Identification and characterization of strawberry FvGELP1
(Fragaria vesca GDSL esterase/lipase)

LUCIA DHANTIKA WITASARI1, FONG-CBIN HUANG2, WILFRIED SCHWAB3,*
1Department of Food and Agricultural Product Technology, Faculty of Agriculture, Universitas Gadjah Mada. Jl. Flora, Bulaksumur, Sleman 55281, Yogyakarta, Indonesia. Tel./fax.: +62-274-588688, *email: dihantie_k@ugm.ac.id
24GENE GmbH. Lise-Meitner-Str. 30, 85354 Freising, Germany
3Biotechnology of Natural Products, Technische Universität München. Liesel-Beckmann-Str. 1, 85354 Freising, Germany

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Abstract. Witasari LD, Huang FC, Schwab W. 2022. Identification and characterization of strawberry FvGELP1 (Fragaria vesca GDSL esterase/lipase). Biodiversitas 23: 907-915. Fruit softening is primarily the result of the hydrolytic enzymes activity. Esterases are reasonable candidates due to their putative role in cell wall components degradation. This study aimed to identify and characterize a new enzyme related to strawberry fruit ripening. Esterase activity was detected in the native PAGE of protein extract isolated from Fragaria x ananassa red fruit. Amino acid sequence analysis of the protein band revealed several esterases as possible candidates. GDSL esterase/lipase from Fragaria vesca (gene27964; FvGELP1) was chosen for cloning purposes and further analysis. Quantitative RT-PCR of FvGELP1 in plant tissues of F. vesca indicated high expression levels in fruit, in particular in early developmental stages. The gene FvGELP1 (1,161 bp) was amplified from F. vesca fruit cDNA and expressed as a 43 kDa HisTag fusion protein in Saccharomyces cerevisiae. FvGELP1 possesses four conserved residues Gly43-Asp44-Ser45-Asn46. FvGELP1 contains Ser45, Asp364, and His367 as the catalytic triad. Esterase assays of FvGELP1 resulted in high levels of the aromatic alcohol products by applying n-naphthyl acetate (oNA), n-nitrophenyl acetate (pNPA), phenyl acetate, and benzyl acetate as substrates. It could be suspected that FvGELP1 plays a role in strawberry fruit ripening and might be involved in the hemicellulose degradation, presumably by deacetylation of the polysaccharide.

Keywords: Fragaria × ananassa, F. vesca, fruit ripening, FvGELP1, GDSL esterase/lipase


INTRODUCTION

Characteristics of the ripe fruit in non-climacteric fruits such as strawberry (Fragaria spp.) are the result of physiological and biochemical changes. Hydrolytic enzymes like hydrodrolases could modify the polysaccharide of the cell wall and trigger fruit softening. Esterases are known also involved in the cell wall component degradation, such as pectin ester in strawberry fruits ripening (Castillejo et al. 2004; Xue et al. 2020). Acetylxyan esterase in combination with cellulases, mannanases, and xylanases may engage in the plant cell walls degradation. A carbohydrate esterase13 and a GDSL esterase/lipase protein (GELP) family member of plant deacetylases have been exhibited to cut acetyl groups from polysaccharides (Gou et al. 2012; Zhang et al. 2017). Recently, DARX1 (deacetylation on arabinosyl sidechain of xylan 1), rice (Oryza sativa) GDSL esterase regulates the conformation of arabinoxylan and the cross-linking mode with cell wall polymers of cellulose (Zhang et al. 2019).

GDSL esterases/lipases are hydrolytic enzymes with wide substrate specificity. Plant GDSL-lipases are known as acylhydrolases which might involve in plant development and growth (Ma et al. 2018; An et al. 2019; Ding et al. 2019a; Watkins et al. 2019), and morphogenesis (Smyth 2017; Yadav et al. 2017; Zhang et al. 2017). EXL6 (extracellular lipase 6) expression in Brassica rapa explained that this gene plays a pivotal role in pollen development (Dong et al. 2016). ZmMs30, a GDSL lipase expressed in maize anthers required for pollen exine and anther cuticle development (An et al. 2019). Besides, the hydrolytic activity of GDSL esterases/lipases has been connected to pathogen defense (Lee et al. 2009; Kim et al. 2013, 2014; Rajarammohan et al. 2018; Ding et al. 2019b), seed germination (Clauss et al. 2008), secondary metabolism (Huang et al. 2015), and the stress tolerance (Naranjo et al. 2006). To facilitate extracellular exportation, GDSL-lipases are synthesized as preproteins restraining signal peptides (Kram et al. 2008). This extracellular exportation might facilitate the degradation of complex polysaccharides in cell walls.

Plants retain a large number of GDSL esterases/lipases family, such as 105 AGELP in Arabidopsis thaliana (Lai et al. 2017), 114 OsGELP in Oryza sativa (Chepyshko et al. 2012), 121 BrGELPs in Brassica rapa (Dong et al. 2016), and 194 GmGELP in soybean (Glycine max) (Su et al.
2020). In addition, Volokita et al. (2011) investigated $57, 96, 126,$ and $130$ GDSL-lipase family members in *Plutella xylostella, Vitis vinifera, Populus trichocarpa,* and *Sorghum bicolor*, respectively. The GDSL-lipase gene family is defined by the distinct GDSL amino acid motif and several highly conserved domains. Similar to SGNH hydrolases, GDSL esterases/lipases contained at least four conserved sequence blocks I, II, III, and V with respective catalytic residues of Ser, Gly, Asn, and His (Upton and Buckley 1995). GDSL-lipases have a flexible catalytic site. They could adjust their conformation in the existence of different substrates and thus, the enzymes have broadly diverse enzymatic activities, such as thioesterase, protease, aryloesterase, and lyso phospholipase activity (Akoh et al. 2004). In plants, GDSL esterases/lipases could show both transferase and hydrolase activities. A GDSL-lipase from *Tanacetum cinerariifolium* possesses transferase (in vivo) and esterase (in vitro) activities in pyrethrins biosynthesis (Kikuta et al. 2012). These activities are comparable to xylanoglucan endotransglycosylases/hydrolases (XTHs) that exhibited transferase and hydrolase activities associated with strawberry fruit ripening (Witasari et al. 2019).

GDSL esterase/lipase in strawberry has not been reported. This study aimed to identify and characterize a new enzyme in strawberry related to fruit ripening. In this current study, we purified native proteins from *Fragaria × ananassa* fruit to investigate their hydrolytic activity and identified a candidate GDSL esterase/lipase from *F. vesca* namely *FvGELP1*, whose recombinant protein was produced in *S. cerevisiae* and biochemically characterized.

### MATERIALS AND METHODS

#### Plant material and reagents

Diploid (*Fragaria vesca* cv. Hawaii 4) and octoploid (*Fragaria × ananassa* cv. Elsanta) strawberry were purchased from KRAEGE Beerenpflanzen, Telgte, Germany (https://kraege.de). These plants were cultivated in a glasshouse (16 h light/8 h dark) in Dünast, Freising, Germany. Chemicals were purchased from Carl Roth (https://www.carlroth.com), Sigma-Aldrich (https://www.sigmaaldrich.com), J.T. Baker (https://www.avantsciences.com), and VWR International (https://www.vwr.com), unless otherwise indicated.

#### Protein extraction

Protein extraction was performed according to Niehaus and Gross (1997) method with modification. *Fragaria × ananassa* red fruits (50 g) were chilled in liquid nitrogen and then grounded in a rotor-stator homogenizer. The strawberry fruit powder was added PVP (10 g) in 100 mL of Tris HCl buffer (50 mM, pH 8.5) and then stirred. The mixture was filtered using muslin and subsequently centrifuged (20,000 g, 20 min). The filtrate was added protease sulfate (2%) under stirring and then centrifuged (20,000 g, 20 min). The supernatant was collected and further fractionated using ammonium sulfate (40-60%). The pellet contained protein was dissolved in 5 mL of Tris-HCl buffer (50 mM, pH 7.5), clarified by centrifugation (20,000 g, 10 min), and then desalted through dialysis using the same buffer.

#### SDS PAGE

The Tris-glycine SDS-PAGE gel (12%) was set in a Bio-rad gel tank (Walker 2009). Ten microgram protein sample was added to 8 μL of 4x loading dye (Carl Roth). The protein samples and a PageRuler Plus Prestained Protein Ladder (Thermo Scientific) were loaded carefully in SDS PAGE gel. Electrophoresis was performed in 1x TAE running buffer at 160 V for 1.5 h. Commassie Blue solution was used to stain the proteins at room temperature (RT), 20 rpm overnight. Finally, the gel was de-stained using 50% methanol and 10% acetic acid solution at RT, 20 rpm for 3 h.

#### Western Blot analysis

SDS gel and filter paper was incubated in semidry blotting buffer (25 mM TRIS base, 200 mM Glycin, 20% (v/v) methanol) for 5-10 minutes. The PVDF membrane (Roth) was activated in methanol for 1 minute and then equilibrated in semidry blotting buffer for 5 minutes. From the bottom part (anode) of semidry blotter was placed in order: 4x filter papers, membrane, polyacrylamide gel, and then 4x filter papers. A current of 10 V (0.8 mA/cm2 gel) was applied for 60 min. The membrane was removed from the blotter and incubated in blocking buffer (5% BSA or milk powder in washing buffer) on a shaker for 60 min at room temperature. The membrane was washed three times for 5 min in washing buffer (20 mM TRIS base, 140 mM NaCl, 0.1% (v/v) Tween 20). The membrane was incubated in a 50 mL falcon tube with 3 mL blocking buffer and 1μl of Anti-His-AP (Abcam) monoclonal antibody with rotation overnight at 4°C. The membrane was washed three times 10 min in washing buffer and then two times 5 min in detection buffer (100 mM Tris (pH 9.5), 100 mM NaCl, 5 mM MgCl2). The membrane was incubated in 20 mL of detection buffer containing 50 μL NBT substrate (5 mg NBT in 100 μL 70% DMF) and 25 μL BCIP (5 mg BCIP Na-salt in 100 μL H2O) for 15 min to 3 h in the dark with shaker until bands appear. Finally, the membrane was washed with water.

#### Native PAGE

Protein extract is dissolved in a non-denaturing sample buffer (Walker 2009). The 12% native PAGE separating gel (4 mL of acrylamide/bis-acrylamide (30%/0.8% w/v), 5.89 mL of Tris-HCl buffer (0.375 M, pH 8.8), 100μL of APS (10% w/v), and 10μL of TEMED) was set in a tris glycine buffer (25 mM Tris, 192 mM glycine). Ten microgramm protein sample and 8 μL of 2x sample buffer (Tris-HCl (62.5 mM, pH 6.8), glycerol (25%), and bromophenol blue (1%) were loaded carefully into each well in a Bio-rad gel tank. Electrophoresis was carried out at 100 V for 3 h at 4°C. Right after electrophoresis, α-naphthyl acetate was loaded as a substrate for detection of esterase activity (Gabriel 1971). Afterward, a diazonium salt was added to visualize the product of α-naphthol.
Protein sequence analysis

The protein band in the native pages were partially sequenced using mass spectrometry as previously described (Franz-Oberdorf et al. 2017). The translated F. vesca genome database (Shulaev et al. 2011) was used to identify the detected amino acid sequences. Peptide quantification and identification was carried out as previously mentioned (Franz-Oberdorf et al. 2017).

Gene expression analysis and phylogenetic tree

Extraction of total RNA from F. vesca cv. Hawaii 4 fruits was performed based on the method described by Liao et al. (2004). Afterward, cDNA and qRT-PCR were carried out according to Witasari et al. (2019). The expression levels of the interspacer 26S-18S RNA (IS) housekeeping gene were utilized to normalize the qRT-PCR data for FvGELP1. Interspacer (IS) primers and gene-specific primers were applied to amplify the IS gene and the target gene, respectively (Table 1). The dilutions of the cDNA of the IS gene and target gene were 8000× and 20×, respectively. Melting curve profiles were analyzed to confirm the absence of unspecific amplicon. The phylogenetic tree was created using Geneious software v. 2020 (https://www.geneious.com).

Cloning and expression of FvGELP1

The FvGELP1 (1,161 bp) was amplified from F. vesca and F. × ananassa cDNA using specific primers (FP_GDSL 27964 and RP_GDSL 27964) (Table 1). First, initial denaturation was done at 95°C for 4 min. Denaturation was conducted at 95°C for 45 sec, followed by annealing at 55°C for 30 sec and elongation at 72°C for 1 min in 35 cycles. Finally, termination was performed at 72°C for 10 min. Cloning and transformation were performed using the PSK+ cloning vector for Escherichia coli NEB 10 cells and the pYES2 expression vector for S. cerevisiae INVSc1 cells. FvGELP1 overexpression was induced by galactose. A HisTrap FF column, 5mL (Thermo Fisher Scientific) connected to a FPLC (AKTA system; GE Healthcare) was utilized to purify FvGELP1. His wash/bind buffer (sodium phosphate buffer (50 mm, pH 7.4), NaCl (0.3 m) and imidazole (30 mm)) at a flow rate of 0.5 mL min⁻¹ was used to equilibrate the column. The target protein was eluted using 1× His elution buffer (sodium phosphate buffer (50 mm, pH 7.4), NaCl (0.3 m), and imidazole (250 mm)) in a flow rate of 0.5 mL min⁻¹ for 20 min. Two milliliter fractions were collected for esterase assays.

Multiple sequence alignment

The full-length amino acid sequence of FvGELP1 was retrieved from the genome sequence of F. vesca ssp. vesca accession Hawaii 4 (Shulaev et al. 2011). The multiple sequence alignment of FvGELP1 and several GDSL esterase/lipase from different species was compiled using Clustal W software.

Esterase assay

Low molecular weight esters such as α-Na, pNPA, phenyl acetate and benzyl acetate were used as substrates based on Gilham and Lehner (2005) method with modification. The sample mixture was 10 µL of FvGELP1 crude extract and 5 µL of 20 mM substrate in 85 µL potassium phosphate buffer (0.1m, pH 6.0). The samples were incubated at 30°C for 24 h with constant shaking (300 rpm). The reaction was stopped using 50 µL methanol followed by centrifugation at 4°C (20,000 g, 10 min). The clear supernatant (50 µL) was used for HPLC-UV analysis.

HPLC-UV analysis

HPLC-UV was achieved using a reverse-phase column (Luna 3u C18(2) 100A, 150 × 2 mm; Phenomenex, https://www.phenomenex.com) in an Agilent 1100 HPLC-UV system (Agilent Technologies, https://www.agilent.com). Water with 0.1% formic acid (A) and methanol with 0.1% formic acid (B) was used as mobile phase. The injection volume was 5 µL. Flow rate was 0.2 mL min⁻¹. A gradient was applied from 0% B to 50% B in 30 min. Within the next 5 min, B was increased to 100% for 15 min. Afterward, B was decreased to 0% within 5 min. These initial conditions were kept for 10 min for system equilibration. UV signals were detected at 280 nm.

Data analysis

Data analysis for protein sequence was achieved using Scaffold 4, v.4.2.1 software (Searle 2010) provided by Chair of Proteomics and Bioanalytics, Technical University of Munich, Germany. qRT-PCR data analysis were performed using ΔΔCt method (Livak and Schmittgen 2001). HPLC-UV data was analyzed based on the method by Ring et al. (2013).

Table 1. Primers used for FvGELP1 cloning

<table>
<thead>
<tr>
<th>Primer name</th>
<th>Vector</th>
<th>Sequence (5' → 3')</th>
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</thead>
<tbody>
<tr>
<td>FP_GDSL 27964</td>
<td>-</td>
<td>ATGCTTGGGAAATGGAGATTTGGGAG</td>
</tr>
<tr>
<td>RP_GDSL 27964</td>
<td>-</td>
<td>GCTCTATAGACACGCTGAGTATGGG</td>
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<tr>
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<tr>
<td>RP_GDSL_PYES2_HIS</td>
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<td>-</td>
<td>ACCGGAGTGACAATTTAGGACG</td>
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<tr>
<td>RP_GDSL_qPCR</td>
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RESULTS AND DISCUSSION

Hydrolase activity and protein sequence analysis

Native proteins were extracted from *Fragaria × ananassa* red fruit to search enzymes candidate associated with the fruit ripening. Target proteins from *F. × ananassa* red fruit were isolated using ammonium sulfate precipitation (40-60%). This protein extract was further separated through SDS PAGE (Figure 1a) and native PAGE (Figure 1b). An esterase assay in the native PAGE gel revealed a positive band indicating α-naphthol release from the respective ester and thus hydrolase activity. An insoluble yellow to red colored product was formed after the coupling of α-naphthol with a diazonium salt (Figure 1b). The protein band presenting esterase activity was cut from the native PAGE gel and then delivered to the Chair of Proteomics and Bioanalytics at Technical University of Munich, Germany for amino acid sequencing (Figure 1). The data interpretation revealed various esterases candidates for instance pectinesterase 1 (PE1), PE3, PE34, and GDSL esterase/lipase (Figure 1c).

Castillejo et al. (2004) has characterized several pectinesterase genes from *F. × ananassa* identified as FaPE1, FaPE2, FaPE3, and FaPE4. Accordingly, GDSL esterase/lipase At5g14450, Precursor (putative), gene27964 (namely *FvGELP1*) was selected for cloning and biochemical analysis in this study.

Gene expression analysis and phylogenetic tree

Gene expression analysis of *FvGELP1* was performed in a transcriptome data set of *F. vesca* varieties including Hawaii 4, Yellow Wonder, and Reine de Vallées by Härtl et al. (2017). High expression levels of *FvGELP1* were found in green fruit of achenes and receptacles in all varieties (Figure 2). During strawberry fruit ripening, decreasing expression levels were detected. In addition, expression levels in receptacles were higher than in achenes. Thus, *FvGELP1* might involve in strawberry fruit ripening. Furthermore, *FvGELP1* showed the highest expression level among 25 candidate GDSL esterase/lipase genes in the receptacle of *F. vesca* Hawaii 4 fruits (Figure 3). Among these genes, *FvGELP1* showed high similarity with gene29811 (GDSL esterase/lipase At5g45920 (putative)) and gene28412 (GDSL esterase/lipase At5g14450, Precursor (similar to)) based on phylogenetic tree (Figure 4). The NGS data of *FvGELP1* in *F. vesca* var. Hawaii 4 fruit at different ripening stages was then verified by qRT-PCR.

Quantitative real-time PCR of *FvGELP1* in *F. vesca* Hawaii 4

The expression levels of *FvGELP1* in *F. vesca* fruit, leaf, and flower tissues, qRT-PCR analysis was presented in Figure 5. The qRT-PCR data of *FvGELP1* genes in different tissues and development stages could provide reference to molecular mechanisms of plant growth and development. The highest expression levels of the gene was detected in large green fruit. It elevated significantly from small green fruit to large green fruit but subsequently declined throughout fruit ripening. This suggested that *FvGELP1* may play pivotal roles in developmental stages. In other tissues, the expression of *FvGELP1* in flower was greater than in old and young leaves. *FvGELP1* expression in different tissues implied that *FvGELP1* might play diverse roles in various tissues and during development. Similarly, BrGELPs in *Brassica rapa* were expressed in various tissues, including floral organs (Dong et al. 2016). In soybean, *GmGELP22*, *GmGELP149*, and *GmGELP186* showed high transcription levels in most tissues throughout the growth period. Whereas *GmGELP10*, 79, 115, 124, and 180 exhibited high expression in young leaves, flowers, pods, and pod shells (Su et al. 2020).

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**Figure 1.** Protein bands of an ammonium sulfate extract from *F. × ananassa* fruit: A. SDS PAGE, B. Native PAGE, C. Possible esterase candidates of targeted band. The yellow band (red box) indicated positive esterase activity.
Figure 2. Gene expression levels of gene27964 in three *F. vesca* var. Hawaii 4 (HW4), Reine des Vallées (RdV), and Yellow Wonder (YW). A. Expression levels in achenes (Ac), B. receptacle (Rc) presented as nRPM (normalized read per million).

Figure 3. Gene expression level of candidate GDSL esterase/lipase in the receptacle of *F. vesca* var. Hawaii 4. Putative genes were arranged in decreasing order of their expression levels, presented as nRPM (normalized read per million).

Figure 4. Phylogenetic tree of GDSL esterase/lipase candidate genes from *F. vesca*. Gene27964 (*FvGELP1*) is in black frame box.

Multiple sequence alignment of *FvGELP1*

The primary amino acid sequence of *FvGELP1* consists of specific conserved residues for the GDSL family. The catalytic triad and conserved motif of *FvGELP1* were explained by multiple sequence alignment with others GDSL esterase/lipase enzyme (Figure 6). GDSL lipases established a lipolytic enzymes subclass indicated by a specific GDSL motif in the N-terminal of Gly-Asp-Ser-Leu (Akoh et al. 2004). The respective residues in *FvGELP1* are Gly^{43}-Asp^{44}-Ser^{45}. BnSCE3/BnLIP2 (*Brassica napus*) and OsEst1 (*Oryza sativa*) have an Ile / Leu exchange (Clauss et al. 2008; Hamada et al. 2012). *FvGELP1* contains Ser^{45}, Asp^{46}, and His^{50} as the catalytic triad similar to other GDSL-motif proteins (Upton and Buckley 1995). The seryl residue is located in block I, while aspartyl and histidyl residues are part of block V. In addition, the SGNH hydrolases are
designated as a subgroup of the GDSL family depending on the existence of Serine in block I, Glycine in block II, Asparagine in block III, and Histidine in block V residues (Mølgaard et al. 2000). FvGELP1 belongs to SGNH hydrolases within the GDSL subclass. It is characterized by the existence of the conserved residues Ser, Gly, Asn, and His in the conserved peptide block I, block II, block III and block V, respectively (Mølgaard et al. 2000; Ling et al. 2006). Each of the conserved residues shows an essential function in enzyme catalysis. The Ser residue acts as the catalytic nucleophile. In addition, the Ser together with the Gly and the Asn residues contribute as proton donors to the oxyanion hole. The His residue serves as a base which deprotonating the hydroxyl group, thus generating the active site Ser more nucleophilic (Akoh et al. 2004). Furthermore, GDSL esterases/lipases have a flexible active site that is able to change their conformation with the binding of different substrates.

Figure 6. Multiple sequence alignment of FvGELP1. Sequences resemble the subsequent accession numbers and species: GLIP1 (NP_198915.1, A. thaliana), OsEST1 (AK061229.1, Oryza sativa), WLD1 (AK067429), RHA 1 (UniProtKB-Q00017, Aspergillus aculeatus), and BnSCE3 (AAX62802.1, Brassica napus). The blue lines box indicates a fully conserved residue. Four conserved peptide blocks (block I, block II, block III, and block V) in the SGNH-hydrolases family are in the red frame box (Ling et al. 2006). The catalytic triad of Ser, Asp, His residues in blocks I and V are marked by red triangles.
Cloning and expression of FvGELP1

The correct size bands (1.2 kb) have been amplified from cDNA of F. vesca and F. × ananassa fruits (excluding from F. × ananassa small green fruit) (Figure 7). According to Shulaev et al. (2011), the gene27964 consists of 1,161 bp. These amplified fragments were cloned into PSK+ plasmid and transformed into E. coli NEβ10. The sequence alignment of the genes from F. × ananassa and F. vesca resulted in 51% and 100% identity with FvGELP1, respectively. In addition, translation analysis of the nucleotide sequence amplified from cDNA of F. × ananassa fruits revealed many stop codons. Therefore, FvGELP1 amplified from F. vesca fruit cDNA was selected for further cloning and heterologous expression in S. cerevisiae. FvGELP1 was expressed as a 43 kDa His-tagged fusion protein (Figure 8). GDSL esterases/lipases have a molecular weight of 22-60 kDa (Akoh et al. 2004).

Esterase assay of FvGELP1

Esterase assays were performed using small molecule esters such as α-NA, pNPA, phenyl acetate, and benzyl acetate as substrates to investigate the enzymatic activity of FvGELP1. GDSL esterases/lipases exhibit a broad range of substrate specificity. FvGELP1 esterase assays revealed positive results for phenyl acetate, benzyl acetate, pNPA, and αNA. It released high content of aromatic alcohol products (Figure 9). These suggest that FvGELP1 is a promiscuous hydrolase catalyzing a range of low molecular weight esters. The results also indicated that FvGELP1 shows the activity of carboxylesterases.

A p-nitrobenzyl (pNB) carboxy-esterase from Bacillus subtilis hydrolyzed simple organic esters for instance benzyl acetate, pNB-acetate and αNA (Chen et al. 1995). Cbes-AcXE2 (a Caldicellulosiruptor bescii acetyl xylan esterase) catalyzed phenyl acetate, p-nitrophenyl butyrate (pNPB), and pNPA with equivalent efficiency. Phenyl acetate as the most preferred substrate showed $K_M$ and specific activity of 0.85 mM and 142 U/mg, respectively (Soni et al. 2017). OsEST1 from Oryza sativa strictly recognizes small molecule esters. It demonstrated high enzymatic activity for αNA with $V_{\text{max}}$ of 63.7 μmol min$^{-1}$ mg$^{-1}$ and $K_M$ of 172 μM. Its relative activity for α-naphthyl butyrate (αNB) was significantly lower than αNA. Furthermore, OsEST1 showed negligible activity using triglycerides as substrates such as tributyrin and olive oil. The latest implied that OsEST1 is not a lipase (Hamada et al. 2012). Eno1d8 from Medicago sativa exhibited esterase activity for acetyl and butyryl esters as substrates however not for longer chain aliphatic esters (Pringle and Dickstein 2004). GLP2, GDSL lipase 2 protein from Arabidopsis thaliana showed lipase activity. It catalyzed pNP acetate, and pNP butyrate hydrolysis (Lee et al. 2009). Although the preliminary enzymatic activity of FvGELP1 has been determined, further research is needed to study the biological role of FvGELP1 throughout strawberry fruit ripening.

Figure 8. Recombinant FvGELP1 produced in S. cerevisiae: A. SDS PAGE, B. western blot analysis. M: protein marker, CE: crude extract, FT: flow through, W: wash, EL1 and EL2: elution

Figure 7. The amplified bands from cDNA of F. vesca and F. × ananassa fruits. A. Amplification of gene27964 from F. × ananassa (1-5) and F. vesca (6) fruit. 1: small green, 2: large green, 3: white, 4: tuning, 5: red fruit of F. × ananassa, 6: ripe fruit of F. vesca. M: DNA marker. Target gene27964 (1.161 bp) bands are shown by an arrow. B. Restriction enzyme analysis of recombinant FvGELP1 using SmaI and XhoI. M: DNA marker, 1: gene27964 and PSK+ plasmid band
In conclusion, this study is successfully identified and characterized a new enzyme in strawberry namely FvGELP1 (Fragaria vesca GDSL esterase/lipase). FvGELP1 showed hydrolase activity against small molecule esters such as α-NA, pNPA, benzyl acetate, and phenyl acetate. Therefore, FvGELP1 might involve in strawberry fruit ripening, possibly by deacetylation of the polysaccharide.

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