Data in Brief 10 (2017) 38–40

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Microarray dataset on the genome-wide expression profile of an *M. smegmatis amtR* mutant (JR258) compared to *M. smegmatis* mc^{2}155

Michael Petridis [a], Gregory M. Cook [a,b,*]

[a] *Department of Microbiology and Immunology, Otago School of Medical Sciences, University of Otago, Dunedin 9054, New Zealand*
[b] *Maurice Wilkins Centre for Molecular Biodiscovery, The University of Auckland, Private Bag 92019, Auckland 1042, New Zealand*

ARTICLE INFO

Article history:
Received 13 September 2016
Received in revised form
14 October 2016
Accepted 15 November 2016
Available online 23 November 2016

ABSTRACT

The dataset presented here describes a microarray experiment to identify the AmtR regulon of *Mycobacterium smegmatis* comparing the transcription profile of a *M. smegmatis amtR* mutant to *M. smegmatis* wild-type. The raw and processed microarray data are available in the ArrayExpress database under Accession Number E-MTAB-4857 and interpretation of this data is found in the research article "Structure and function of AmtR in *Mycobacterium smegmatis*: implications for post-transcriptional regulation of urea metabolism through a small antisense RNA" (Petridis et al., in press) [1].

Specifications Table

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

DOI of original article: http://dx.doi.org/10.1016/j.jmb.2016.09.009
* Correspondence to: Department of Microbiology and Immunology, University of Otago, P.O. Box 56, Dunedin 9054, New Zealand.
E-mail addresses: michael.petridis@otago.ac.nz (M. Petridis), gregory.cook@otago.ac.nz (G.M. Cook).

http://dx.doi.org/10.1016/j.dib.2016.11.049

Type of data	*Text file,.xlsx file (Excel)*
How data was acquired	*Scanned Genepix 4000A scanner. Images were quantified using Spotfinder (TIGR). Total normalization and LOWESS normalization with MIDAS software (TIGR)*
Data format	*Raw, processed*
Experimental factors	*A markerless deletion of the amtR gene in the background of M. smegmatis mc^2155 was created.*
Experimental features	*Expression profiles of a M. smegmatis amtR mutant and M. smegmatis mc^2155 were determined during aerobic growth in Hartmans de Bont minimal medium.*
Data source location	*Not applicable*
Data accessibility	*Data within this article are available in the ArrayExpress database (https://www.ebi.ac.uk/arrayexpress/) under Accession Number E-MTAB-4857.*

Value of the data

- Description of the AmtR regulon gives insight into its role in the regulation of nitrogen metabolism in actinomycetes.
- Our data can be used to further clarify gene regulation through the two canonical transcription regulators AmtR and GlnR in response to nitrogen availability.
- The data can be used to characterize global regulatory networks in mycobacteria.

1. Data

Both raw and processed microarray data have been deposited in ArrayExpress with the Accession Number E-MTAB-4857 (https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-4857/). The dataset summarize changes in the transcription profile of a *Mycobacterium smegmatis amtR* mutant compared to *M. smegmatis* wild-type. Raw data files are the result of four independent biological replicates including two dye swaps and the columns IA and IB in the raw data files correspond to Cy3 and Cy5 values, respectively. The processed data file contains the combined differential gene expression data including statistical analysis.

2. Experimental design, materials and methods

2.1. Construction of amtR deletion mutant

For a detailed description for the *amtR* deletion mutant construction, see Petridis et al. [1].

2.2. Microarray analysis and quantitative real-time PCR

Total RNA from *M. smegmatis* wild-type and *M. smegmatis* JR258 Δ*amtR* was extracted as previously described [2]. The quality of the RNA (RIN > 9) was confirmed with the Bioanalyzer 2100 and the concentration was determined using a NanoDrop ND-100 spectrophotometer. RT-PCR was performed using SuperScript III (Invitrogen) according to the manufacturers instructions for cDNA synthesis and Phusion High-Fidelity PCR Kit (New England Biolabs) for PCR. Microarray analysis was performed using arrays provided by the Pathogen Functional Genomics Research Center (PFGRC) funded by the National Institute of Allergy and Infectious Diseases using protocols SOP# M007 and M008 from The Institute of Genomic Research (TIGR) [3]. The arrays were scanned using a Genepix 4000 A scanner and images were quantified using Spotfinder (TIGR) [3]. Total normalization and LOWESS normalization of the data were performed with the MIDAS software (TIGR) [3]. All data have been deposited in ArrayExpress with the Accession Number E-MTAB-4857.

Acknowledgements

This work was supported by the Maurice Wilkins Centre for Molecular Biodiscovery and a Marsden Grant from the Royal Society of New Zealand. G.M.C. was supported by a James Cook Fellowship from the Royal Society of New Zealand. MP was supported by a University of Otago Doctoral Scholarship, the Webster Center for Infectious Diseases and the Otago School of Medical Sciences.

Transparency document. Supplementary material

Transparency data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.11.049.

Appendix A. Supplementary material

Supplementary data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.11.049.

References

[1] M. Petridis, C. Vickers, J. Robson, J.L. McKenzie, M. Bereza, A. Sharrock, et al., Structure and function of AmtR in *Mycobacterium smegmatis*: implications for an AmtR/GlnR competitive binding mechanism for transcriptional regulation of urea metabolism, J. Mol. Biol. 428 (2016) 4315–4329.
[2] M. Petridis, A. Benjak, G.M. Cook, Defining the nitrogen regulated transcriptome of *Mycobacterium smegmatis* using continuous culture, BMC Genom. 16 (2015) 821.
[3] P. Hegde, R. Qi, K. Abernathy, C. Gay, S. Dharap, R. Gaspard, et al., A concise guide to cDNA microarray analysis, Biotechniques 29 (2000) 548–562.