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Data Article

Data set for transcriptome analysis of *Escherichia coli* exposed to nickel

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ABSTRACT

Ni is recognized as an element that is toxic to humans, acting as an allergen and a carcinogenic agent, and it is also toxic to plants. The toxicity of Ni has been understudied in microorganisms. The data presented here were obtained by submitting the model bacterium *Escherichia coli* K-12 to nickel stress. To identify expressed genes, RNA-Seq was performed. Bacteria were exposed to 50 μM $NiCl_2$ during 10 min. Exposure to Ni lead to the deregulation of 57% of the *E. coli* transcripts. Further analysis using DAVID identified most affected biological pathways. The list of differentially expressed genes and physiological consequences of Ni stress are described in "Ni exposure impacts the pool of free Fe and modifies DNA supercoiling via metal-induced oxidative stress in *Escherichia coli* K-12" (M. Gault, G. Effantin, A. Rodrigue, 2016) [1].

Specifications Table

Subject area	*Biology*
More specific subject area	*Bioinformatics and microbiology*
Type of data	*Tables, figure*

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How data was acquired	*High-throughput RNA-sequencing*
Data format	*Filtered and analyzed with statistical tests*
Experimental factors	*The bacteria were grown in minimal medium until early log-phase where 50 μM $NiCl_2$ was added, after 10 min bacteria were harvested and frozen*
Experimental features	*Total RNA was extracted using the frozen acid-phenol method. ARNr were excluded. Directional libraries were sequenced on Illumina Hiseq2500 in single reads.*
Data source location	*Laboratory "Microbiologie, Adaptation et Pathogénie", UMR5240, INSA Lyon, France*
Data accessibility	*Data are with this article and deposited in NCBI's Gene Expression Omnibus (GEO), accessible through GEO Series accession number GEO:* GSE76167 http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE76167

Value of the data

- Ni, as many transition metals, is essential as a trace element to living organisms whereas it becomes toxic when present in excess. At present, the description of Ni toxicity in bacteria is under-studied although this metal is a widespread element bacteria are in contact with.
- The data shows differentially expressed genes under Ni stress that could be compared to differentially expressed genes in other metal-stress conditions or other stress conditions.
- Analysis of the biological pathways impacted when cells are exposed to Ni will help to understand the molecular mechanisms of Ni- or metal-stress.
- Identification of Ni-deregulated genes could lead to biotechnological applications such as the design of whole cell biosensors.

1. Data

The RNA-Seq and gene expression datasets were deposited in NCBI's Gene expression Omnibus [2], accessible through GEO series accession number GEO: GSE76176. Fig. 1 shows the distribution of deregulated genes in *E. coli* upon exposure to 50 μM Ni. 2545 genes were deregulated considering a Fold-Change (FC) of 1.5, representing 57 % of the 4440 annotated transcripts of *E. coli* K-12 strain W3110. Gene Ontology was applied to classify differentially expressed genes according to their biological function (see Fig. 1 in [1]). GO Terms that were enriched in the list of differentially expressed genes were identified using the DAVID tools (Database for Annotation, Visualization and Integrated Discovery) [3,4]. Pathways that were significantly affected were mapped using KEGG and are listed in Table 1.

2. Experimental design, materials and methods

2.1. Strains and growth conditions

E. coli K-12 cells were grown at 37 °C in minimal medium supplemented with glucose until O. $D._{600\ nm}$= 0.3 and then treated with 50 μM $NiCl_2$ during 10 min. These conditions lead to maximal expression of the Ni-stress marker gene *rcnA* (see Fig. S1A and S1B in [1]).