Data Article

Microarray expression profile of circular RNAs in lung tissues from rats with lipopolysaccharide-induced acute respiratory distress syndrome

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ABSTRACT

The data presented in this article are related to the research article entitled “The expression profiles of circRNAs in lung tissues from rats with lipopolysaccharide-induced acute respiratory distress syndrome (ARDS): A microarray study.” (Wan et al., 2017) [1]. ARDS remains a common and devastating syndrome. The development of circRNA microarray has facilitated the study of the role of circRNAs in regulating gene expression in ARDS. This research was designed to explore the expression profile of circRNAs in lung tissues from rats with lipopolysaccharide-induced ARDS. The field dataset is made publicly available to enable critical or extended analyzes.

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Keywords:
Microarray
Circular RNAs
Lipopolysaccharide
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Specialization Table

| Subject area          | Chemistry/Biology            |
|-----------------------|------------------------------|
| More specific subject area | Rat with ARDS                |
| Type of data          | Table                        |
| How data was acquired | Arraystar Rat CircRNA Array (8×15K, Arraystar) |
| Data format           | Raw and analyzed             |
| Experimental factors  | Lung tissues from 3 rats with lipopolysaccharide-induced ARDS vs. 3 normal rat lung tissues |
| Experimental features | Microarray expression profile analysis of circRNAs in rats with lipopolysaccharide-induced ARDS |
| Sample source location | Changsha, China             |
| Data accessibility    | Data are available via a web application (https://www.ncbi.nlm.nih.gov/geo/info/linking.html) |

Value of the data

- We first performed microarray detection on the expression profiles of circRNAs in lung tissues from rats with lipopolysaccharide-induced ARDS. The data are important and can be consulted by the other researchers in future research in this research area.
- Using circRNA microarray data, the other researchers can compare the circRNA expression profiles in ARDS lung tissues with others methods.
- This data allows the other researchers and research students to extend the statistical analyses.

1. Data

The dataset of this article provides information on the expression profiles of circRNAs in lung tissues from rats with lipopolysaccharide-induced ARDS. Microarray and sample annotation data were deposited in Gene Expression Omnibus under accession number GSE102523. Direct link to deposited data is [https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE102523](https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE102523).

2. Experimental design, materials and methods

2.1. Tissue samples and RNA preparation

Lung tissue samples were collected from Sprague Dawley rats undergoing lipopolysaccharide-induced ARDS and normal rats [1, 2]. Total RNA was isolated from 3 ARDS rat lung tissue samples and 3 normal rat lung tissues using TRIzol Reagent (Invitrogen, USA).

2.2. Labeling and hybridization

Sample labelling and microarray hybridization were performed according to the Arraystar’s standard protocols (Arraystar, Rockville, Maryland, USA) [1]. In short, total RNA was treated with Ribonuclease R (RNase R) (Epicenter, Madison, WI, USA) to remove linear RNAs. Then, enriched circRNAs were amplified and transcribed into fluorescent cRNA using a random priming method based on Arraystar Super RNA Labeling protocol. After the concentration and specific activity were measured using a NanoDrop ND-1000, the labelled cRNAs (pmol Cy3/μg cRNA) were then hybridized onto
**RNA Sample QC**
The purity and concentration of total RNA samples were determined with NanoDrop ND-1000. Results were provided in Sample QC report.

**RNA Labeling**
Total RNA from each sample was treated with Rnase R to enrich circular RNA. The enriched circular RNA was then amplified and transcribed into fluorescent cRNA utilizing randon primer according to Arraystar Super RNA Labeling protocol (Arraystar, Inc.).

**Array Hybridization**
The labeled cRNAs were hybridized onto the Arraystar Rat circRNA Arrays (8x15K, Arraystar), and incubated for 17 hours at 65°C in an Agilent Hybridization Oven.

**Array Scanning**
After washing, slides were scanned with the Agilent Scanner G2505C.

**Data Collection and Analysis**

The Arraystar Rat circRNA Arrays (8x15K, Arraystar). The circRNA expression microarray slides were incubated for 17 hours at 65°C in an Agilent Hybridization Oven. After washing the slides, the hybridized arrays were fixed and scanned with an Agilent G2505C Scanner.

It is worthy of note that part of the probes in rat chip were designed by using mouse and human orthology sequence, hoping to find similar circRNAs in rat through the junction site on account of High Gene homology.
2.3. Microarray and quality control

The acquired scanned images were imported into Agilent Feature Extraction software (version 11.0.1.1) for raw data extraction. The R software package limma package (R version 3.1.2) was used for quantile normalization and subsequent data processing. After quantile normalization of the raw data, low intensity filtering was performed, and the circRNAs that at least 2 out of 6 samples have flags in “P” or “M” (“All Targets Value”) were retained for further analyses. CircRNAs exhibiting P-value less than 0.05 and fold change greater than 2.0 were considered as significantly differentially expressed circRNAs.

The experiment workflow is listed in Fig. 1.

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Transparency document. Supporting information

Transparency data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2017.10.018.

References

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