Data in Brief 1 (2014) 15–18

Contents lists available at ScienceDirect

Data in Brief

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

Data Article

Data for a comparative proteomic analysis of chloroplast biogenesis (*clb*) mutants

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ARTICLE INFO

Article history:
Received 17 July 2014
Received in revised form
28 July 2014
Accepted 28 July 2014
Available online 12 August 2014

Keywords:
Chloroplast development
Comparative proteomics
clb mutants
Arabidopsis thaliana

ABSTRACT

This data article contains data related to the research article titled **Proteomic analysis of chloroplast biogenesis (clb) mutants uncovers novel proteins potentially involved in the development of *Arabidopsis thaliana* chloroplasts** (de Luna-Valdez et al., 2014) [1]. This research article describes the 2-D PAGE-based proteomic analysis of wild-type and four mutant lines (*cla1-1*, *clb2*, *clb5* and *clb19*) affected in the development of *Arabidopsis thaliana* chloroplasts. The report concludes with the discovery of three proteins potentially involved in chloroplast biogenesis. The information presented here represent the tables and figures that detail the processing of the raw data obtained from the image analysis of the 2-D PAGE gels.

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http://dx.doi.org/10.1016/j.dib.2014.07.001

Specifications table

Subject area	Biology
More specific subject area	*Plant proteomics*
Type of data	*Tables and fiures*
How data was acquired	***Electron microscopy***: *Images were extracted from* [2,3,4] ***2-D PAGE and image analysis***: *GS-800 densitometer* (*Bio-Rad Hercules, CA, EUA*); *image analysis software PD-Quest 8.0.1* (*Bio-Rad Hercules, CA, EUA*) ***Mass Spectrometry***: Matrix-Assisted Laser Desorption/Ionization-Time of Flight; Autoflex, Bruker Daltonics, Billerica, MA, USA
Data format	*Processed.*
Experimental factors	*No pretreatment of samples was performed.*
Experimental features	*Total protein was extracted from mutant and wild-type plants by triplicate. 2-D PAGE gel images were generated and compared in order to discover reliable (T-test $P < 0.01$) spots with abundance shift of at least ± 2-fold.*
Data source location	*NA.*

Value of the data

- The data further validate the information presented in de Luna-Valdez et al. (2014) [1].
- The data present alternative ways of visualizing the abundance of the proteins under study.
- The data provide specifics on the biochemical processes affected in all the analyzed clb mutants.

Direct link to deposited data in public repository
The data is directly available in this article and related to de Luna-Valdez et al. (2014) [1].

1. Experimental design

Total protein was extracted from 16-days old mutant and 8-days old wild-type plants by triplicate. 2-D PAGE gel images were generated and compared in order to discover reliable (*T*-test $P < 0.01$) spots with abundance shift of at least ± 2-fold. Protein identification was performed using MALDI-TOF Mass spectrometry.

2. Material and methods [1]

2.1. Plant material and growth conditions

Arabidopsis thaliana heterozygous mutant lines corresponding to *cla1-1* (At4g15560) [2], *clb2* (At3g11945) [3], *clb19* (At1g05750) [4], *clb5* (At3g04870) [3,5], *emb1241* (SALK_045238), *pbp1* (SAIL_773_D06), and *atrabe1b* (SALK_069644) were used in this study (Fig. S1, S2). Seeds were surface-sterilized using solutions of 100% C_2H_6O and 1% NaClO, then cultured on 0.5X Murashige & Skoog media supplemented with 0.05 g/l 2-(N-morpholino)ethanosulfonic acid, 0.5 g/l sucrose, 100 mg/l myo-inositol, 1 mg/l nicotinic acid, 1 mg/l pyridoxine-HCl, 10 mg/l thiamine-HCl, and 8 g/l phyto agar. Seedlings from the four mutant lines that presented the wild-type phenotype and the first pair of true leaves were harvested after 8 days of culture. These were then pooled for processing as the wild-type protein samples used in this study. In order to minimize the effect of using plants in different developmental stages (detection of development-related proteins), pigment-deficient plants were collected after 16 days of culture; at this time, all the seedlings display at least the first pair of true leaves. Three biologically independent seedling batches were generated for further processing.