

OPEN ACCESS

APPROVED BY
Frontiers Editorial Office,
Frontiers Media SA, Switzerland

*CORRESPONDENCE
Ke Liu

☑ liuke@shvri.ac.cn
Zhiyong Ma
☑ zhiyongma@shvri.ac.cn

RECEIVED 30 May 2025 ACCEPTED 02 June 2025 PUBLISHED 13 June 2025

CITATION

Tao K, He C, Zhang T, Xiao C, Du L, Li Z, Shao D, Wei J, Li B, Qiu Y, Ma Z and Liu K (2025) Correction: Evidence of WNV infection in migratory birds passing through Xinjiang, china, using viral genome amplicon approach. *Front. Microbiol.* 16:1638113. doi: 10.3389/fmicb.2025.1638113

COPYRIGHT

© 2025 Tao, He, Zhang, Xiao, Du, Li, Shao, Wei, Li, Qiu, Ma and Liu. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these

Correction: Evidence of WNV infection in migratory birds passing through Xinjiang, china, using viral genome amplicon approach

Kunsheng Tao¹, Chan He¹, Tong Zhang¹, Changguang Xiao¹, Lifei Du², Zongjie Li¹, Donghua Shao¹, Jianchao Wei¹, Beibei Li¹, Yafeng Qiu¹, Zhiyong Ma^{1*} and Ke Liu^{1*}

¹Shanghai Veterinary Research Institute, Chinese Academy of Agricultural Science, Shanghai, China, ²Hunan Institute of Animal and Veterinary Science, Changsha, China

KEYWORDS

West Nile virus, migratory bird, amplicon, fecal samples, epidemiology

A Correction on

Evidence of WNV infection in migratory birds passing through Xinjiang, China, using viral genome amplicon approach

by Tao, K., He, C., Zhang, T., Xiao, C., Du, L., Li, Z., Shao, D., Wei, J., Li, B., Qiu, Y., Ma, Z., and Liu, K. (2025). *Front. Microbiol.* 16:1468530. doi: 10.3389/fmicb.2025.1468530

In the published article, there was an error in the legend for Figure 3D as published. [(**D**) Phylogenetic analysis of WNV fragments. The phylogenetic analysis was performed using the DNAstar software.]. The corrected legend appears below.

[(D) Phylogenetic analysis of WNV fragments. The phylogenetic analysis was performed using the R code.].

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.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.