

CORRECTION

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Correction to: Evaluation of the impact of six different DNA extraction methods for the representation of the microbial community associated with human chronic wound infections using a gel-based DNA profiling method

Ayomi Dilhari¹, Asanga Sampath¹, Chinthika Gunasekara¹, Neluka Fernando¹, Deepaka Weerasekara², Chris Sissons³, Andrew McBain⁴ and Manjula Weerasekera^{1*}

Correction to: AMB Expr (2017) 7:179

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Following publication of the original article (Dilhari et al. 2017), the authors identified an error in Figs. 1 and 3.

The corrected figures are given below.

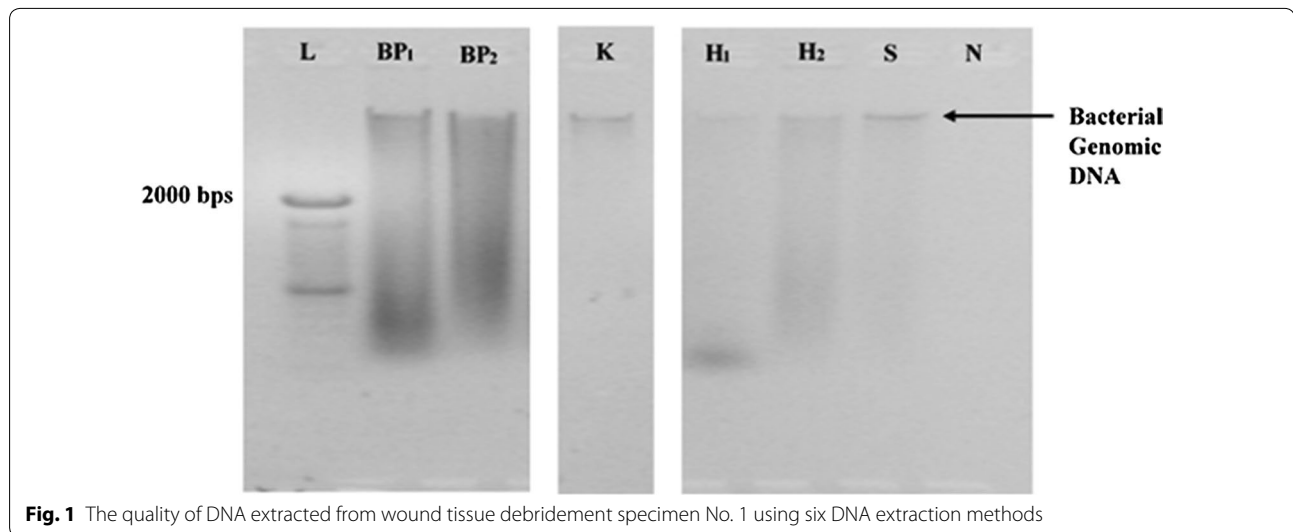


Fig. 1 The quality of DNA extracted from wound tissue debridement specimen No. 1 using six DNA extraction methods

The original article can be found online at <https://doi.org/10.1186/s13568-017-0477-z>.

*Correspondence: mmweera@yahoo.com; mmweera@sjp.ac.lk

¹ Department of Microbiology, Faculty of Medical Sciences, University of Sri Jayewardenepura, Gangodawila, Nugegoda, Sri Lanka

Full list of author information is available at the end of the article



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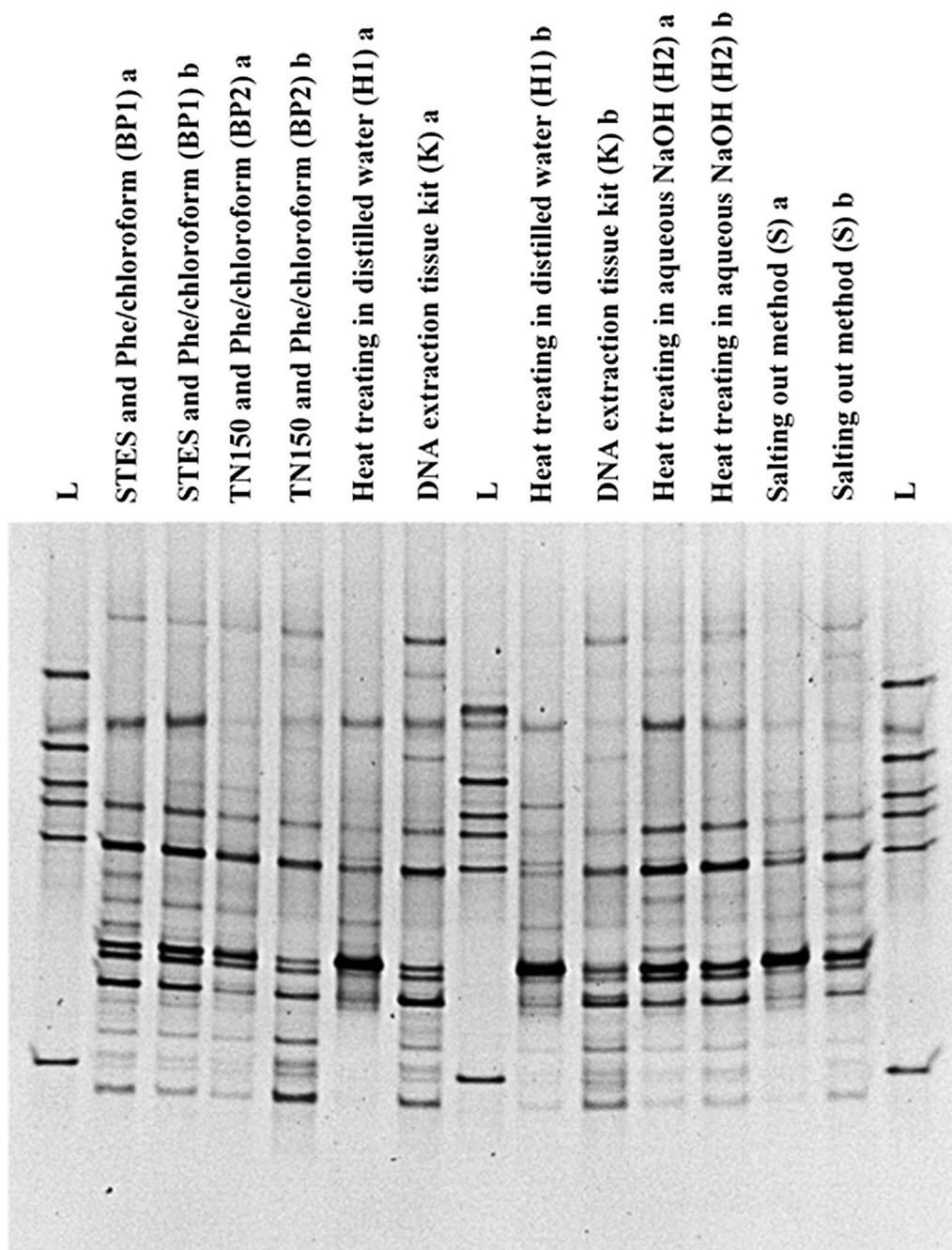


Fig. 3 A comparison of DGGE profiles of PCR amplified bacterial 16S rRNA gene for the specimen No: 1. DNA was extracted using six different DNA extraction methods using 25 mg of wound tissue debridement specimen no. 1. Bacterial fingerprinting profile is based on 30–55% denaturing gradient. “L” lanes represent the in house bacterial reference panel which includes *S. aureus*, *Acinetobacter* spp, Group B *Streptococcus* spp., *E. faecalis*, Group A *Streptococcus* spp. and *E. coli* from top to bottom respectively. Other lanes show bacterial fingerprinting profile of each extraction method in duplicate (a, b) for the specimen No. 1, collected from a subject with a chronic wound

Author details

¹ Department of Microbiology, Faculty of Medical Sciences, University of Sri Jayewardenepura, Gangodawila, Nugegoda, Sri Lanka. ² Department of Surgery, Faculty of Medical Sciences, University of Sri Jayewardenepura, Gangodawila, Nugegoda, Sri Lanka. ³ Department of Pathology and Molecular

Medicine, University Otago, Wellington, New Zealand. ⁴ Faculty of Biology, Medicine and Health, The University of Manchester, Manchester M13 9PT, UK.

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