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Data Article

De novo transcriptome assembly associated with fumonisin production by the rice pathogen *Fusarium fujikuroi*

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ABSTRACT

The present study employed a next-generation sequencing method to assemble a *de novo* transcriptome database designed to distinguish gene expression changes exhibited by the fumonisin-producing fungus *Fusarium fujikuroi* when grown under 'fumonisin-producing' compared to 'non-fumonisin-producing' conditions. The raw data of this study have been deposited at DNA Data Bank of Japan (DDBJ) under the accession ID DRA006146.

Specifications Table

Subject area	Agriculture, Food safety
More specific subject area	Mycotoxins; Genes induced during fumonisin production
Type of data	Table, text file, figure

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How data was acquired	*De novo* transcriptome assembly was constructed using next-generation mRNA sequencing techniques using by the Illumina HiSeq 2000 sequencing system
Data format	Raw (FASTQ) sequences
Experimental factors	A *F. fujikuroi* strain was cultured for 7 days for total RNA extraction, sequencing, *de novo* transcriptome assembly and annotation
Experimental features	The gene expression changes exhibited by the fumonisin-producing fungus *F. fujikuroi* when grown under 'fumonisin-producing' compared to 'non-fumonisin-producing' conditions were studied
Data source location	Kanto region, Japan
Data accessibility	The raw data have been deposited at DNA Data Bank of Japan (DDBJ). http://trace.ddbj.nig.ac.jp/DRASearch/submission?acc=DRA006146

Value of the data

- The novel data base was constructed from a *F. fujikuroi* fungal strain which is postulated to be a source of fumonisin contamination of major crops such as rice and corn produced in Japan, due to its high prevalence in the country.
- The data presents an assemble of a *de novo* transcriptome library, with the aim of identifying changes to the gene expression profile of *F. fujikuroi* specimens grown under "fumonisin-producing" versus "non-fumonisin-producing"' culture conditions.
- Further analysis of the data presented here may enable the identification of novel genomic networks, and thereby promote a better understanding of the fumonisin induction pathway.

1. Data

Data reported here describe the fumonisin concentration, sequencing results obtained from the *de novo Fusarium fujikuroi* mRNA transcriptome (Table 1) and the conducted Gene Ontology (GO) functional analysis (Supplementary Fig. 1a-c). In addition, up- and down-regulated ($>$ 2-fold) genes under the two culture methods on fumonisin production were acquired by homology search using the tblastn (NCBI rice bakanae disease protein database) (Supplementary Table 1). A total of four raw sequence data were deposited into DDBJ DRA data base and can be accessed with the Bio Project accession number PRJDB6333.

(http://trace.ddbj.nig.ac.jp/BPSearch/bioproject?acc=PRJDB6333) under the Bio Sample accession numbers SAMD00093543.

(http://trace.ddbj.nig.ac.jp/BSSearch/biosample?acc=SAMD00093543) and SAMD00093544 (http://trace.ddbj.nig.ac.jp/BSSearch/biosample?acc=SAMD00093544).

1.1. Fumonisin (FB1) concentration

No FB1 was detected ($<$ 1 μg/L) either at the initiation of, or after 7 days of MO409 strain exposure to the non-fumonisin-producing growth conditions. In contrast, the concentration of FB1 reached 13 and 940 μg/L at the initiation of, and after 7 days of MO409 strain exposure to the fumonisin-producing growth conditions, respectively.