Data in Brief 4 (2015) 500–509

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data for proteomic profiling of Anthers from a photosensitive male sterile mutant and wild-type cotton (*Gossypium hirsutum* L.)

Ji Liu [a], Chaoyou Pang [a], Hengling Wei [a], Meizhen Song [a], Yanyan Meng [b], Jianhui Ma [c], Shuli Fan [a,*], Shuxun Yu [a,*]

[a] State Key Laboratory of Cotton Biology, Institute of Cotton Research, Chinese Academy of Agricultural Sciences, Anyang 455000, Henan Province, China
[b] Hubei Provincial Key Laboratory for Protection and Application of Special Plants in Wuling Area of China, College of Life Sciences, South Central University for Nationalities, Wuhan 430064, Hubei Province, China
[c] College of Life Sciences, Henan Normal University, Xinxiang 453007, Henan Province, China

ARTICLE INFO

Article history:
Received 15 June 2015
Received in revised form
23 June 2015
Accepted 23 June 2015
Available online 9 July 2015

Keywords:
Photosensitive
Male sterility
Tapetum
Exine
Proteome
Pollen development

ABSTRACT

Cotton is an important economic crop, used mainly for the production of textile fiber. Using a space mutation breeding technique, a novel photosensitive genetic male sterile mutant CCRI9106 was isolated from the wild-type upland cotton cultivar CCRI040029. To study the male sterile mechanisms of CCRI9106, histological and iTRAQ-facilitated proteomic analyses of anthers were performed. This data article contains data related to the research article titled *iTRAQ-Facilitated Proteomic Profiling of Anthers From a Photosensitive Male Sterile Mutant and Wild-type Cotton (Gossypium hirsutum L.)* [1]. This research article describes the iTRAQ-facilitated proteomic analysis of the wild-type and a photosensitive male sterile mutant in cotton. The report indicated that exine formation defect is the key reason for male sterility in mutant plant. The information presented here represents the tables and figures that detail the processing of the raw data obtained from iTRAQ analysis.

DOI of original article: http://dx.doi.org/10.1016/j.jprot.2015.05.031
* Corresponding authors.
E-mail addresses: liujicricaas@163.com (J. Liu), chypang@163.com (C. Pang), henglingwei@163.com (H. Wei), songmz@cricaas.com.cn (M. Song), baiyun405@163.com (Y. Meng), mjhui1983@163.com (J. Ma), fansl@cricaas.com.cn (S. Fan), yu@cricaas.com.cn (S. Yu).

http://dx.doi.org/10.1016/j.dib.2015.06.022

Specifications table.

Subject area	Biology
More specific subject area	Plant proteomics
Type of data	Table and figure
How data was acquired	Plant phenotype: DP72 light microscope (Olympus, Japan) Scan electron microscopy: scanning electron microscopy S-530 (HITACHI, Japan) Mass spectrometry: AB SCIEX Triple TOF 5600 System (AB SCIEX, USA) Quantitative real-time PCR: ABI 7500 real-time PCR system (Applied Biosystems, USA)
Data format	Processed
Experimental factors	No pretreatment of samples was performed
Experimental features	Total anther protein was extracted from mutant and wild-type plants by triplicate using a TCA–acetone method. Three replicates iTRAQ-facilitated proteomic analysis were conducted for protein identification and quantification. Any protein changed with $a \geq 1.5$-fold difference and a p-Value ≤ 0.05 in at least two replicates would thus be considered as a significant DEP in our data.
Data source location	Cotton anther samples were collected in Anyang, Henan Province, China. iTRAQ-facilitated proteomic analysis were conducted in Beijing Genomics Institute, Shenzhen, Guangdong Province, China.
Data accessibility	The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository with the dataset identifier PXD002209. The reviewer account: username, reviewer23539@ebi.ac.uk; password: 3ts0ERFU.

Value of the data

- An iTRAQ-based proteomic analysis in cotton anthers.
- Identification of 6,121 high-confidence proteins in cotton anther.
- There are 325 proteins show differential expression patterns between WT and MT.
- The data enrich the understanding of the molecular regulatory mechanisms of male sterility.

1. Experimental design

Using a space mutation breeding technique, a novel photosensitive genetic male sterile mutant CCRI9106 was isolated from the wild-type upland cotton cultivar CCRI040029. Histological and iTRAQ-facilitated proteomic analyses of anthers were performed to explore male sterility mechanisms of the mutant.

2. Materials and methods

2.1. Plant growth and anther collection

Two *G. hirsutum* L. genotypes, a PGMS mutant CCRI9106 and its WT line, CCRI040029, were used in this study. CCRI040029 was an elite upland variety bred in our lab, and the mutant line, CCRI9106, was created by space mutation in 2010 [2]. They were grown in an agronomic field in Anyang (Henan, China) from April to October (Fig. S1), and in Sanya (Hainan, China) from October to early April (Fig. S2). Thirty rows (8 m in length × 0.8 m in width) were prepared for each genotype, and every 10 rows formed one replicate. To test the pollen fertility, anthers were stained with Alexander's solution. Additionally, anthers from both MT and WT at different development stages were collected for further analysis.

2.2. Scan electron microscopy

For SEM (Fig. S3), anthers were infiltrated with 2.5% (v/v) glutaraldehyde in phosphate buffer (0.1 M, pH 7.2), dehydrated in a graded series of ethanol (from 30% to 100%), treated in acetone for