

CORRECTION

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Corrigendum: A Comparison of Techniques for Collecting Skin Microbiome Samples: Swabbing Versus Tape-Stripping

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A Corrigendum on

A Comparison of Techniques for Collecting Skin Microbiome Samples: Swabbing Versus Tape-Stripping

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In the original article, there was an error in the sequence of the forward primer used in the real-time PCR.

The forward primer 5'-ACTGAGACACGGYCCA-3' in the original text should read 5'-ACT GAGAYACGGYCCA-3'. The primer with the corrected sequence was actually used in the study; therefore, the results are not affected.

A correction has been made to Materials and Methods, Real-Time PCR:

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To determine the copy number of the 16S rRNA gene in the DNA extracted from the swab or adhesive tape, real-time PCR was performed. The 16S rRNA gene was amplified using universal primer pairs (F: 5'-ACTGAGAYACGGYCCA-3'; R: 5'-CTGCTGGCACGDAGTTAGC C-3') (Wang and Qian, 2009) and a universal probe (5'-VIC-ACTGCTGCCTCCCGTA-NFQ-MGB-3') (Gao et al., 2010) with the Thunderbird Probe qPCR Mix (Toyobo Co., Ltd., Osaka, Japan). A standard curve was drawn from a known amount of the 16S rRNA gene [100, 10, 1, and 0.1 pg of *Propionibacterium acnes* genomes, which are equivalent to 7.23×10^4 , 7.23×10^3 , 7.23×10^2 , and 7.23×10^1 16S rRNA genes, respectively (Nadkarni et al., 2002; Miura et al., 2010; Stoddard et al., 2015)]. All the reactions were performed with the Mx3005P System (Agilent Technologies, CA, United States). The copy number of 16S rRNA gene was compared for the same size of skin area (4.4 × 4.4-cm square; Supplementary Figure 1, open squares).

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.

REFERENCES

- Gao, Z., Perez-Perez, G. I., Chen, Y., and Blaser, M. J. (2010).

 Quantitation of major human cutaneous bacterial and fungal populations. *J. Clin. Microbiol.* 48, 3575–3581. doi: 10.1128/JCM.00 597-10
- Miura, Y., Ishige, I., Soejima, N., Suzuki, Y., Uchida, K., Kawana, S., et al. (2010).
 Quantitative PCR of *Propionibacterium acnes* DNA in samples aspirated from sebaceous follicles on the normal skin of subjects with or without acne. *J. Med. Dent. Sci.* 57, 65–74. doi: 10.11480/jmds.570108
- Nadkarni, M. A., Martin, F. E., Jacques, N. A., and Hunter, N. (2002). Determination of bacterial load by real-time PCR using a broad-range (universal) probe and primers set. Microbiology 148(Pt 1), 257–266. doi: 10.1099/00221287-148-1-257
- Stoddard, S. F., Smith, B. J., Hein, R., Roller, B. R., and Schmidt, T. M. (2015). rrnDB: improved tools for interpreting rRNA gene abundance in bacteria and

- archaea and a new foundation for future development. *Nucleic Acids Res.* 43, D593–D598. doi: 10.1093/nar/gku1201
- Wang, Y., and Qian, P. Y. (2009). Conservative fragments in bacterial 16S rRNA genes and primer design for 16S ribosomal DNA amplicons in metagenomic studies. PLoS ONE 4:e7401. doi: 10.1371/journal.pone.0007401

Conflict of Interest Statement: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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