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Data Article

Gel-based and gel-free proteome data associated with controlled deterioration treatment of *Glycine max* seeds

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ABSTRACT

Data presented here are associated with the article: “In-depth proteomic analysis of soybean (*Glycine max*) seeds during controlled deterioration treatment (CDT) reveals a shift in seed metabolism” (Min et al., 2017) [1]. Seed deterioration is one of the major problems, affecting the seed quality, viability, and vigor in a negative manner. Here, we display the gel-based and gel-free proteomic data, associated with the CDT in soybean seeds. The present data was obtained from 2-DE, shotgun proteomic analysis (label-free quantitative proteomic analysis) using Q-Exactive, and gene ontology analysis associated with CDT in soybean seeds (Min et al., 2017) [1].

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Specifications Table

Subject area	Biology
More specific subject area	Plant science, Proteomics, Controlled Deterioration Treatment (CDT)
Type of data	Tables and Figures
How data was acquired	MALDI-TOF/TOF-MS (ABI4800, Applied Biosystems, Framingham, MA, USA) and QExactive™ Orbitrap High-Resolution Mass Spectrometer (Thermo Fisher Scientific, USA) coupled with UHPLC Dionex UltiMate® 3000 (Thermo Fisher Scientific, USA) system
Data format	Raw, Analyzed
Experimental factors	CDT in soybean seeds
Experimental features	CDT related proteins were characterized
Data source location	Department of Functional Crop, National Institute of Crop Science (NICS), Rural Development Administration (RDA), Miryang, South Korea (latitude 35N)
Data accessibility	Data within this article and the ProteomeXchange Consortium via the PRIDE [6] partner repository with the dataset identifier PXD006064

Value of the data

- The presented data show a shift in diverse metabolic processes in soybean seeds under CDT stress condition.
- A total of 1626 proteins were identified from label-free quantitative proteome analysis by Q-Exactive and 31 proteins from 2-DE under CDT.
- This data provide new evidences on CDT associated changes in low abundance proteins (LAPs) proteome profiles and metabolic process in soybean seeds.

1. Data

The dataset reported here was obtained from the proteome analysis of CDT exposed soybean seeds, analyzed by gel-based (1-DE and 2-DE) and gel-free (label-free proteome) approaches (Figs. 1 and 2). [Supplementary Table 1–4](#) representatively show list of identified proteins from gel-based ([Supplementary Table. 1](#)) and gel-free ([Supplementary Table 2–5](#)) proteomic analysis. Furthermore, gene ontology and pathway analysis indicated major metabolic changes during CDT in soybean seeds [1].

2. Experimental design, materials and methods

2.1. Plant materials

Soybean seeds were collected from the experimental field of National Institute of Crop Science (NICS), Rural Department Administration (RDA) at Miryang, Korea. The soil was supplemented with a standard RDA N-P-K fertilizer (N-P-K=3-3-3.3 kg/10 acre). Seeds were harvested in October (average temperature 23.5 ± 3.5 °C, average day length 12 h 17 min).

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