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Data article

Gene expression profiling data of *Schizosaccharomyces pombe* under nitrosative stress using differential display

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ABSTRACT

Excess production of nitric oxide (NO) and reactive nitrogen intermediates (RNIs) causes nitrosative stress on cells. *Schizosaccharomyces pombe* was used as a model to study nitrosative stress response. In the present data article, we have used differential display to identify the differentially expressed genes in the fission yeast under nitrosative stress conditions. We have used pure NO donor compound detaNONOate at final concentrations of 0.1 mM and 1 mM to treat the cells for 15 min alongside control before studying their gene expression profiles. At both the treated conditions, we identified genes which were commonly repressed while several genes were induced upon both 0.1 mM and 1 mM treatments. The differentially expressed genes were further analyzed in DAVID and categorized into several different pathways.

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Specifications table

Subject area	*Biology*
More specific subject area	*Molecular biology*

Abbreviations: NO, Nitric oxide; RNIs, Reactive nitrogen intermediates; DAVID, Database for annotation, visualization and integrated discovery; GO, Gene ontology; KEGG, Kyoto encyclopedia of genes and genomes

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Type of data	*Tables and figures*
How data was acquired	*Polymerase Chain Reaction (Applied Biosystems PCR System 9700), Denaturing Poly-acrylamide Gel Electrophoresis (Bio-Rad Sequi-Gen GT System) DNA sequencing using BigDye® Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems) and Applied Biosystems 3700 sequencer.*
Data format	*Analyzed using statistical tests*
Experimental factors	*Fission yeast cells were treated with pure NO donor compound detaNONOate at final concentrations of 0.1 mM and 1 mM alongside controls for 15 min.*
Experimental features	*RNA was extracted from the control and treated cells and converted to cDNA. PCR was performed using degenerate primers, products separated by denaturing poly-acrylamide gel electrophoresis. Differentially expressed transcripts were sequenced to identify the genes.*
Data source location	*Department of Biochemistry, University of Calcutta, Kolkata, West Bengal, India*
Data accessibility	*Data is with this article*

Value of the data

- The data shows the differentially expressed genes in the fission yeast under nitrosative stress which could be compared to differentially expressed genes in other stress conditions
- Comparison of the data with differentially expressed genes in other stress conditions could help in better understanding of the gene expression patterns under nitrosative stress
- The affected pathways under nitrosative stress could be compared to those affected under other stress conditions
- Based on the data detailed pathway oriented studies could be undertaken to understand the mechanism of nitrosative stress action

1. Data

To identify the differentially expressed genes in the fission yeast under nitrosative stress, cells were treated with two different doses of pure NO donor i.e. 0.1 mM and 1 mM for 15 min. It was previously reported that fission yeast *Schizosaccharomyces pombe* cells are much more sensitive to a concentration of 3 mM of detaNONOate than to 1 mM [1,2] in terms of cell growth, lowering the mitotic index, while cell viability is maintained at 95%. The differentially expressed genes are listed in Table 1. Treatment of the wild type *S. pombe* cells with NO donor compound detaNONOate at a concentration of 1 mM resulted in 9 genes to be repressed while 30 genes were identified as induced (Table 2). The differential expressions of 8 genes were confirmed by Real-Time (RT) PCR analysis. The gene expression profiles (up regulation or down regulation) obtained by differential display analysis and by RT-PCR are similar as listed in Table 3. Gene Ontology (GO) terms that were enriched in the differentially expressed gene lists were searched using the online tool DAVID. In order to identify the different pathways affected under nitrosative stress, the information provided in KEGG was referred. Genes were classified as belonging to the different pathways that were affected upon treatment with pure NO donor compound. Fig. 1 shows the 18 pathways that were significantly affected ($p < 0.01$) when the wild type *S. pombe* cells were treated with 0.1 mM concentration of pure NO donor

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