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Data Article

Datasets for transcriptomic analyses of maize leaves in response to Asian corn borer feeding and/or jasmonic acid



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ABSTRACT

Corn is one of the most widely grown crops throughout the world. However, many corn fields develop pest problems such as corn borers every year that seriously affect its yield and quality. Corn's response to initial insect damage involves a variety of changes to the levels of defensive enzymes, toxins, and communicative volatiles. Such a dramatic change secondary metabolism necessitates the regulation of gene expression at the transcript level. In this paper, we summarized the datasets of the transcriptome of corn plants in response to corn stalk borers (*Ostrinia furnacalis*) and/or methyl jasmonate (MeJA). Altogether, 39,636 genes were found to be differentially expressed. The sequencing data are available in the NCBI SRA database under accession number SRS965087. Our dataset will provide more scientific and valuable information for future work such as the study of the functions of important genes or proteins and develop new insect-resistant maize varieties.

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Specifications Table

Subject area	<i>Molecular Biology</i>
More specific sub- ject area	<i>Volatile responses, insect herbivory, plant defense, transcriptomics</i>
Type of data	<i>The cDNA sequencing</i>
How data was acquired	<i>Illumina HiSeq 2500 sequencing platform</i>
Data format	<i>Raw reads in FASTQ format</i>
Experimental factors	<i>ACB damage, exogenous MeJA</i>
Experimental features	<i>Maize leaves were subjected to ACB feeding and/or application of exogenous MeJA before extraction of total RNA.</i>
Data source location	<i>Harbin, Heilongjiang province, China</i>
Data accessibility	Data is with this article are available in the NCBI SRA database under accession number SRS965087.

Value of the data

- The RNA-seq data allow the readers to access the transcriptomic profile of corn in response to Asian corn borer damage and MeJA stress.
- The data evaluate the utility of illumina platform for RNA-sequencing.
- Analyses of the significantly differentially expressed genes under Asian corn borer and MeJA treatment provide new targets for the development of insect-resistant maize varieties.
- Studies reveal maize defensive mechanism to the feeding of Asian corn borer and MeJA treatment.

1. Data

Over 50 million raw reads were generated for each experimental treatment (75,612,000 reads for maize exposed to Asian corn borer (ACB) feeding; 62,189,006 for jasmonic acid exposure; 61,528,872 for exposure to both treatments; 53,089,614 for the control). Data is available at the NCBI SRA database under accession number SRS965087.

2. Experimental design, materials and methods

2.1. Insect and plant resources

A colony of *Ostrinia furnacalis* (ACB) was maintained at College of Life Sciences, Heilongjiang University (Heilongjiang province, China) on an artificial diet (5 g vitamin C, 40 g yeast extract, 50 g barley powder, 60 g soybean powder, 14 mL ethylic acid (36%), 20 g agar powder, 1 g benzoic acid, 3 g sodium benzoate in 1000 mL ddH₂O). The ACB were reared at 28 °C under a 14 h light: 10 h dark photoperiod. Corn seeds of variety Longdan46 were provided by the Maize Research Institute of Heilongjiang Academy of Agricultural Science and cultivated in a greenhouse at 25 ± 1 °C, 60% humidity, and a 14 h light: 10 h dark photoperiod.

2.2. Insect feeding and MeJA treatments

Corn plants with four to five leaves were treated with ACB larvae (labeled as “CornOf2”), MeJA (labeled as “CornJA1”), or both (labeled as “CornJAOf2”). The control group was treated with 5 mL of

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