


CORRECTION

Open Access



Correction to: Bioprospection of actinobacteria derived from freshwater sediments for their potential to produce antimicrobial compounds

Zothanpuia¹, Ajit Kumar Passari¹, Vincent Vineeth Leo¹, Preeti Chandra², Brijesh Kumar², Chandra Nayak³, Abeer Hashem^{4,5}, Elsayed Fathi Abd_Allah⁶, Abdulaziz A. Alqarawi⁶ and Bhim Pratap Singh^{1*} 

Correction to: *Microb Cell Fact* (2018) 17:68

<https://doi.org/10.1186/s12934-018-0912-0>

Upon publication of this article [1], it was brought to our attention that Figs. 3, 4 and 5 are incorrectly presented in the original version of the article. The figures were inadvertently swapped in the original submission and published. Figure 3 should be treated as Fig. 5; Fig. 4 should be 3 and Fig. 5 should be Fig. 4.

The corrected figures are given in this erratum (Figs. 3, 4, 5).

Page no. 4 of the original publication under section Detection of antibiotics using UPLC–ESI–MS/MS, last sentence should be “Instrumentation and analytical conditions were performed using the standardized methods as described in our previous paper (Fig. 4) [19].

Similarly, Page no. 8 of original publication under section Detection and quantification of antibiotics using

the UPLC–MRM method should be “MS/MS Spectra of standard reference analytes i.e. trimethoprim, fluconazole, ketoconazole and rifampicin showed as Fig. 5 was used from our earlier publication [19].

Page no. 7 of the original publication Figure 3 legend needs to be changed as Fig. 3 MRM extracted ion chromatogram of reference analyte: **a** trimethoprim, **b** fluconazole, **c** ketoconazole, **d** rifampicin.

Page no. 9 of the original publication, Figure 4 should be Fig. 4 MS/MS spectra of reference analytes; **a** trimethoprim, **b** fluconazole, **c** ketoconazole, **d** rifampicin (as per [19]).

Page no. 10 of the original publication, Figure 5 should be Fig. 5 Maximum likelihood (ML) phylogenetic tree constructed using amino acid sequences for **a** PKS type II gene; **b** NRPS gene and **c** phzE gene. The scale bar represents the amino acid changes.

*Correspondence: bhimpratap@gmail.com

¹ Molecular Microbiology and Systematics Laboratory, Department of Biotechnology, Mizoram University, Aizawl, Mizoram 796004, India
Full list of author information is available at the end of the article



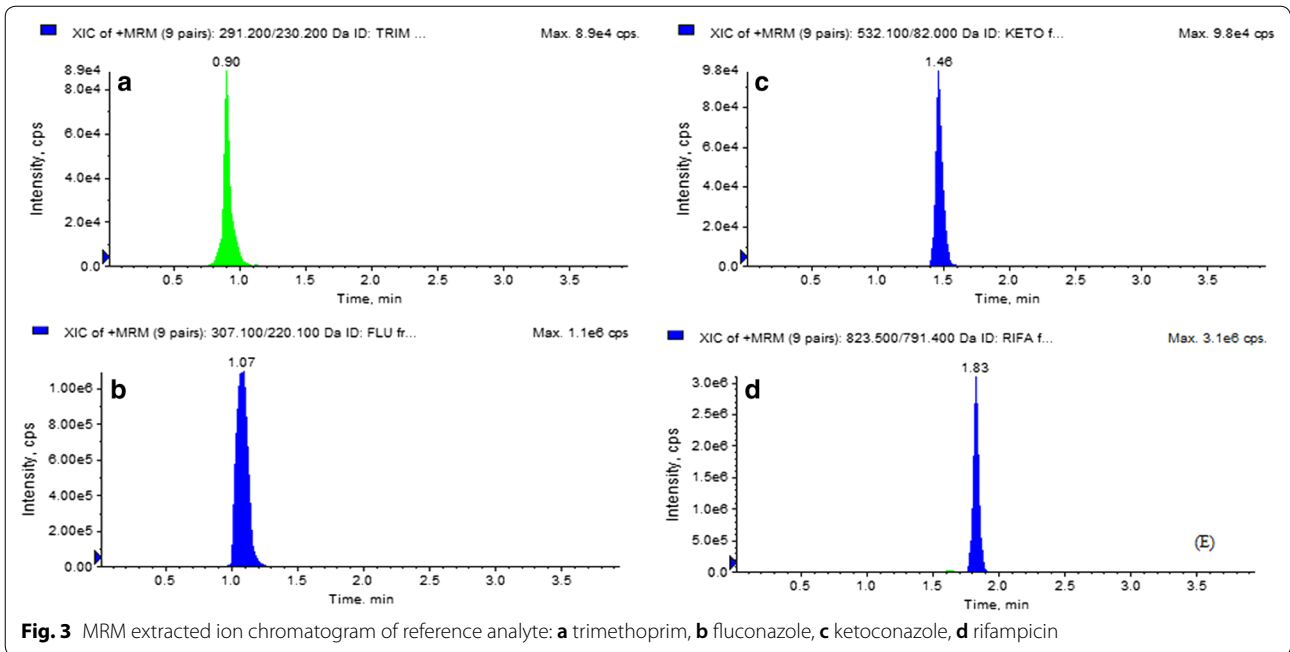


Fig. 3 MRM extracted ion chromatogram of reference analyte: **a** trimethoprim, **b** fluconazole, **c** ketoconazole, **d** rifampicin

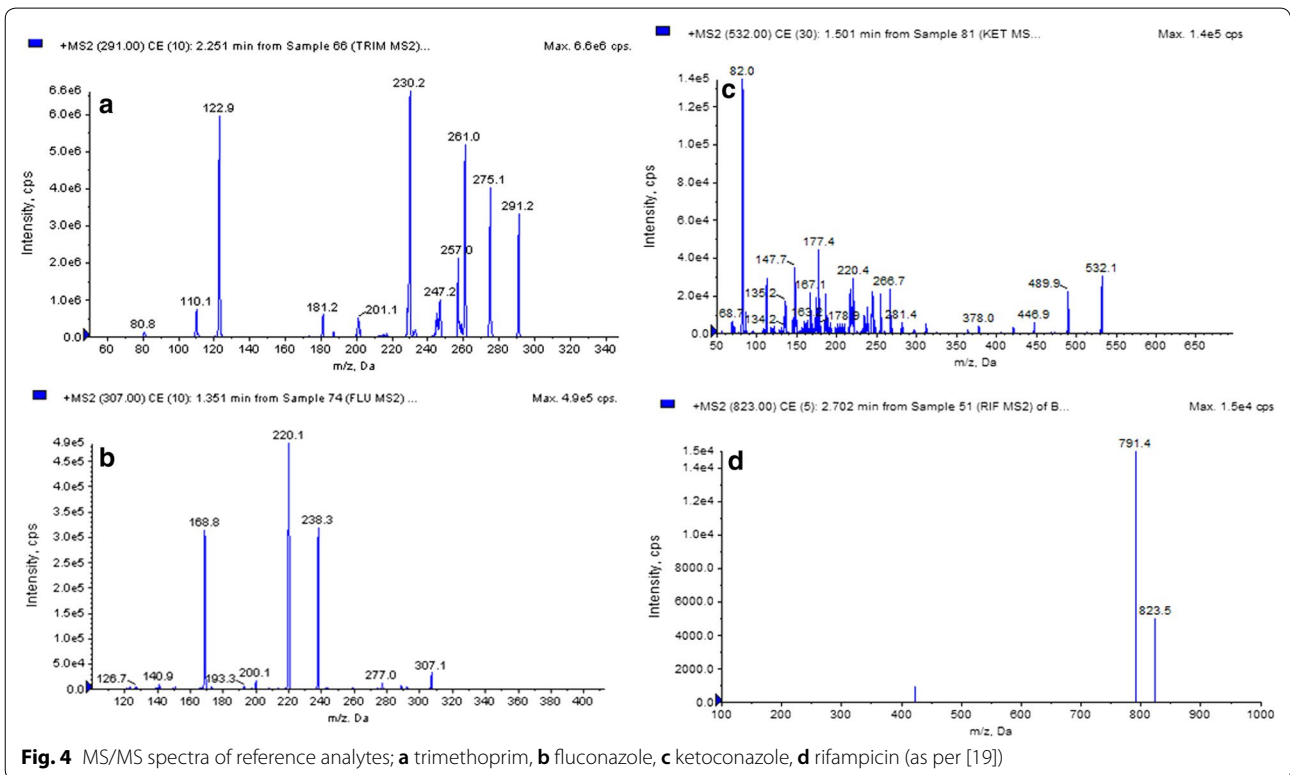


Fig. 4 MS/MS spectra of reference analytes; **a** trimethoprim, **b** fluconazole, **c** ketoconazole, **d** rifampicin (as per [19])

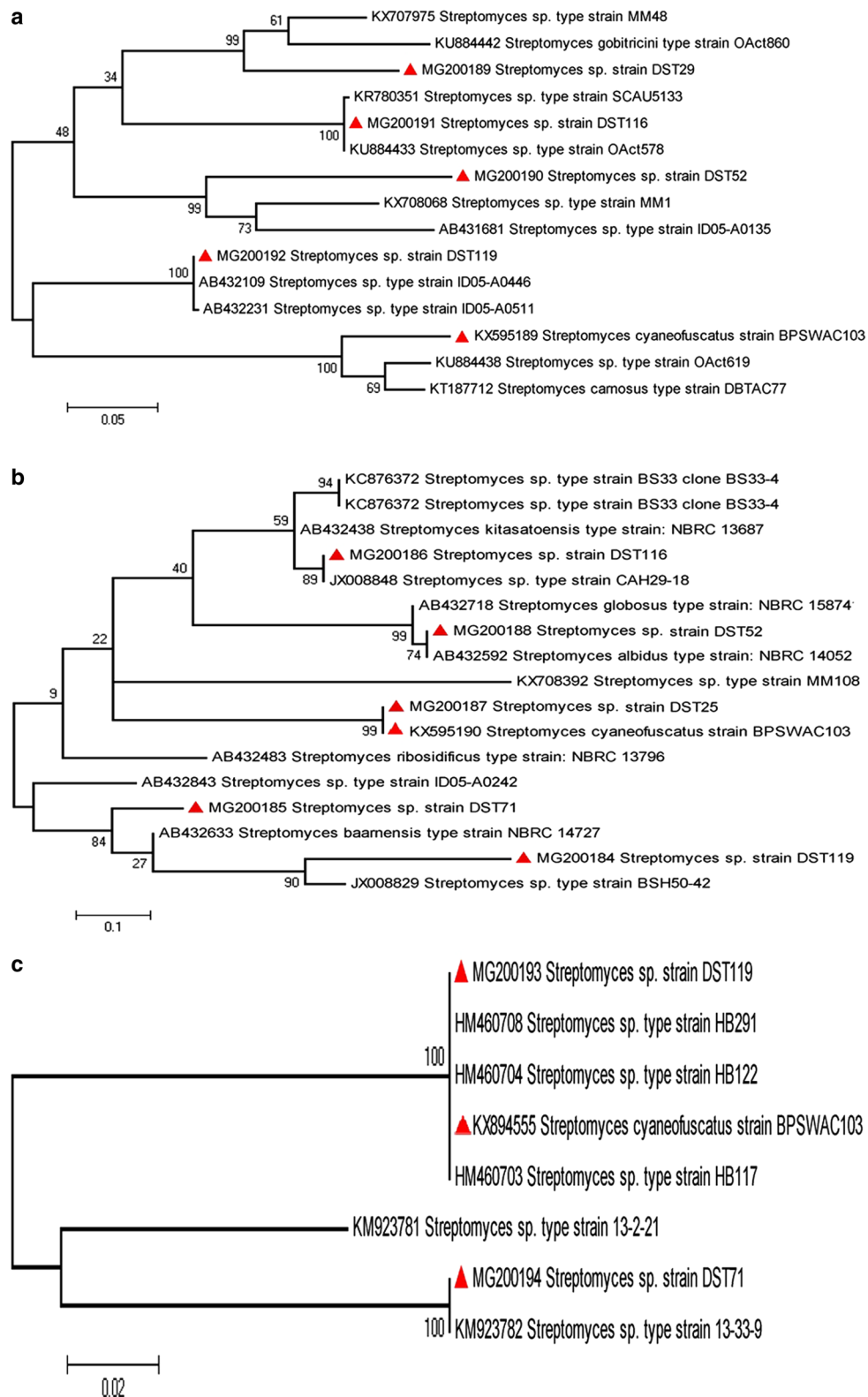


Fig. 5 Maximum likelihood (ML) phylogenetic tree constructed using amino acid sequences for **a** PKs type II gene; **b** NRPS gene and **c** phzE gene. The scale bar represents the amino acid changes

Author details

¹ Molecular Microbiology and Systematics Laboratory, Department of Biotechnology, Mizoram University, Aizawl, Mizoram 796004, India. ² SAIF, CSIR-Central Drug Research Institute (CSIR-CDRI), Lucknow 226012, India. ³ University of Mysore, Manasagangotri, Mysore, India. ⁴ Botany and Microbiology Department, College of Science, King Saud University, P.O. Box 2460, Riyadh 11451, Saudi Arabia. ⁵ Mycology and Plant Disease Survey Department, Plant Pathology Research Institute, ARC, Giza 12511, Egypt. ⁶ Department of Plant Production, Faculty of Food & Agricultural Sciences, P.O. Box 2460, Riyadh 11451, Saudi Arabia.

The original article can be found online at <https://doi.org/10.1186/s12934-018-0912-0>.

Publisher's Note

Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Published online: 05 June 2018

Reference

1. Zothanpuia, Passari AK, Leo VV, Chandra P, Kumar B, Nayak C, Hashem A, Abd_Allah EF, Alqarawi AA, Singh BP. Bioprospection of actinobacteria derived from freshwater sediments for their potential to produce antimicrobial compounds. *Microb Cell Fact*. 2018;17:68. <https://doi.org/10.1186/s12934-018-0912-0>.