



# Corrigendum: Changes in the Carbon Metabolism of *Escherichia coli*During the Evolution of Doxycycline Resistance

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Keywords: carbon metabolism, evolution, antibiotic resistance, DOX, Escherichia coli

# A Corrigendum on

# **OPEN ACCESS**

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Eric Altermann, AgResearch Ltd. New Zealand

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## Specialty section:

This article was submitted to Antimicrobials, Resistance and Chemotherapy, a section of the journal Frontiers in Microbiology

Received: 11 January 2022 Accepted: 13 January 2022 Published: 08 February 2022

## Citation:

Yang Y, Mi J, Liang J, Liao X, Ma B, Zou Y, Wang Y, Liang J and Wu Y (2022) Corrigendum: Changes in the Carbon Metabolism of Escherichia coli During the Evolution of Doxycycline Resistance. Front. Microbiol. 13:852577.

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by Yang, Y., Mi, J., Liang, J., Liao, X., Ma, B., Zou, Y., Wang, Y., Liang, J., and Wu, Y. (2019). Front. Microbiol. 10:2506. doi: 10.3389/fmicb.2019.02506

In the original article, there was an error. The methods used to extract and purify RNA were not well described.

A correction has been made to Materials and Methods, Transcriptome Sequencing and Analysis of Escherichia coli section, paragraph 1:

"Total RNA of Escherichia coli was extracted using a E.Z.N.A Bacterial RNA Kit (R6950-01, OMEGA, USA) according to the manufacturer's instruction. A total of 3 µg of RNA per sample was used as input material for RNA sample preparation. Sequencing libraries were generated using the NEBNext<sup>®</sup> Ultra<sup>TM</sup> Directional RNA Library Prep Kit for Illumina<sup>®</sup> (NEB, USA) according to the manufacturer's recommendations, and index codes were added to attribute sequences to each sample. Ribo-Zero rRNA Removal Kit (Bacteria) (Illumina, MRZB12424) was used for removal of rRNA from total RNA preparations. Fragmentation was carried out using divalent cations under elevated temperature in NEBNext First Strand Synthesis Reaction Buffer (5×). First strand cDNA was synthesized using random hexamer primers and M-MuLV reverse transcriptase (RNaseH-). Second-strand cDNA synthesis was subsequently performed using DNA polymerase I and RNase H. In the reaction buffer, dNTPs with dTTP were replaced by dUTP. Remaining overhangs were converted into blunt ends via exonuclease/polymerase activities. After adenylation of 3' ends of DNA fragments, NEBNext adaptors with hairpin loop structures were ligated to prepare the samples for hybridization. To preferentially select cDNA fragments that were 150-200 bp in length, the library fragments were purified with the AMPure XP system (Beckman Coulter, Beverly, USA). Then, 3 µl of USER enzyme (NEB, USA) was used with size-selected, adaptor-ligated cDNA at 37°C for 15 min, followed by 5 min at 95°C before PCR. Then, PCR was performed with Phusion high-fidelity DNA polymerase, universal PCR primers, and Index (X) primer. Finally, products were purified (AMPure XP system), and library quality was assessed on am Agilent Bioanalyzer 2100 system."

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The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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