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Data article

Data set from a comprehensive phosphoproteomic analysis of rice variety IRBB5 in response to bacterial blight

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ABSTRACT

Bacterial blight (BB) caused by *Xanthomonas oryzae pv. oryzae* (*Xoo*) has become one of the most devastating diseases for rice, a major food source for over half of the world populations. To investigate the roles of protein phosphorylation in rice bacterial blight resistance, a quantitative phosphoproteomic study was conducted in rice variety IRBB5 at 0 h and 24 h after *Xoo* infection. 2367 and 2223 phosphosites on 1334 and 1297 representative proteins were identified in 0 h and 24 h after *Xoo* infection, respectively, out of which 762 proteins were found to be differentially phosphorylated. In associated with the published article "A comprehensive quantitative phosphoproteome analysis of rice in response to bacterial blight" in BMC Plant Biology (Hou et al., 2015) [1], this dataset article provided the detailed information of experimental designing, methods, features as well as the raw data of mass spectrometry (MS) identification. The MS proteomics data could be fully accessed from the ProteomeXchange Consortium with the dataset identifier PXD002222.

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Specifications Table

Subject area	*Biology*
More specific subject area	*Rice phosphoproteomics*
Type of data	*Table, excel files*
How data was acquired	*Easy-nLC1000 liquid chromatography system (Thermo) Q Exactive Plus (Thermo)*
Data format	*Raw, analyzed*
Experimental factors	*Rice plants of IRBB5 were obtained from China National Rice Research Institute (CNRRI). IRBB5 plants were inoculated with the Chinese representative strain of Xoo (Zhe173) at the booting stage by the leaf clipping method* [2]. *The concentrations of Xoo suspension is up to* 3×10^8 cfu/mL. *After inoculation, around* 5 cm *long IRBB5 leaves close to the clip position were collected immediately after Xoo inoculation* (0 h) *and at* 24 h *after inoculation* (24 h).
Experimental features	*Non-gel, label-free, quantitative phosphoproteomics*
Data source location	*China National Rice Research Institute, Hangzhou,* 311400, *P.R.China*
Data accessibility	*The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium* [3] *via the PRIDE partner repository with the dataset identifier PXD*002222. *Other datasets are directly provided with this article.*

Value of the data

- This data provided over 2000 phosphosites and phosphopeptides information of rice leaf proteins.
- The differential phosphorylation pattern indicates the potential function of phosphoproteins in rice disease resistance.

1. Data, experimental design, materials and methods

1.1. Experimental design

The leaf total protein of rice variety IRBB5 was isolated at the 0 h and 24 h after *Xoo* infection respectively. After the proteins were digested by trypsin, the peptides were enriched byTiO2 beads and applied for LC–MS/MS identification to explore the protein phosphorylation sites, intensities and dynamics (Supplemental Fig. 1).

1.2. Plant growth conditions and bacterial blight inoculation

Rice plants of IRBB5 (*xa*5) were obtained from National Rice Research Institute (CNRRI). IRBB5 (*xa*5) seedlings were grown in the net house of CNRRI. The cultivation and management of the rice in the net house proceeded as usual. IRBB5 plants were inoculated with the Chinese representative strain of *Xoo* (Zhe173) at the booting stage by the leaf clipping method [2]. The concentrations of *Xoo* suspension is up to 3×10^8 cfu/mL.

1.3. Total protein extraction

After inoculation, around 5 cm long IRBB5 leaves close to the clip position were collected immediately after *Xoo* inoculation (0 h) and at 24 h after inoculation (24 h). The total proteins were extracted using the urea-extraction method. Briefly, 1 g of rice leaf tissue was grinded into fine powder, lysed with 5 mL lysis buffer (150 mM Tris pH8.0, 8 M urea, 1 × phosphoprotein protease