

CORRECTION

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Correction: Diversity and composition of gut microbiota in healthy individuals and patients at different stages of hepatitis B virus-related liver disease

Meng-Ju Lin¹, Tung-Hung Su^{2,3*}, Chieh-Chang Chen², Wei-Kai Wu⁴, Shih-Jer Hsu², Tai-Chung Tseng^{2,3,4}, Sih-Han Liao⁵, Chun-Ming Hong⁶, Hung-Chih Yang², Chun-Jen Liu^{2,3,7}, Ming-Shiang Wu² and Jia-Horng Kao^{2,3,4,7*}

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Following publication of the original article [1], it was noted that due to a typesetting mistake, errors were introduced in the caption of Additional files 5–7 in the Supplementary information.

The original article can be found online at <https://doi.org/10.1186/s13099-023-00549-w>.

*Correspondence:

Tung-Hung Su
tunghungsu@ntu.edu.tw
Jia-Horng Kao
kaojh@ntu.edu.tw

¹ School of Medicine, College of Medicine, National Taiwan University, Taipei, Taiwan

² Division of Gastroenterology and Hepatology, Department of Internal Medicine, National Taiwan University Hospital, 1 Chang-Te Street, Taipei 10048, Taiwan

³ Hepatitis Research Center, National Taiwan University Hospital, Taipei, Taiwan

⁴ Department of Medical Research, National Taiwan University Hospital, Taipei, Taiwan

⁵ Section of Gastroenterology, Department of Medicine, National Taiwan University Cancer Center, Taipei, Taiwan

⁶ Division of Hospital Medicine, Department of Internal Medicine, National Taiwan University Hospital, Taipei, Taiwan

⁷ Graduate Institute of Clinical Medicine, College of Medicine, National Taiwan University, 1 Chang-Te Street, Taipei 10048, Taiwan

The publisher apologises to the authors and readers for the inconvenience caused by the error.

That is,

- “HBeAgchronic HBV infection” should be “HBeAg (+) chronic HBV infection”
- “HBeAgchronic hepatitis B” should be “HBeAg (+) chronic hepatitis B”
- “HBeAgchronic HBV infection” should be “HBeAg (–) chronic HBV infection”
- “HBeAgchronic hepatitis B” should be “HBeAg (–) chronic hepatitis B”

It has been corrected in this correction. The original article has been updated.

Additional file 5: Figure S1.

Comparisons of bacterial diversity and richness of patients with HBeAg (+) chronic HBV infection, HBeAg (+) chronic hepatitis B, HBeAg (–) chronic HBV infection, HBeAg (–) chronic hepatitis B, and resolved HBV. **A** A Venn diagram displays the unique and shared ASVs among the four groups. **B** The HBeAg (–) chronic hepatitis B group had the least observed ASVs among the five groups. The HBeAg (–) chronic hepatitis B group had the lowest alpha diversity indices, including **C** Shannon diversity, **D** Simpson diversity, **E** Chao1 index, and **F** Chao2 index. * means $P < 0.05$ and ** means $P < 0.01$.



Additional file 6: Figure S2.

Beta diversity indices of patients with HBeAg (+) chronic HBV infection, HBeAg (+) chronic hepatitis B, HBeAg (–) chronic HBV infection, HBeAg (–) chronic hepatitis B, and resolved HBV. **A** PCoA plot of bacterial beta diversity based on the weighted UniFrac distance. **B** PCoA plot of bacterial beta diversity based on the unweighted UniFrac distance. No separate cluster was found between HBeAg (+) chronic HBV infection, HBeAg (+) chronic hepatitis B, HBeAg (–) chronic HBV infection, HBeAg (–) chronic hepatitis B, and resolved HBV.

Additional file 7: Table S5.

Statistical significance of beta diversity distance matrices among patients with HBeAg (+) chronic HBV infection, HBeAg (+) chronic hepatitis B, HBeAg (–) chronic HBV infection, HBeAg (–) chronic hepatitis B, and resolved HBV.

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Reference

1. Lin M-J, Su T-H, Chen C-C, Wu W-K, Hsu S-J, Tseng T-C, Liao S-H, Hong C-M, Yang H-C, Liu C-J, Wu M-S, Kao J-H. Diversity and composition of gut microbiota in healthy individuals and patients at different stages of hepatitis B virus-related liver disease. *Gut Pathogens*. 2023;15:24. <https://doi.org/10.1186/s13099-023-00549-w>.

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