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Data Article

Data in support of comparative analysis of strawberry proteome in response to controlled atmosphere and low temperature storage using a label-free quantification

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ABSTRACT

To elucidate the mechanisms contributing to fruit responses to senescence and stressful environmental stimuli under low temperature (LT) and controlled atmosphere (CA) storage, a label-free quantitative proteomic investigation was conducted in strawberry (*Fragaria ananassa*, Duch. cv. 'Akihime'). Postharvest volatile compounds were characterized following storage under different conditions. The observed post-storage protein expression profiles may be associated with delayed senescence features in strawberry [2]. A total of 454 proteins were identified in differentially treated strawberry fruits. Quantitative analysis, using normalized spectral counts, revealed 73 proteins common to all treatments, which formed three clusters in a hierarchical clustering analysis.

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Specifications table

Subject area	*Biology*
More specific subject area	*Fruit proteomics*
Type of data	*Table, figure*
How data was acquired	• *Shimadzu QP2010 gas chromatograph–mass spectrometer (GC–MS) (Shimadzu Co., Kyoto, Japan)* • *LTQ XL mass spectrometer (Thermo Fisher) with a Michrom captive spray nano-electrospray ionization (NSI) source, low energy collision-induced dissociation (CID)* • *NCBI Viridiplantae entries, a total of 278115 sequences updated on Dec. 31th 2011 (NIH, Bethesda, MD, USA)*
Data format	*Analyzed*
Experimental factors	*Harvested strawberry (Fragaria ananassa, Duch. cv. 'Akihime') was transferred to the laboratory, sorted to discard damaged and diseased fruits, then calyxes and pedicels were removed. The surface of the strawberries was cleaned with a 2% sodium dodecyl sulfate (SDS) solution, before sorting strawberries into different storage treatments: either in package with controlled atmosphere comprised of 2% O_2 and 12% CO_2, or in air at low temperature, or in air at room temperature. Samples for analysis were immediately frozen in liquid nitrogen, placed in sealable bags and stored at $-80\,^{\circ}C$. Three independent biological replicates were prepared using pooled tissue from twenty individual strawberries.*
Experimental features	• *Solid-phase microextraction (SPME) of volatile compounds* • *Label-free proteomic quantification*
Data source location	*Tianjin, China*
Data accessibility	*Data are available with this article.*

Value of the data

- Label-free approach on analysis of the strawberry proteome in response to storage conditions.
- Coordinated changes in postharvest volatile evolution are characterized.
- Candidate proteins shown here that represent important metabolic pathways may contribute to storage tolerance were identified.

1. Data, experimental design, materials and methods

A total of 454 proteins were identified in differentially treated strawberry fruits. Quantitative analysis, using normalized spectral counts, revealed 73 proteins common to all treatments, which formed three clusters in a hierarchical clustering analysis.

1.1. Plant materials and treatments

Strawberries (*Fragaria ananassa*, Duch. cv. 'Akihime') were harvested from the Xintai Farmhouse, Tianjin Economical and Developmental Area, P.R. China. Harvested strawberry fruits were transferred to the laboratory, sorted to discard damaged and diseased fruits, then calyxes and pedicels were removed. The surface of the strawberries was cleaned with a 2% sodium dodecyl sulfate (SDS) solution, before sorting strawberries into different storage treatments: either in package with CA comprised of 2% O_2 and 12% CO_2, or in air at LT, or in air at RT. Sample fruits for analysis were immediately frozen in liquid nitrogen, placed in sealable bags and stored at $-80\,^{\circ}C$. Three independent biological replicates were prepared using pooled tissue from twenty individual strawberries.