Data in Brief

Microarray analysis of *Neosartorya fischeri* using different carbon sources, petroleum asphaltenes and glucose-peptone

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Abstract

Asphaltenes are considered as the most recalcitrant petroleum fraction and represent a big problem for the recovery, separation and processing of heavy oils and bitumens. *Neosartorya fischeri* is a saprophytic fungus that is able to grow using asphaltenes as the sole carbon source [1]. We performed transcription profiling using a custom designed microarray with the complete genome from *N. fischeri* NRRL 181 in order to identify genes related to the transformation of asphaltenes [1]. Data analysis was performed using the genArise software. Results showed that 287 genes were up-regulated and 118 were down-regulated.

Here we describe experimental procedures and methods about our dataset (NCBI GEO accession number GSE68146) and describe the data analysis to identify different expression levels in *N. fischeri* using this recalcitrant carbon source.

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Table 1

GO classifications of the annotated genes. Annotated genes were separated in biological process, molecular function and Cellular component categories. Number of annotated genes are shown in brackets.

| Upregulated                  | Downregulated               |
|------------------------------|------------------------------|
| Biological process           |                              |
| Localization (9)             | Signaling (3)                |
| Biological regulation (10)   | Response to stimulus (8)     |
| Cellular process (51)        | Metabolic process (44)       |
| Metabolic process (62)       | Localization (6)             |
|                              | Biological regulation (10)   |
|                              | Celluar component organization or biogenesis (9) |
| Molecular function           |                              |
| Binding (49)                 | Transporter activity (4)     |
| Transporter activity (6)     | Structural molecule activity (4) |
| Catalytic activity (56)      | Nucleic acid binding transcription factor activity (7) |
|                              | Enzyme regulator activity (1) |
|                              | Catalytic activity (30)      |
|                              | Antioxidant activity (1)     |
|                              | Binding (37)                 |
| Cellular component           |                              |
| Organelle (18)               | Organelle (19)               |
| Cell (39)                    | Membrane enclosed lumen (8)  |
| Macromolecular complex (13)  | Membrane (9)                 |
|                              | Macromolecular complex (17)  |
|                              | Cell (34)                    |
|                              | Extracellular region (3)      |

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1 g/L KCl, 0.02 g/L FeSO₄·7H₂O, trace element 1 mL/L) supplemented with asphaltenes (400 mg/L). The cultures were incubated at 37 °C and shaken at 100 rpm for 24 h or 17 days for Saboraud and Czapek, respectively. The mycelium was frozen and disrupted with liquid nitrogen. The RNA extraction was performed using a TRI reagent kit (Sigma). RNA quality was tested in agarose gel.

2.2. Probe preparation and hybridization to arrays

For cDNA synthesis dUTP-Cy3 or dUTP-Cy5 was incorporated for each different growth condition, employing the CyScribe First-Strand cDNA labeling kit (Amersham). Incorporation of fluorophore was analyzed by using the absorbance at 555 nm for Cy3 and 655 nm for Cy5. Equal quantities of labeled cDNA were hybridized using hybridization solution UniHyb (TeleChem International Inc.), to the arrays for 14 h at 42 °C.

2.3. Data acquisition and analysis

Acquisition and quantification of array images were performed in GenePix 4100A with GenePix software by Molecular Devices. All images were captured using optimal laser power and 5 μm resolution. For each spot the Cy3 and Cy5 density mean value and the Cy3 and Cy5 background mean value were calculated with software ArrayPro Analyzer from Media Cybernetics.

Microarray data analysis was performed using genArise software, developed by the Computing Unit of the Institute of Cellular Physiology of UNAM (http://www.ifc.unam.mx/genarise/). This software carry out background correction, Lowess normalization, intensity filter, analysis of replicates and selection of differentially expressed genes to identify those that show accurate evidence of differential expression by calculating an intensity-dependent z-score. It uses a sliding window algorithm to calculate the mean and standard deviation within a window surrounding each data point, and define a z-score where z measures the number of standard deviations a data point is from the mean.

\[ z_i = \frac{|R_i - \text{mean}(R)|}{\text{sd}(R)} \]

where \( z_i \) is the z-score for each element, \( R_i \) is the log-ratio for each element, and \( \text{sd}(R) \) is the standard deviation of the log-ratio. With this criterion, the elements with a z-score > 2 standard deviations would be the significantly differentially expressed genes.

In order to perform functional annotation of the genes, sequences were aligned using the blast2go tool [2].

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**Fig. 1.** KEGG pathway reconstructions of metabolism of polycyclic aromatic hydrocarbons (PAH). Up-regulated genes coding for monoxygenase enzyme are shown in red.
3. Discussion

405 genes were differentially expressed (z-score > 2) from which 287 were up-regulated and 118 down-regulated. We obtain GO functional annotation for 203 genes. Results are summarized in Table 1.

41 sequences were encoded for enzymes from which 10 corresponded to oxidoreductases and 4 specifically for monooxygenases, which had been related to aromatic hydrocarbon degradation [3]. We used KEGG annotation in order to find pathway annotation of up-regulated genes (Fig. 1).

References

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