGG
-529 AAGTGTGATGCTAAAAAACAATTAATTACTAGGAAAAATAGACTAGGCATTA
-476 ACATTAACATCTAGTTAAATTTATCTATTTTACGATGTCCAATATCCTGGCCG
-423 CCCAGGCTAAAAGTTTTACTTCTTTTTGTTGCTTCACCCACTTGTTATTCTGTG
-370 AACAAAATTC AATATACAGCTAATCATGTCACTTTCAAATATCAATGATCGG
-317 AGTGATAATAATTGATTAAGTTTTAGATAAAGGCACGACTCAGCACAACAAGA
-264 ATTCTTTTCAAAAAGTAATCAAAACAAGAAAAGTATCGATACCTTCCCACCAT
-211 TCACGTGGCATCTATTATTACATGCAAAATTCACATTATGACCAAAACAATAAA
      IV
-158 TCAAAATTTATTCCTAGTAAATGCCATACTGTACTTTTTAAAAAATTCGAATAT
-105 TATATTTCAAAAAATTAGCGTATATATAGTTTTTCGACAACTTGATAATATAT
-52 ATATAAAAACATAAAATTTAAAAGTAAAAACA AAAATAGAACGTTGAAATTA

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Figure 5. DNA sequence of the PMEU1 Promoter. Shown are the longest direct repeats (numbered in bold), mirror repeats (arrows in opposite directions), putative TATA box (doubled underlined), translation start site (bold) and putative cis-acting elements (roman numbered and boxed). The software used to find the promoter characteristics is explained in the body of the paper.

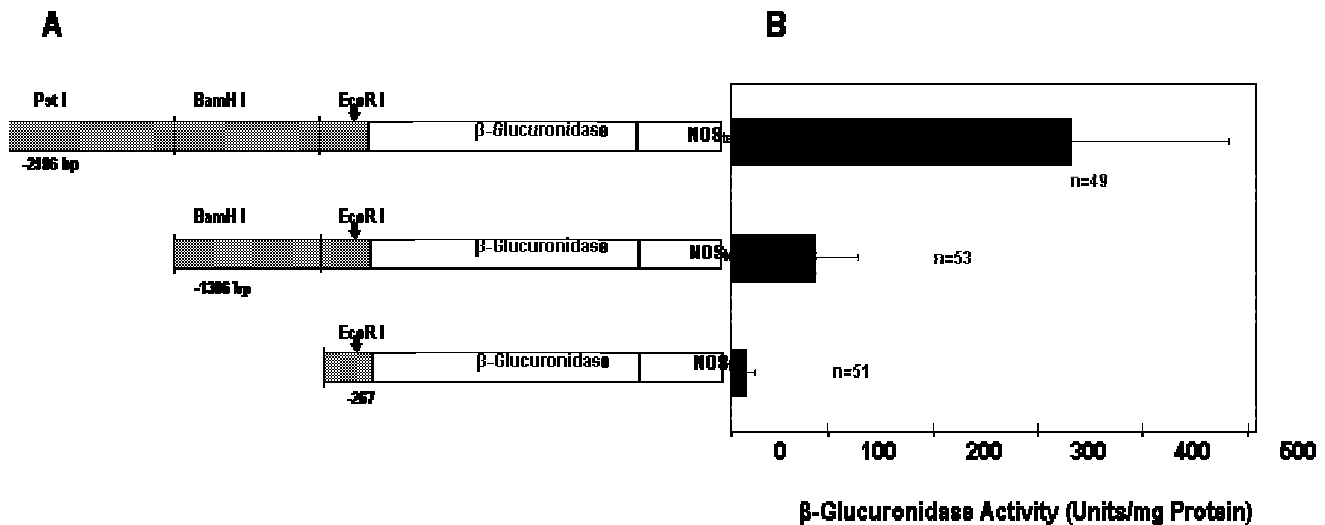


Figure 6. Chimeric PMEU1 promoter constructs and average of GUS activity in the transgenic tobacco plants.

A. The chimeric constructs used in plant transformation. Numbers below the shadowed bar are indicating the size of the *pmeu1* promoter in each construct. Arrow is indicating the translation start site for the *pmeu1* transcribed region.

B. Average of GUS activity from leaf of about 50 tobacco transgenic plants analyzed. Shown are the average and standard deviation values. Differences in GUS activity levels among all three constructs were statistically significant ($p < 0.05$).

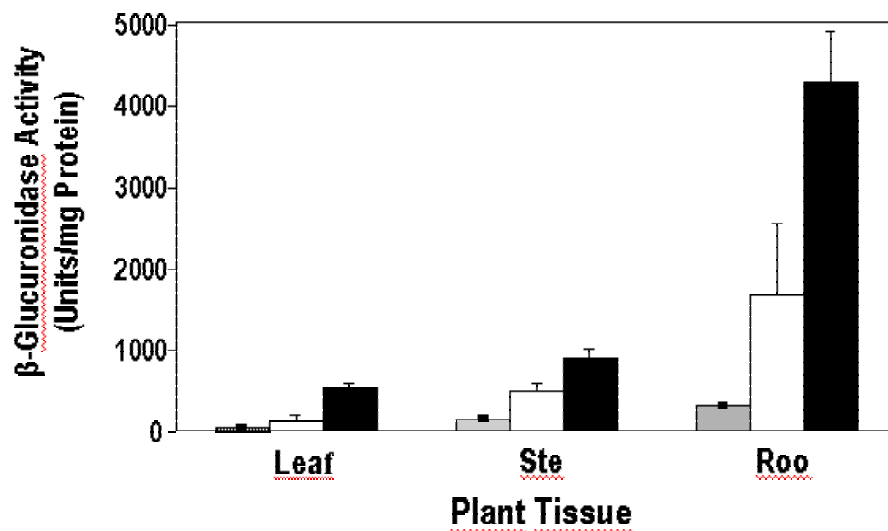


Figure 7. Average of GUS activity for root, stem and leaf of tobacco transgenic plants. Six independent transgenic tobacco plants harboring each of the three constructs were used to determine the average of GUS activity in root, stem and leaf. Shaded, white and black bars are the average of GUS activity for plants harboring 0.267 kb of promoter size, 1.306 kb of promoter and 2.59 kb, respectively. Lines in bars are indicating the standard deviation. Both average and standard deviation values were calculated by transforming back the square root transformed data used in the statistical analysis. Root and leaf values are statistically significant ($p < 0.05$). GUS activity for the constructs including 1.306 kb and 2.59 kb of promoter size showed significant differences when comparing root with leaf and stem. For the construct including 0.267 kb of promoter size, statistical analysis did not detect differences ($p > 0.05$).