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Data Article

Label-free proteome data of susceptible and resistant rice cultivars in response to *Xanthomonas oryzae* pv. *oryzae* inoculation

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ABSTRACT

Here we report the data associated with the article: "Comparative proteome profiling of susceptible and resistant rice cultivars identified an arginase involved in rice defense against *Xanthomonas oryzae pv. oryzae*" [1]. Bacterial blight disease caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) is one of the most devastating diseases of rice across the globe; however, the underlying molecular mechanism of rice-*Xoo* interaction is currently not well understood. In this manuscript, we report the proteome profiles of rice leaves generated using a label-free quantitative proteomic analysis using QExactive™ Orbitrap High-Resolution Mass Spectrometer, MapMan, and rice interactome viewer [1].

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Specifications Table

Subject	Biology
Specific subject area	Plant science, Proteomics, Plant-pathogen interaction
Type of data	Table, Figure
How the data were acquired	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
Description of data collection	Leaf proteomes of *Xoo* susceptible (Dongjin) and resistant (Hwayeong) cultivars were analyzed after 0, 3d, and 6d in response to inoculation of K1 strain of *Xoo*
Data source location	Plant Immunity Laboratory, Department of Plant Science, Pusan National University, Miryang, South Korea (latitude 35 N)
Data accessibility	With this article. All raw data are deposited in the ProteomeXchange with the dataset identifier PXD027569. Direct FTP link to data: http://proteomecentral.proteomexchange.org/cgi/GetDataset?ID=PXD027569
Related research article	R. Gupta, C.W. Min, S. Son, G.H. Lee, J.W. Jang, S.W. Kwon, S.R. Park, S.T. Kim, Comparative proteome profiling of susceptible and resistant rice cultivars identified an arginase involved in rice defense against *Xanthomonas oryzae* pv. *oryzae*, Plant Physio. Biochem. 171 (2022) 105–114 [1].

Value of the Data

- Data reported here show the comparative protein profiles of two rice cultivars that are susceptible (Dongjin) and resistant (Hwayeong) to *Xoo* strain KACC10859 (K1).
- This data show that the proteins related to photosynthesis and photorespiration were majorly decreased in resistant cultivar while proteins associated with jasmonic acid biosynthesis, protein modification, and proteolysis were majorly increased.
- Researchers working in the area of plant-pathogen interaction can use this dataset to check the abundance pattern of 4214 identified rice proteins in response to *Xoo* inoculation.
- Further, the information derived from this dataset can be translated to other pathosystems to predict the abundance of various host plant proteins in response to pathogen attack.
- Taken together, this data provide a list of potential protein candidates that can be targeted in the future to generate the *Xoo* resistant rice cultivars.

1. Data Description

The dataset reported here was obtained from the proteome analysis of two rice cultivars Dongjin and Hwayeong challenged with the K1 strain of *Xoo*. A shotgun proteomics approach was utilized for the identification of proteins and a label-free approach was utilized for their quantification. Downstream data processing and filtering were performed using Perseus software (Fig. 1) and functional annotation of the *Xoo* responsive proteins in the two cultivars was carried out by MapMan analysis (Figs. 2,3 and 5). Interactions among the Hwayeong specific proteins were analyzed by rice interactome viewer (Fig. 4). Supplementary Tables 1, 2, and 3, representatively show the list of *Xoo* responsive rice proteins (Supplementary Table. 1), Hwayeong and Dongjin specific proteins (Supplementary Table. 2), and results of interactome analysis (Supplementary Table. 3).

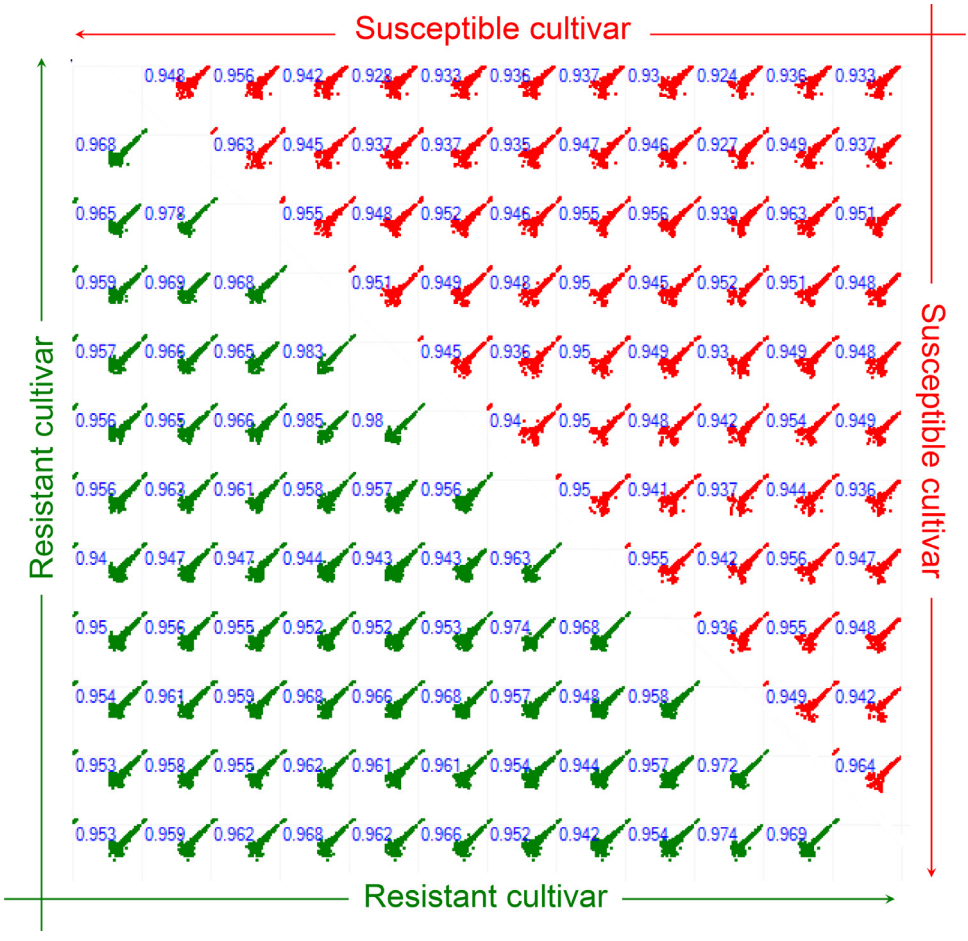

Fig. 1. Multi-scatterplots showing pearson correlation coefficient values among different replicates of the samples.

2. Experimental Design, Materials and Methods

2.1. Plant materials

Oryzae sativa ssp. *japonica* cultivars Dongjin and Hwayeong seeds were surface-sterilized sequentially with 70% ethanol for 1 min and 5% sodium hypochlorite for 5 min. These seeds were then planted in the soil after their complete washing in deionized water and allowed to germinate and at 28 °C with a 16 h/8 h day/night cycle.

2.2. Xoo *treatment and protein extraction*

Xoo strain KACC10859 (K1) showing compatible and incompatible interactions with Dongjin and Hwayeong rice cultivars was used for the experimentation. *Xoo* was cultured in PSA agar media and was inoculated on rice leaves using a clipping method as described previously [2]. Extraction of rice leaf proteins and enrichment of low-abundance proteins were carried out as described in detail previously [3]. In brief, 1 g of Dongjin and Hwayeong leaves harvested after

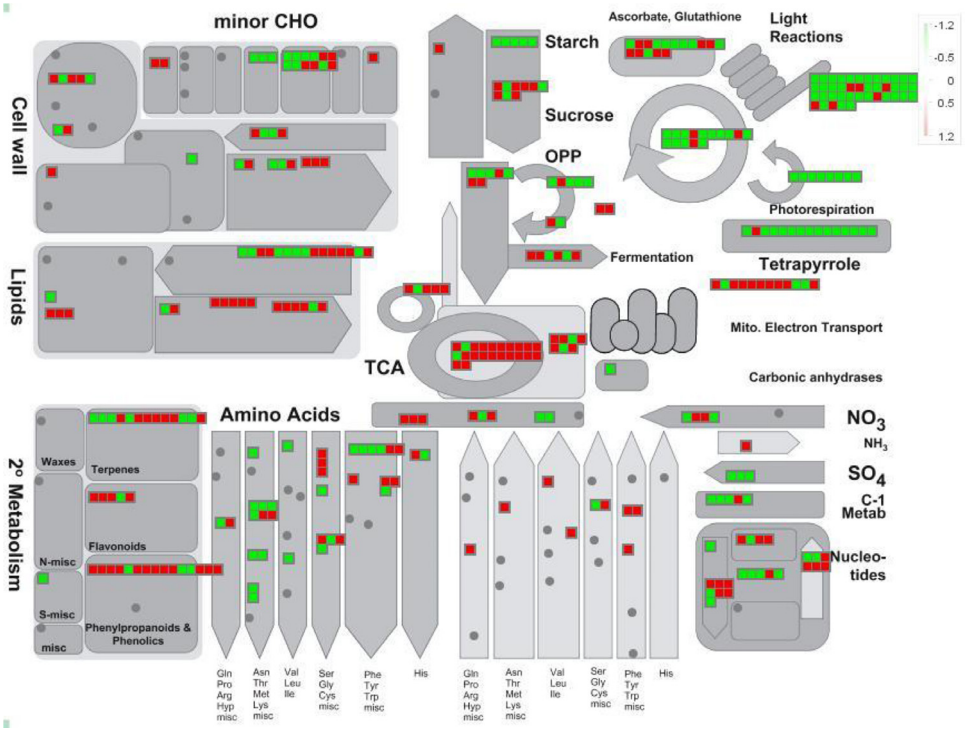

Fig. 2. Major CHO metabolism overview category of MapMan showing differential modulation of Dongjin and Hwayeong proteins corresponding to clusters 1 and 2 of Fig. 2A.

0,3 and 6 days were powdered using liquid nitrogen followed by the addition of 10 mL of Tris-Mg/NP-40 buffer and centrifugation at 12,000 × *g* for 15 min at 4 °C. The supernatant obtained after centrifuge was treated with 0.1% Protamine Sulfate (w/v, in deionized water) for 30 min to enrich the low-abundance proteins which were subsequently used for the proteome analysis.

2.3. Label-free quantitative proteome analysis with Q-Exactive

The isolated proteins were carried out label-free quantitative proteome analysis using QExactive ™ Orbitrap High-Resolution Mass Spectrometer (Thermo Fisher Scientific, USA) coupled with UHPLC Dionex UltiMate ® 3000 (Thermo Fisher Scientific, USA) system as described previously [1]. In brief, rice leaf proteins were digested using in-solution trypsin digestion and further mass spectrometry analysis was carried out as described in detail previously [1] (Supplementary Tables. 1 and 2). The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [4] partner repository with the dataset identifier PXD027569 and can be accessed at https://www.ebi.ac.uk/pride/archive/projects/PXD027569.

2.5. Statistical test and functional classification

Analysis of raw mass spectrometry data and label-free quantitative proteome analysis was carried out using the MaxQuant software with integrated Andromeda search engine [5]. Further downstream data processing and the statistical test were performed using Perseus software

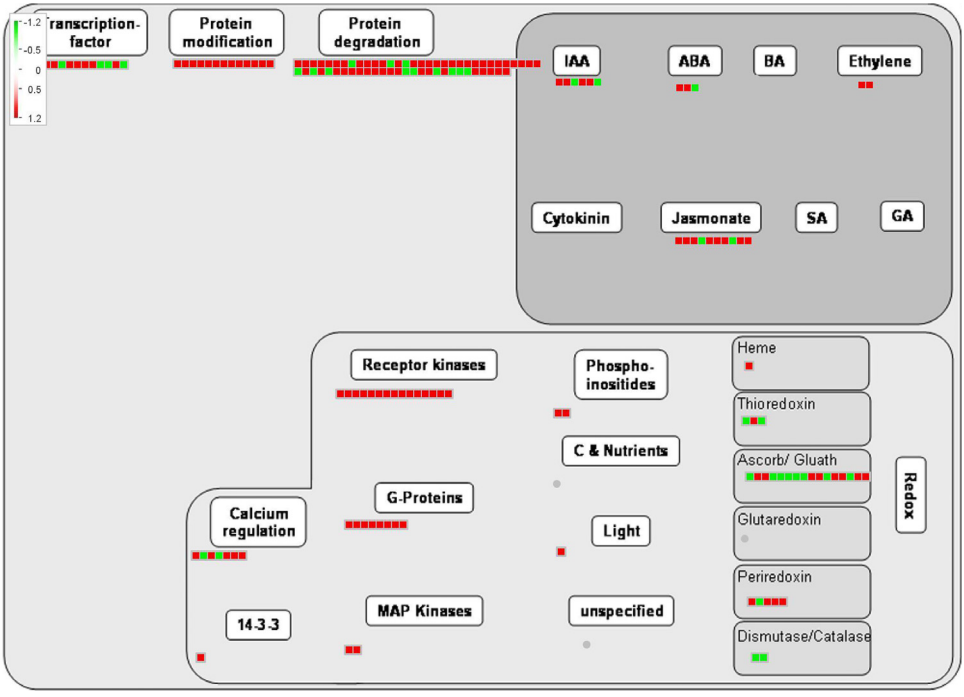

Fig. 3. Regulation overview category of MapMan showing differential modulation of Dongjin and Hwayeong proteins corresponding to clusters 1 and 2 of Fig. 2A.

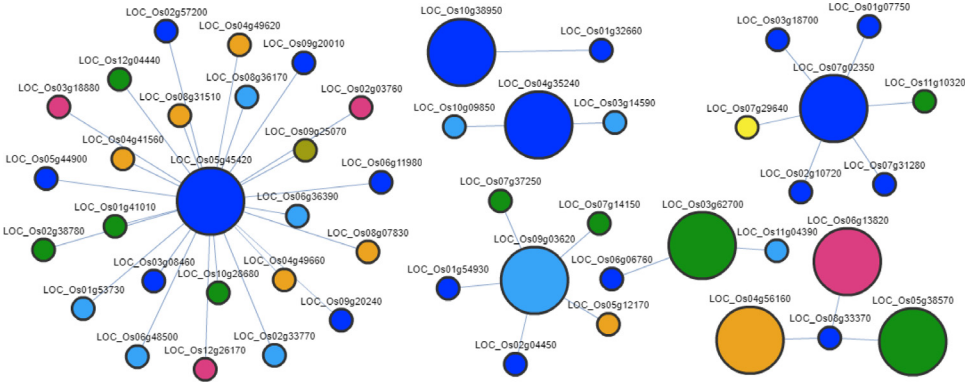

Fig. 4. Interaction network showing experimentally confirmed interactions among the Hwayeong specific proteins.

[6]. Multiple sample test was performed to find out significant differences (≥1.5 fold change, Benjamini-Hochberg-based FDR < 0.05) in the protein abundance following *Xoo* treatment (Supplementary Tables. 1 and 2). Differential proteins were functionally annotated using MapMan software [7].

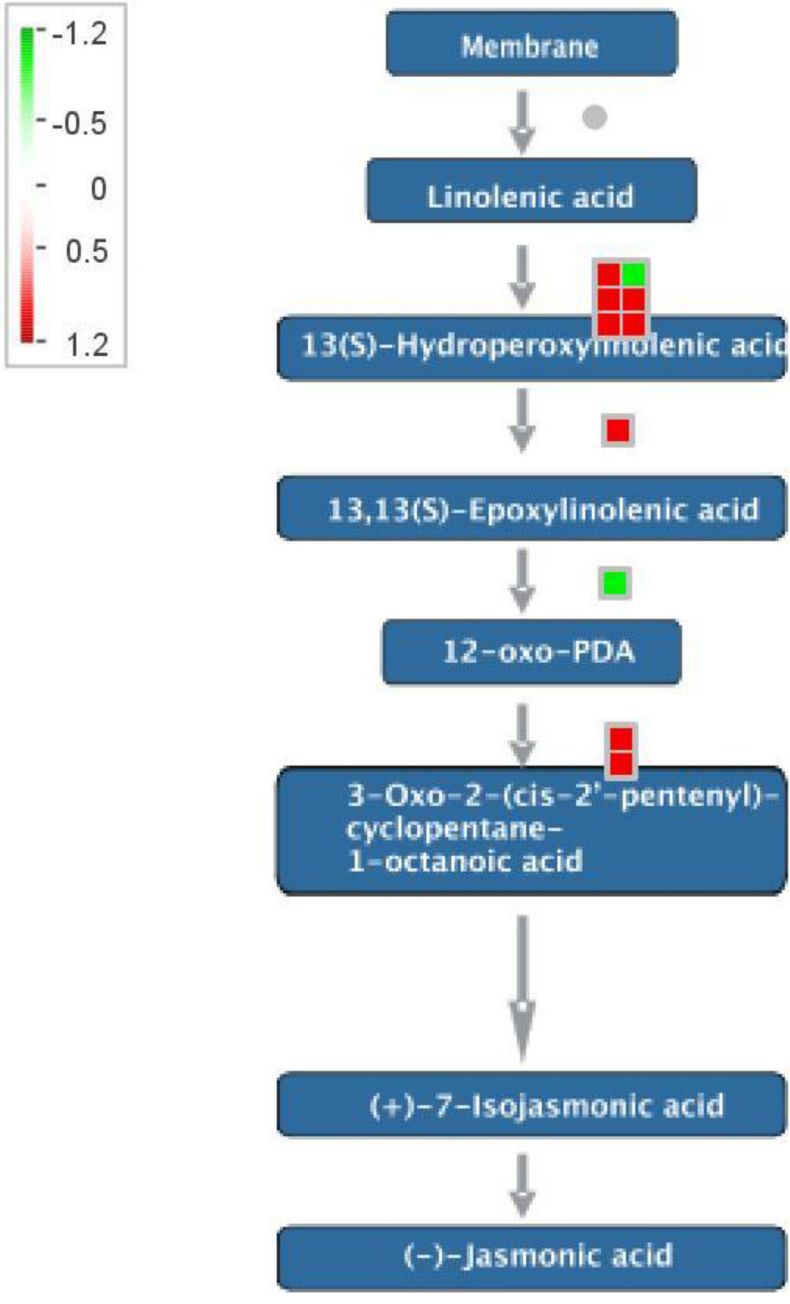

Fig. 5. Jasmonic acid biosynthesis pathway showing significantly modulated proteins marked by red (increased abundance) and green (decreased abundance) color scheme.

Ethics Statements

No animal experiments were performed in this study.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

CRediT Author Statement

Ravi Gupta: Conceptualization, Methodology, Software, Writing – original draft; **Cheol Woo Min:** Data curation; **Sang-Ryeol Park:** Supervision; **Sun Tae Kim:** Supervision, Writing – review & editing.

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Supplementary Materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2022.107890.

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