ORIGINAL PAPER

Comparative analysis of fruit volatiles and related gene expression between the wild strawberry *Fragaria pentaphylla* **and cultivated** *Fragaria* **×** *ananassa*

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Received: 18 January 2017 / Revised: 1 May 2017 / Accepted: 17 June 2017 / Published online: 27 June 2017 © Springer-Verlag GmbH Germany 2017

Abstract *Fragaria pentaphylla*, one of several wild strawberry species, produces white or red fruits. The white fruits have a stronger aroma than the red. In this study, solidphase microextraction was used in combination with gas chromatography–mass spectrometry to compare volatiles during fruit development and maturation from the two fruit types of *F. pentaphylla* and the cultivated $F \times \alpha$ *ananassa*. A total of 38 volatile compounds were identifed in $F \times \alpha$ *nanassa*, while 61 and 53 volatile compounds were identifed in the white and red fruits of *F. pentaphylla*, respectively. The predominant volatiles in white ripe fruits of *F. pentaphylla* were 3(2*H*)-furanone 4-methoxy-2,5 methyl (24.71%), butanoic acid, 2-methyl, methyl ester (10.43%), trans-2-hexenal (9.23%). The main volatiles in red ripe fruits of *F. pentaphylla* were 2-hexenal (21.23%), 1-hexanol (13.29%) and 2-hexen-1-ol acetate (13.00%). While the main volatiles in ripe fruits of $F \times \alpha$ *ananassa* were butanoic acid, ethyl ester (25.80%), 2-hexenal (23.47%) and butanoic acid, 2-methyl (10.09%). In addition, cyclopropane propyl was frst found in the white fruits

Electronic supplementary material The online version of this article (doi[:10.1007/s00217-017-2935-x](https://doi.org/10.1007/s00217-017-2935-x)) contains supplementary material, which is available to authorized users.

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of wild *F. pentaphylla* at high levels (4.83%). As the intense aroma of the white fruits of *F. pentaphylla* is characteristic of high 3(2*H*)-furanone 4-methoxy-2,5 methyl production. RNA-seq was used for quantitative analysis of volatilesrelated gene expression. Integrative analysis of GC–MS data and RNA-seq data from fruits of *F. pentaphylla* indicated that reduction of sugar in red fruits of *F. pentaphylla* might lead to a relatively lower DMF and higher aldehydes and alcohols compared with that in white fruits.

Keywords Strawberry · Volatile compounds · SPME–GC/ MS · RNA-seq

Abbreviations

Introduction

Strawberry (*Fragaria* × *ananassa*) is a popular fruit crop worldwide [[1\]](#page-15-0). In 2012, global strawberry production reached 4.5 million tons, two times more than the sum of all other berries ([http://faostat.fao.org/\)](http://faostat.fao.org/). Cultivated strawberries, however, often lack favour and fragrance [\[2\]](#page-15-1), and production of berries with diverse aroma patterns requires breeding of strawberry cultivars. Compared to cultivated strawberries, wild strawberries (*Fragaria* species) produce smaller fruits and lower yields, but more diverse aroma patterns, which are directly related to the production of volatile compounds. Comparisons of the volatile compounds of wild *Fragaria* species and cultivated strawberries may provide valuable information for future breeding efforts to produce more appealing cultivars.

Different patterns of volatiles in cultivated strawberries and other wild strawberries have been reported [\[3,](#page-15-2) [4](#page-15-3)]. More than 360 compounds have been found in cultivated strawberry (*F.* × *ananassa*), predominantly esters, aldehydes, furanones, sulfuric and terpenic compounds [[5–](#page-15-4)[9](#page-15-5)]. Among them, the most abundant aroma compounds are methylbutanoate, ethyl butanoate, ethyl hexanoate and methyl 2-methylbutanoate [[10,](#page-15-6) [11\]](#page-15-7). However, the major favour compounds in wild *F. vesca* are methyl anthranilate, butyl formate, octyl acetate, decyl acetate, benzyl acetate, carveyl acetate, decyl butanoate, methyl nicotinate and methyl *N*-formylanthranilate [[12\]](#page-15-8). Furthermore, the monoterpene linalool is more abundant in cultivated strawberries, while terpenoids and ketones are present at higher levels in wild berries [\[3](#page-15-2), [4\]](#page-15-3). However, with the exception of *F. vesca* [\[2\]](#page-15-1), *F. moschata* L. [[2](#page-15-1)], and *F. virginiana* Mill. [[13](#page-15-9)], little focus has been placed on the volatile chemical patterns of the other wild *Fragaria* spp.

Fragaria pentaphylla, one of the wild strawberry species, produces white or red fruits. The white fruits have a stronger aroma than the red [[14](#page-15-10)] and therefore provide a good model to study volatility patterns and their impact on aroma and favour. In this study, solidphase microextraction was used in combination with solid phase microextraction and gas chromatography– mass spectrometry (SPME–GC/MS) and RNA-seq techniques for quantitative analysis of volatile compounds and their related gene expression, respectively. Volatile compounds from two types of *F. pentaphylla* fruits were compared to the cultivated $F_r \times \alpha$ *ananassa* during fruit development and maturation. The results expand our knowledge of the biosynthesis and regulation of volatiles, which play important roles in the breeding of cultivated strawberries.

Materials and methods

Fruit collection

Wild strawberry *F. pentaphylla* with unripened fruit were collected in July 2012 in Mao County (31°41′16″N, 103°52′41″E), Chengdu City, Sichuan Province, China. The plants were transplanted to a walk-in growth chamber at Taizhou University, Zhejiang Province, China. The plants were grown at day/night temperatures of 20/15 °C, with a photoperiod of 10/14 h, with 75% constant humidity. When the fruits were ripened, 18 red fruits of *F. pentaphylla* were random collected and six fruits were mixed as one sample, three samples of fruits were used for the analysis. And the same was repeated for white fruits. The fruits were immediately frozen in liquid nitrogen and stored at −80 °C for RNA-seq.

The cultivated strawberry *F. ananassa* Duch. cv '*Benihoppe*' was bought in November 2012 from a cooperative society in Linhai City, Zhejiang Province, China, and transplanted to the walk-in growth chamber under the same conditions noted above. In June 2015, when the cultivated and wild strawberries were fowering, hand cross-pollination was conducted to produce fruits. Two fruits per plant were collected at three ripening stages $[14]$ $[14]$: the unripe stage $(S1)$, the intermediate stage $(S2)$, and the ripe stage (S3), which corresponded to 22, 28, and 36 days after full bloom, respectively. Six fruits from different plants were mixed as one sample. The fruits were immediately frozen in liquid nitrogen and stored at −80 °C until chemical analysis.

Analysis of aroma volatiles

Strawberry fruit fesh was ground using a mortar, and 5 g was placed into a 15-mL vial which was fushed with nitrogen, then, the sample was equilibrated with stirring at 35 °C for 30 min in a water bath. After equilibration, a solid-phase microextraction (SPME) fbre (Supelco, Bellefonte, PA, USA), coated with an absorbent phase of polydimethylsiloxane/carboxen/divinylbenzene (PDMS/ CAR/DVB) was exposed to the headspace of the vial for 30 min, after which the fbre was inserted into a GC–MS (Agilent Technologies, Inc., Palo Alto, CA, USA) desorption 3 min for analysis. All the samples were prepared in triplicate.

Volatiles analysis was done with reference to method described previously with some modifcation [[15\]](#page-15-11). GC– MS analysis was performed on the Agilent 7890B (GC) coupled with a 5975C mass spectrometer (EI mode, 70 eV) (Agilent Technologies, Inc., Palo Alto, CA, USA). Helium was used as the carrier gas at a flow rate of 1 mL/

min with a splitless injection. Volatile compounds were separated using a DB-5 MS column (30 m \times 0.32 mm, 0.25 μ m) under the following conditions: 1 min at 50 °C, followed by an increase from 50 to 320 °C at a rate of 5 °C/min, where the temperature was maintained until the procedure was manually stopped. The injector and the interface temperature were 220 and 280 °C, respectively. The m/z range was from 29 to 450. Compound identification was performed using the data system library (NIST 11).

Volatile compounds was confrmed by comparing the mass spectra of the samples with the data system library (NIST 11), retention index (RI) and authentic references. Retention index (RI) of volatiles was calculated using the mixture of n-alkanes (C7–C40, purchased from Sigma-Aldrich, St. Louis, MO, USA) as standards. The standards compounds (hexanal, (*E*)-2-hexenal, 3(2*H*)-furanone,4 methoxy-2,5 methyl) were purchased from Sigma-Aldrich (St. Louis, MO, USA).

Expression analysis of aroma‑volatile genes by RNA‑seq

Total RNA was extracted from six red and six white fruit samples of ripe stage, and then quantifed. Total RNA was extracted in the TRIzol reagent (Life Technologies) according to the manufacturer's protocol. RNA concentration was quantifed using a Nanodrop 2000 spectrophotometer (Thermo Fisher Scientifc Inc., Wilmington, DE, USA) and the ratio of absorbance at 260 and 280 nm was calculated to evaluate the quality of RNA. Subsequently, mRNA was purifed using NEXTfex™ Poly(A) Beads and cDNA libraries were prepared. The cDNA libraries were quantifed using a Qubit 2.0 (Thermo Fisher Scientifc Inc., Wilmington, DE, USA), and the size distribution was assessed on an Agilent 2100 Bioanalyzer (Agilent Technologies, Inc. Santa Clara, CA, USA). The cDNA libraries were sequenced on an Illumina NextSeq 500 sequencing instrument (Illumina Inc., San Diego, CA, USA). All experiments were conducted at Tianke Hi-New Technology Co. Ltd. in Zhejiang Province, China. Raw RNAseq reads were trimmed for low quality, clean reads were determined by their error rate, Q20, Q30, and GC-contents. Then the clean reads were mapped to the *F. vesca* genome using Bowtie software, the number of mapped clean reads for each UniGene was counted and then normalized into RPKM value (reads per kb per million reads, which was widely used to calculate the UniGene expression) [\[16](#page-15-12)], and then the gene expression was represented as $log₂$ (foldchange) with the gene expression level in white ripe fruits as reference. Expression fold change of genes was calculated using DESeq [[17\]](#page-15-13). Any gene with an adjusted *p* value of $\langle 0.05 \rangle$ and \log_2 (fold change)| > 1 was determined to be differentially expressed gene (DEGs) [[18\]](#page-15-14).

KEGG enrichment analysis was conducted as the following. Firstly, the number of genes per pathway was calculated by mapping all of DEGs to the KEGG database [\(www.Genome.jp/keg/\)](http://www.Genome.jp/keg/), then the signifcantly enriched DEGs were found using the binormal test. The pathway with the Q value ≤ 0.05 is defined as pathway that is significantly enriched in the differentially expressed genes.

Statistical analysis

The signifcance of the different volatile profles was determined by one-way analysis of variance (ANOVA) using SPSS, version 17.0 (SPSS Inc., 2009). Principal component analysis (PCA) of the volatile compounds was performed using Soft Independent Modelling of Class Analogies (SIMCA-P, V.11.5) in Unscrambler (Camo Process AS, Oslo, Norway). Heat map was obtained using the Cluster Software package and the Multi Experiment Viewer.

Results

Qualitative analyses of volatile compounds

A total of 61 volatile compounds were identifed in the white fruits of *F. pentaphylla*, of which 29, 26, and 38 compounds were detected in the S1, S2 and S3 stages, respectively. Fifty-three volatile compounds were identifed in the red fruits of *F. pentaphylla,* of which 17, 20, and 35 compounds were detected in the S1, S2 and S3 stages, respectively. Thirty-eight volatile compounds were detected in cultivated fruits of *F.* × *ananassa*, of which 10, 8, and 33 compounds were detected in the S1, S2 and S3 stages, respectively (Table [1\)](#page-3-0). In the ripened white fruits of *F. pentaphylla*, the profile was as follows (Fig. [1a](#page-10-0)): aldehydes (fve compounds), 15.86%; alcohols (seven compounds), 7.41%; hydrocarbons (three compounds), 7.82%; acids (two compounds), 5.58%; ketones (one compound), 24.71%; esters (16 compounds), 37.72%; and other compounds (four), 0.90%. In the ripened red fruits of *F. pentaphylla*, the profle of the volatiles was as follows: aldehydes (four compounds), 30.71%; alcohols (fve compounds), 21.97%; hydrocarbons (three compounds), 1.30%; acids (two compounds), 1.61%; ketones (two compounds), 9.50%; esters (13 compounds), 31.65%; and other compounds (six), 3.26%. In the ripened fruits of *F.* × *ananassa*, the profle of the volatiles was as follows: aldehydes (two compounds), 23.62%; alcohols (three compounds), 5.02%; hydrocarbons (one compounds), 0.35%; acids (three compounds), 11.80%; ketones (four compounds), 6.46%; esters

Table 1 continued

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 Amounts of volatiles were expressed by total peak area Relative amounts of volatile compounds were expressed by relative peak area

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Fig. 1 Variation in the relative peak area (**a**) and total peak areas (**b**) of the volatile compounds of the white fruits of *F. pentaphylla* (*W*), red fruits of *F. pentaphylla* (*R*) and cultivated fruits of *F.* \times *ananassa* (*C*) at the unripe (*S1*), intermediate (*S2*) and ripe stages (*S3*)

(18 compounds), 51.85%; and other compounds (two), 0.89%. As shown in Fig. [1b](#page-10-0), the total amounts of volatile compounds in both the red and white fruits of *F. pentaphylla* was higher than that in $F \times \alpha$ *ananassa* ($p < 0.01$), while no signifcant difference occurred between the red and white fruits of *F. pentaphylla.*

The main volatile compounds in the white ripe fruits of *F. pentaphylla* were 3(2*H*)-furanone 4-methoxy-2,5 methyl (DMF) (24.71%), butanoic acid, 2-methyl, methyl ester (10.43%), trans-2-hexenal (9.23%), 2-hexen-1-ol, acetate (6.28%), and hexanal (5.72%). The content of DMF declined during the early stages and then rose rapidly, reaching its highest value (24.71%) at maturity (Fig. [2](#page-11-0); Table [1](#page-3-0)). 2-Methyl butanoic acid methyl ester was not detected in the early stages, but reached a relative content of 10.43% at maturity. The content of 2-hexenal and hexanal continuously decreased with fruit maturity; 2-hexenal dropped from 41.77% in the unripe stage to 9.23% at maturity, while hexanal fell from 13.10 to 5.72%. The content of 2-hexen-1-ol acetate was slightly lower during early development and then sharply increased to a maximum value of 6.28% at maturity. In addition, cyclopropane propyl was found in the white fruits of wild *F. pentaphylla* at high levels (4.83%), which is the frst report of this compound in white fruit strawberries.

In the red ripe fruits of *F. pentaphylla*, the main volatiles detected were 2-hexenal (21.23%), 1-hexanol (13.29%), 2-hexen-1-ol acetate (13.00%), hexanal (8.94%), 2-hexenol (7.71%), and DMF (7.19%). 2-Hexenal increased from 13.32 to 21.23%, while the content of 1-hexanol and 2-hexenol increased to 12.82 and 7.44%, respectively. 2-Hexen-1-ol acetate increased early and then decreased to 13.00% at the ripe fruit stage. The maximum amount of DMF appeared in unripe fruit (S1), decreased rapidly to the lowest value (S2) and then increased slightly to 7.19% at the ripe fruit stage.

The main components in ripe fruits of $F \times \alpha$ *ananassa* were butanoic acid ethyl ester (25.80%), 2-hexenal (23.47%), 2-methyl butanoic acid (10.09%), and hexanoic acid ethyl ester (8.75%), DMF (5.31%). The two main esters (butanoic acid ethyl ester and hexanoic acid ethyl ester) were observed only in ripe fruits. The highest value of 2-hexenal occurred in the unripe fruit stage (S1) at 80.41% and then gradually decreased to 23.47% at maturity.

PCA and heat map analysis showed that the volatile compounds of the wild and cultivated species were well differentiated in CS2 and CS3 (Figs. [2,](#page-11-0) [3\)](#page-12-0).

RNA‑seq analysis and aroma‑related gene expression in the red and white fruits of *F. Pentaphylla*

An averaged 9,705,633 and 10,179,395 raw reads were produced from red fruit and white fruit, respectively. After the fltering out of the low-quality reads, an average of 9,646,731 and 10,102,495 clean reads remained for red fruit and white fruit, respectively. The reads from red fruit and white fruit were mapped approximately 53.93 and 53.28% of the reference genome (*F. vesca*), respectively (Table [2\)](#page-12-1).

Totally, 2271 DEGs were found between the red and white fruits of *F. pentaphylla*, of which 1164 up-regulated and 1107 down-regulated in red fruits of *F. pentaphylla* compared to the white fruits (Fig. [4a](#page-13-0)). In total, 20 categories of biological processes were enriched in the DEGs, and the most enriched pathway was "Biosynthesis of secondary metabolites" (Fig. [4b](#page-13-0)).

Fig. 2 Heat map analysis of all strawberries and volatile compounds during maturation. *Red colour* represents low levels, and *green colour* represents high levels. *WS1* indicates the white fruits of *F. pentaphylla* at the unripe stage; *WS2* at the intermediate stage; and *WS3*

at the ripe stage. *RS1* indicates the red fruits of *F. pentaphylla* at the unripe stage; *RS2* at the intermediate stage; and *RS3* at the ripe stage. *CS1* indicates the fruits of *F.* × *ananassa* at the unripe stage; *CS2* at the intermediate stage; and *CS3* at the ripe stage

To elucidate the genetic regulation of the volatile biosynthesis, the genes were fltered for these involved in the volatile biosynthesis pathway of *F. pentaphylla* (Supplementary Table 1). As fatty acid derivatives, aldehyde and alcohol are derived from the degradation of C18 unsaturated fatty acids (linoleic or linolenic acids) through "the lipoxygenase pathway" (Fig. [5\)](#page-14-0). The key step for producing aldehyde is the deoxygenation of unsaturated fatty acids, catalysed by lipoxygenase (LOX). Among nine identifed LOXs, four genes were signifcantly up-regulated in wild red fruits, resulting in the content of hexanal, the product of LOX, in red fruits was higher than that in white fruits as expected (red: 235.01, white: 112.04) (Supplementary Table 1). The aldehydes produced from the unsaturated fatty acid can be further degraded by alcohol dehydrogenases (ADHs). Among 15 identifed ADHs, fve genes were signifcantly expressed with two signifcantly up-regulated genes and three signifcantly downregulated genes in the red fruits. As the product of ADH, the content of hexenol in red and white fruits was 162.6 and 27.67, respectively (Supplementary Table 1). Finally, an ester can be generated from an alcohol by the catalysis of acyl transferases (AATs). Among two identifed AATs, only one gene was found to be signifcantly down-regulated in the red fruits (Fig. [5\)](#page-14-0). As the product of AAT, the content

Fig. 3 PCA score plot of the main sources of variability between strawberry samples. *WS1* indicates the white fruits of *F. pentaphylla* at the unripe stage; *WS2* at the intermediate stage; and *WS3* at the ripe stage. *RS1* indicates the red fruits of *F. pentaphylla* at the unripe stage; *RS2* at the intermediate stage; and *RS3* at the ripe stage. *CS1* indicates the fruits of $F \times \alpha$ *ananassa* at the unripe stage; *CS2* at the intermediate stage; and *CS3* at the ripe stage

of hexen-1-ol, acetate in red and white fruits was 162.6 and 27.67, respectively (Supplementary Table 1). Interestingly, a glyoxysome malate dehydrogenase was found to be signifcantly up-regulated in the red fruits.

Discussion

Composition of aroma

Although more than 360 compounds have been previously reported in strawberries [[19\]](#page-15-15), less than 20 compounds contribute signifcantly to strawberry favour in a proportional way [[11,](#page-15-7) [20\]](#page-15-16). According to the threshold value [\[20](#page-15-16)], the top 10 key aroma compounds (parts per billion) were β-ionone (0.007), DMF (0.03), DHF (0.04), ethyl butanoate (0.13), (*Z*)-3-hexenal (0.25), methyl anthranilate (3), linalool (6), eugenol (11), (*E*)-2-hexenal (16), and heptanone-2 (50).

Aroma furanones, which always present as DMF and DHF in fruit, are considered to be important volatile compounds with a caramel-like odour [\[21](#page-15-17)]. They always exist at very low levels in fruits; however, we found DMF to be the highest single compound in the white fruits, representing 24.71% of the total volatiles, far greater than the percentage observed in the wild red and cultivated fruits. In addition to DMF, 2-hexenal, hexanal, 2-hexen-1-ol, 2-hexen-1-ol acetate, and acetic acid hexyl ester were found at high levels in *F. pentaphylla*. Although all these compounds confer a positive, sweet favour to the aroma, only 2-hexenal has a relatively low threshold aroma value (17 ppb), contributing a green odour. The other compounds were considered to offer little contribution to favour because the threshold aroma value of these compounds is far more than that of the key aroma compounds mentioned above. Although the relative abundance of 2-hexenal in the wild white fruits was approximately 0.44 times less than that in the wild red fruits and cultivated fruits, considering the highest total amount of volatiles and highest level of DMF in the white fruits, we inferred that the aroma of the wild white fruits of *F. pentaphylla* is far stronger than that of the wild red and cultivated fruits, which is consistent with the description in "fora of China" and report by Risser and Navatel [\[14](#page-15-10)], more than that, it even better than those of other wild strawberries, such as *F. vesca,* characterized by high levels of methyl anthranilate [\[20](#page-15-16)].

The characteristic compounds (DMF and 2-hexenal) in the wild white fruits may confer a positive, pleasant character to their favour and possess important properties, such as attractant, anti-carcinogenic, and fungicidal properties [\[22](#page-15-18), [23](#page-15-19)].

For the frst time, we report the identifcation of cyclopropane propyl and cyclohexanol in strawberries. Although

RS3 means red fruits at ripe stage, -1,-2,-3 means triplicate. WS3 means white fruits at ripe stage, -1,-2,-3 means triplicate

Fig. 4 Analysis of the differentially expression genes (DEGs) between the red fruits and white fruits of *F. pentaphylla.* **a** Histogram of different expressed genes ($p < 0.05$). **b** Statistics of pathway enrichment; *Total* means total numbers of DEGs between the red ripe

fruits and white ripe fruits of *F. pentaphylla*; *Up* means up-regulated DEGs; *Down* means down-regulated DEGs; *Red vs White* means the white fruits were used as the reference; *White vs Red* means the red fruits were used as the reference

alkanes have little impact on favour [[19\]](#page-15-15), the extent to which these novel compounds contribute to favour still needs to be studied.

Synthetic pathway of aroma

Furanones are unique group of favour molecules with extremely low odour thresholds. It has been suggested that furanones are synthesized from p-fructose 1,6-bisphosphate. Although it is not clear how the furanone ring is synthesized and which enzymes are involved [\[24](#page-15-20)], studies in yeast and tomato suggest that phosphorylated carbohydrates serve as potential precursors of furanones [\[25](#page-15-21), [26](#page-15-22)]. Hexose and pentose are primary photosynthetic products and may serve as excellent aroma precursors of furanones without degradation of the carbon skeleton [\[6](#page-15-23)]. They originate from the degradation of starch through glycolytic pathway, so the total soluble sugar content in fruits may be strongly infuenced by the biosynthesis of furanones; the lower sugar content found in wild red fruits and corresponding low DMF level supports this speculation.

Furthermore, DMF decreases dramatically from unripe to ripened wild red fruits. Availability of carbohydrates for DMF synthesis reduces because a large amount of carbohydrates are needed for the biosynthesis of anthocyanins at the colour-changing stage in red fruits [\[27](#page-15-24)].

Aldehydes are synthesized via the lipoxygenase (LOX) pathway from C18 unsaturated fatty acids, which undergo deoxygenation catalysed by LOX and hydroperoxide lyase (HPL) [[28\]](#page-15-25). The aldehydes are further reduced by alcohol dehydrogenase and then by alcohol acyl transferases (AATs) to esters [[29\]](#page-15-26). These compounds are associated with fresh green fragrances [[30](#page-15-27)] and are known as "greenleaf volatiles" (GLV) [[29\]](#page-15-26); their content always decreases as fruits ripen, and they are often produced in response to wounding and pest attack [\[31,](#page-15-28) [32](#page-15-29)]. We observed a continuous decrease in "GLV" content in the white fruits of *F. pentaphylla* and fruits of *F.* × *ananassa.* In contrast, in the red fruits of *F. pentaphylla*, GLVs showed a continuously increasing abundance during fruit development. Moreover, signifcantly up-regulated *LOX* expression and higher content of hexanal were found in the red

Fig. 5 Features of carbon and lipid metabolism in *F. pentaphylla*. $Log₂$ (fold change) of differentially expressed genes between the red and white strawberries of *F. pentaphylla* (*Red vs White*, *p* < 0.05) are presented as *bars*. The *bar* above zero means the gene expression level was up-regulated in red fruits compared with that in white fruits. The *bar* below zero means the gene expression level was downregulated in red fruits compared with the white that in white fruits. The compounds marked in *gray box* means it was higher in red fruits than that in white fruits, while the compounds marked in *white box*

means it was lower in red fruits than that in white fruits. *R* wild red fruit, *W* wild white fruit, *LOX* lipoxygenase, *ADH* alcohol dehydrogenase, *AAT* alcohol acyl transferases, *UFGT* favonoid-3-*O*-glucosyltransferase, *F1,6P* fructose 1,6-diphosphate, *DMF* 3(2*H*)-furanone 4-methoxy-2,5 methyl, *3-PGA* 3-phosphoglycerate, *PEP* phosphoenolpyruvic acid, *ShikA* shikimate, *Phe* phenylalanine, *Tyr* tyrosine, *Glc* glucose, *Pg* pelargonidin, *Pg3glc* 3-*O*-β-glucopyranosides of pelargonidin, *Cy* cyanin, *Cy3glc* 3-*O*-β-glucopyranosides of cyanidin

fruits compared with the white fruits of *F. pentaphylla.* These results imply that red fruit-bearing plants experience selection pressures, although there was little difference in wounding between the wild white and red fruits. At the end of LOX pathway, only one signifcantly downregulated AAT and lower product conversion rate (Supplementary Table 2) in red fruits compared with the white fruits, suggesting that hexenol might have other degradation pathways. Feussner et al. [[33](#page-15-30)] reported an alternative pathway associated with the expression of *LOX* and lipid metabolism. Unsaturated fatty acids are catalysed to their corresponding hydroxides, which are later degraded via glyoxysomal β-oxidation. Recently, Fan et al. [[34\]](#page-15-31) also suggested that lipids may metabolize to starch via glyoxysomal β-oxidation in oleaginous *Chlorella* spp. The signifcant up-regulation of glyoxysomal malate dehydrogenase and 3-ketoacyl-CoA thiolase in wild red fruits supports the metabolic fux of unsaturated fatty acids to the tricarboxylic acid cycle via a LOX-dependent pathway in red fruits. Although energy use is less effective in this pathway $[35]$ $[35]$, it may be sufficient to compensate for the energy loss as glucose is metabolized during the synthesis of anthocyanin in red fruits. Therefore, we speculated that the reduction of sugar and correspondingly low DMF leads to increased LOX activity, ultimately resulting in a high level of aldehydes and alcohols (Fig. [5](#page-14-0)). Having known that the glyoxylate cycle plays a central role in the use of stored oil in oilseeds [[36\]](#page-15-33), more studies should be conducted to verify the presence of the glyoxylate cycle in fruits.

Acknowledgements This work was fnancially supported by the National Natural Science Foundation of China (No. 31261120580).

Compliance with ethical standards

Confict of interest The authors declare that they have no confict of interest.

Compliance with ethical requirements This research does not contain any studies with human or animal subjects.

References

- 1. Hancock JF (1999) Strawberries. CAB International, Oxford
- 2. Negri AS, Allegra D, Simoni L, Rusconi F, Tonelli C, Espen L, Galbiati M (2015) Comparative analysis of fruit aroma patterns in the domesticated wild strawberries "Profumatadi Tortona" (*F. moschata*) and "Reginadelle Valli" (*F. vesca*). Front. Plant Sci 6(56):1–13
- 3. Ulrich D, Olbricht K (2013) Diversity of volatile patterns in sixteen *Fragaria vesca* L. accessions in comparison to cultivars of *Fragaria* × *ananassa*. J Appl Bot Food Qual 86:37–46
- 4. Ulrich D, Olbricht K (2014) Diversity of metabolite patterns and sensory characters in wild and cultivated strawberries. J Berry Res 4:11–17
- 5. Menager I, Jost M, Aubert C (2004) Changes in physicochemical characteristics and volatile constituents of strawberry (Cv. Cigaline) during maturation. J Agric Food Chem 52:1248–1254
- 6. Bood KG, Zabetakis I (2002) The biosynthesis of strawberry favor (II): biosynthetic and molecular biology studies. J Food Sci $67(1):2-8$
- 7. Forney CF (2001) Horticultural and other factors affecting aroma volatile composition of small fruit. Horttechnology 11:529–538
- 8. Azodanlau R, Darbellay C, Luisier JL, Villettaz JC, Amado R (2003) Quality assessment of strawberries (*Fragaria* species). J Agric Food Chem 51:715–721
- 9. Azodanlau R, Darbellay C, Luisier JL, Villettaz JC, Amado R (2004) Changes in favour and texture during the ripening of strawberries. Eur Food Res Technol 218:167–172
- 10. Larsen M, Poll L (1992) Odour thresholds of some important aroma compounds in strawberries. Z Lebensm Unters FA 195:120–123
- 11. Schieberle P, Hofmann T (1997) Evaluation of the character impact odorants in fresh strawberry juice by quantitative measurements after sensory studies on model mixtures. J Agric Food Chem 45:227–232
- 12. Pyysalo T, Honkanen E, Hirvi T (1979) Volatiles of wild strawberries, *Fragaria vesca* L., compared to those of cultivated berries, *Fragaria ananassa* cv. Senga Sengana. J Agric Food Chem $27:19 - 22$
- 13. Ulrich D, Komes D, Olbricht K, Hoberg E (2007) Diversity of aroma patterns in wild and cultivated *Fragaria* accessions. Genet Resour Crop Evol 54:1185–1196
- 14. Risser G, Navatel JC (1997) Phenologic stages of strawberry plant. In strawberry: plant and varieties. Ctif, Paris
- 15. Cheng H, Chen JL, Li X, Pan JX, Xue SJ, Liu DH, Ye XQ (2015) Differentiation of the volatile profles of Chinese bayberry cultivars during storage by HS–SPME–GC/MS combined with principal component analysis. Postharvest Biol Technol 100:59–72
- 16. Mortazavi A, Williams BA, McCue K, Schaeffer L, Wold B (2008) Mapping and quantifying mammalian transcriptomes by RNA-Seq. Nat Methods 5(7):621–628
- 17. Anders S, Huber W (2010) Differential expression analysis for sequence count data. Genome Biol. doi[:10.1186/](https://doi.org/10.1186/gb-2010-11-10-r106) [gb-2010-11-10-r106](https://doi.org/10.1186/gb-2010-11-10-r106)
- 18. Love MI, Huber W, Anders S (2014) Moderated estimation of fold change and dispersion for RNA-seq data with DESeq 2. Genome Biol 15:550–570
- 19. Schwab W, Davidovich-Rikanati R, Lewinsohn E (2008) Biosynthesis of plant-derived favor compounds. Plant J 54:712–732
- 20. Ulrich D, Hoberg E, Rapp A, Kecke S (1997) Analysis of strawberry favour discrimination of aroma types by quantifcation of volatile compounds. Z Lebensm Unters FA 205:218–223
- 21. Latrasse A (1991) Fruits III. In: Maarse H (ed) Volatile compounds in food and beverages. Marcel Dekker, Inc., New York, USA
- 22. Farine JP, Le Quere JL, Duffy J, Everaerts C, Brossut R (1994) Male sex pheromone of cockroach *Eurycotis foridana* (Walker) (Blattidae, Polyzosteriinae): role and composition of tergites 2 and 8 secretions. J Chem Ecol 20:2291–2306
- 23. Slaughter JC (1999) The naturally occurring furanones: formation and function from pheromone to food. Biol Rev 74:259–276
- 24. Roscher R, Bringmann G, Schreier P, Schwab W (1998) Radiotracer studies on the formation of 2,5-dimethyl-4-hydroxy-3(2H)-furanone in detached ripening strawberry fruits. J Agric Food Chem 46:1488–1493
- 25. Sasaki M, Nunomura N, Matsudo T (1991) Biosynthesis of 4-hydroxy-2(or5)-ethyl-5(or 2)-methyl-3(2*H*)-furanone by yeasts. J Agric Food Chem 39:934–938
- 26. Hauck T, Hubner Y, Bruhlmann F, Schwab W (2003) Alternative pathway for the formation of 4,5-dihydroxy-2,3-pentanedione, the proposed precursor of 4-hydroxy-5-methyl-3(2*H*)-furanone as well as autoinducer-2, and its detection as natural constituent of tomato fruit. BBA 1623:109–119
- 27. Petroni K, Tonelli C (2011) Recent advances on the regulation of anthocyanin synthesis in reproductive organs. Plant Sci 181(3):219–229
- 28. Feussner I, Wasternack C (2002) The lipoxygenase pathway. Annu Rev Plant Biol 53:275–297
- 29. Olias JM, Sanz C, Rios JJ, Perez AG (1995) Substrate specifcity of alcohol acyltransferase from strawberry and banana fruit. In: Rouseff RL, Leahy MM (eds) Fruit favors: biogenesis, characterization and authentication. American Chemical Society, Washington, DC, USA
- 30. Poll L, Lewis MJ (1986) Volatile components of elderberry juice. Lebensm Wiss Technol 19:258–262
- 31. Matsui K (2006) Green leaf volatiles: hydroperoxide lyase pathway of oxylipin metabolism. Curr Opin Plant Biol 9:274–280
- 32. Hamilton-Kemp TR, Archbold DD, Collins RW, Yu KS (2003) Emission patterns of wound volatile compounds following injury of ripe strawberry fruit. J Sci Food Agric 83:283–288
- 33. Feussner I, Kuhn H, Wasternack C (2001) The lipoxygenase dependent degradation of storage lipids. Trends Plant Sci 6:268–273
- 34. Fan JH, Ning K, Zeng XW, Luo YC, Wang DM, Hu JQ, Li J, Xu H, Huang JK, Wan MX, Wang WL, Zhang DJ, Shen GM, Run CL, Liao JJ, Fang L, Huang S, Jing XY, Su XQ, Wang AH, Bai LL, Hu ZM, Xu J, Li YG (2015) Genomic foundation of starch-to-lipid switch in oleaginous *Chlorella* spp. Plant Physiol 169:2444–2461
- 35. Gerhardt B, Fischer K, Balkenhohl TJ, Pohnert G, Kühn H, Wasternack C, Feussner L (2005) Lipoxygenase-mediated metabolism of storage lipids in germinating sunfower cotyledons and β-oxidation of (9Z,11E,13S)-13-hydroxy-octadeca-9,11-dienoic acid by the cotyledonary glyoxysomes. Planta 220:919–930
- 36. Peter JE, Ian AG (2001) Re-examining the role of the glyoxylate cycle in oil seeds. Trends Plant Sci 6(2):72–77