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Reply to: Evidence of widespread sequencing errors in global avian influenza study

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The primary issue arose due to an error during the sequence submission process to GISAID. Following GISAID's advice for bulk submissions, we used the command-line software "FluCLI" to upload our data. During reformatting of files for submission, an analysis file originally prepared for phylogenetic tree construction and containing both our study sequences and reference sequences was inadvertently uploaded. In addition, sample identifiers were reformatted incorrectly, which led to duplication and mixing of study and reference sequences. Importantly, in our original analyses, we did not find such anomalies. We would like to apologize for the confusion caused by the erroneous sequences. The sequences have been corrected both in GISAID and in GenBank, under the same accession numbers provided in the original manuscript (GISAID: EPI_ISL_19613337 to EPI_ISL_19613573/EPI_ISL_19812857-EPI_ISL_19812874; GenBank: PV422873-PV423054, PV422241-PV422430, and PV440337-PV440372, now version 2). Additional data from this work are available from the following link: https://doi.org/10.7910/DVN/KJDNGF (In accordance with each country's data protection laws, these data are provided strictly upon a valid request according to collaborative agreements. They must not be used to model, predict, or otherwise infer health or commercial applications. The data are not permitted for use in generative AI modeling, dashboard development, or border-related health prediction systems.

Appearance of HA and NA sequences from disparate regions over prolonged time periods sharing 100% nucleotide identity (Main text second paragraph from Matters Arising)

Sequence uploading error led to the appearance of implausible 100% repeated nucleotide identities and patterns of apparent evolutionary stasis that were observed by the correspondents. According to Chen and Holmes (2006) and as highlighted by the authors, substitution rates of AIV varied between 1.8 and 8.4×10^{-3} per site per year. For HA it was 3.92×10^{-3} per site per year (95% highest probability density range: $2.43–5.40 \times 10^{-3}$). For the NA, the mean substitution rate was 3.61×10^{-3} per site per year (95% highest probability density range: $2.29–4.92 \times 10^{-3}$). Based on the values by Chen and Holmes (2006)[1], a rough estimate for the mutation rate in the HA can be 6.7 (3.5–9.1) per year, while the mutation rate for NA may be calculated as 5.1 (3.2–7) mutations per year. Kim et al. (2022)[2] evaluated the effects of host on the AIV mutation rates and found that mutation rates were higher for viruses infecting wild shorebirds and chickens compared to wild and domestic ducks. Even though the host of the collected fecal samples or the exact date of dropping data is unavailable, our sequences are consistent with the expected rate of influenza virus evolution (Supplementary Fig. 1 and Supplementary Table 1-2).

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TempEst analysis (Main text second and third paragraph from Matters Arising)

We also conducted a TempEst analysis using the correct sequence data. We downloaded the available full sequences of NA from Asia collected between 1996/1/1 and 2024/12/31 and uploaded to GISAID. In total, 817 sequences were downloaded. The phylogeny was inferred using the Maximum Likelihood method and the General Time Reversible model of nucleotide substitutions. We found that the tree constructed with the correct sequences didn't have any outliers belonging to our study sequences (Supplementary Fig. 1).

Thus, the conclusions in our published manuscript were based on correctly generated data, while the erroneous sequences in GISAID were the result of a submission mistake. We sincerely apologize for this error and for the confusion it has caused. We have worked with GISAID to withdraw the affected entries and replace them with the corrected sequence data. We are currently reviewing and strengthening our internal submission and data-handling processes to ensure that such errors do not occur again in the future. We sincerely thank the authors for their detailed work in identifying this issue.

Clarification on Australia's avian influenza status (Main text second, third and fourth paragraph from Matters Arising)

We wish to clearly emphasize that our study does not, in any way, question Australia's status as free from avian influenza. We never mentioned this in our study or discussed it. We fully agree with the correspondents that Australia has a strong surveillance and infection-control system and a well-documented history of rapid detection and eradication of avian influenza outbreaks. We are grateful for the correspondents' clarification on this point and sincerely thank them for highlighting the importance of maintaining accuracy in how such findings are interpreted. The phylogenetic tree constructed based on correct sequence data clearly shows that our sequences are not 100% identical to the two sequences reported in Australia in 2020 (Supplementary Fig. 2v).

At the same time, it is important to recognize that influenza viruses, including H7 lineages, can share genetic similarities across regions, and that related or convergent genetic constellations may appear in other parts of the world due to under-sampled reservoirs. Influenza is a global virus with shared variants circulating across multiple regions, and the limited surveillance coverage in many areas means that similar or related lineages may remain undetected outside well-monitored countries such as Australia. The COVID-19 pandemic highlighted the risks of attributing viral "origins" to a single country in the absence of comprehensive global data. Such attributions are not scientifically robust and may unfairly stigmatize specific countries. Our study makes no claims that Australia is a source of infection, nor do our findings provide any evidence that would call Australia's current avian influenza-free status into question (Our study does not even mention Australia). Furthermore, we emphasize that our research is in no way sufficient to support any theory about the origin of influenza variants, nor to provide information that would identify any specific region or country as the primary source of such variants. This limitation is clearly mentioned in our study.

Flyways and global circulation (Main text second, third and fourth paragraph from Matters Arising)

We would like to apologize again for the sequence uploading error which made the HA and NA sequences obtained from Papua New Guinea 100% identical to previously submitted sequences. We have compared the correct sequences from Papua New Guinea with reference sequences in supplementary Tables 1 and 2, provided a complete Excel file containing all BLAST results (Supplementary Data 1), and generated phylogenetic trees with the reference sequences (Supplementary Fig. 2 (a)-(v)). When the correct sequences are used, we did not observe any 100% similarities.

Regarding the discussion of flyways, we would like to emphasize that Papua New Guinea lies within the East Asian–Australasian Flyway, which also intersects with several other major migratory pathways. These include the West Asian–East African Flyway, the Black Sea/Mediterranean Flyway, and the Central Asian Flyway via northern Siberia, Russia, and Alaska[1–4]. In addition, Papua New Guinea is indirectly connected to the Pacific and Mississippi Americas Flyways through northern migratory routes of East Asian–Australasian Flyway[1–4]. The Pacific and Mississippi Americas Flyways also overlap with the Atlantic Americas Flyway in both the northern and southern hemispheres. Much migration of land and waterbirds occurs in a north–south direction, but there are also well-documented examples of east–west migration[1–4]. Additionally, there are the North Indian Ocean Flyway, East Indian Ocean Flyway, West Pacific Ocean Flyway, and Atlantic Ocean Flyway, all of which interconnect and overlap with the major continental flyways[1–14]. Seabird movements are influenced by resource availability and prevailing winds, making them complex and often difficult to predict[12–14].

Our study region also contains more than 100,000 small islands or islets, around 98% of which are remote or rural and therefore not subject to any form of testing or monitoring in the past. Consequently, there are significant gaps in available data. Climate change is rapidly altering these ecosystems, further complicating our ability to understand virus circulation. This extensive overlap makes it biologically plausible that avian influenza viruses circulating in one region may be detected in distant geographic areas. Moreover, migratory patterns are increasingly shaped by environmental stressors such as climate change, habitat loss, logging, mining, and extreme weather events, all of which can alter traditional routes and stopover sites. Our study was conducted between late 2021 and early 2023, during which time the North/South Indian Ocean experienced a total of 14 cyclonic storms (World Meteorological Organization (WMO), https://wmo.int). The Philippines and Indonesia experienced several severe weather events, while Madagascar and Mozambique were repeatedly struck by destructive tropical cyclones, including the record-breaking Cyclone Freddy in 2023 (World Meteorological Organization (WMO), https://wmo.int). Yemen experienced a rare but severe cyclone strike in 2023, and Somalia suffered major flooding in the same year, alongside its worst drought in 40 years. Similarly, Madagascar endured multi-year droughts interspersed with cyclones. The Maldives and Papua New Guinea also faced climate-related stress, including drought, sea-level rise, and indirect cyclone impacts (World Meteorological Organization (WMO), https://wmo.int). The Philippines experienced frequent, intense typhoons linked to El Niño (World Meteorological Organization (WMO), https://wmo.int), while Sri Lanka and Myanmar faced climate pressures on agriculture, compounded by conflict and economic instability. Collectively, these events can disrupt ecosystems, alter bird migratory pathways, and displace human populations in search of food and shelter, further increasing the complexity of disease ecology in these regions[12–16].

At the same time, there remain major gaps in influenza surveillance. In northern regions such as Siberia and northern Mongolia, as well as across much of Central Asia, Africa, and South and East Asia, systematic surveillance is limited or absent[5,6]. Only a handful of countries routinely conduct surveillance studies and release sequence data from wild birds or poultry, and many do not release any data at all. These regions are also heavily affected by conflict, poverty, political instability, and weak infrastructure, which further restricts disease monitoring and data sharing. Our study period also overlapped with the global COVID-19 pandemic, during which much existing surveillance capacity was diverted to pandemic

management, leaving influenza and other pathogens under-monitored; the global restriction of movements also hampered disease surveillance. In addition, large parts of Asia, the Pacific, and Africa are characterized by millions of backyard and smallholder poultry farms, most of which are rarely, if ever, subject to surveillance for avian influenza[7]. These regions also host some of the highest levels of biodiversity worldwide, including thousands of bird and mammal species, but very little influenza sequence data is available from the last two decades[8,9]. Surveillance often focuses on areas where it is easier to catch birds or on locations known for historical outbreaks, industrial farming areas, neglecting many crucial, hard-to-reach areas. This creates a spatial and temporal bias in the available data. Surveillance in Papua New Guinea, the Solomon Islands, much of the Pacific[10–14], Sri Lanka, the islands in the Philippines, Indonesia, the Maldives, Yemen, Somalia, Madagascar, and Mozambique is minimal. This does not mean influenza is absent in the Pacific, South/ East Asia, the Middle East, or West Africa, only that it is under-sampled. Viruses introduced into these Islands may circulate silently.

At present, most influenza genomic data come from high-income countries with advanced surveillance infrastructure, whereas much of the rest of the world lacks such capacity. Given these realities, our global understanding of influenza circulation remains incomplete. Without testing across all regions and species, it is not possible to determine with certainty where specific variants first arise or what their true origins may be. We therefore caution against assuming that certain transmission patterns are impossible. Under-sampling, lack of historical data, and significant gaps in global surveillance mean that the true diversity, circulation, and evolutionary dynamics of avian influenza viruses remain only partially understood.

H3 clade assignment (Main text fifth paragraph from Matters Arising))

We also acknowledge the issue regarding H3 HA clade assignment. This arose from the automated NextClade platform, which occasionally assigns avian H3 sequences to human-specific clades instead of reporting them as “unassigned.” While this is a limitation of the platform, we recognize that it was our responsibility to validate these assignments before including them in the manuscript. We respectfully thank the correspondents for kindly highlighting this, and we have correted the record by updating these as “unassigned” clades in our paper, as an author’s correction.

Ethical and regulatory approvals (Main text six paragraph from Matters Arising)

Our study did not involve direct sampling from live or protected animals, nor did it involve the collection of material from birds’ nests or directly from bird colonies. All materials consisted of bird feces collected from the environment, representing environmental waste samples. These samples are essentially leftover substances present in the public domain, with no commercial or recreational value. For this reason, they do not fall under the scope of the Convention on International Trade in Endangered Species (CITES) or the Nagoya Protocol, both of which regulate the use of biological resources. We confirmed this with the relevant authorities before starting this project.

We carefully confirmed with the relevant local authorities that no special permits were required for the type of environmental fecal waste sampling undertaken in this study. No bird genomes were sequenced, and no viruses were cultured. All samples were collected directly into a DNA/RNA preservation buffer (DNA/RNA Shield, Zymo Research), which renders the material non-infectious and non-culturable, while preserving only nucleic acids. The solution lyses cells and preserves genetic material for downstream applications, such as sequencing and PCR, while ensuring samples remain safe for handling by inactivating viruses, bacteria, fungi, and parasites, as well as other protein or organic substances. This method is currently used by self-heritage test services, which utilize postal services to transport samples. This is exempt from the requirement for permits, as it falls under nucleotide materials, which do not require such approval. We have already checked these requirements with the relevant authorities; they assured us that such requirements are not necessary. The analyses and sequencing were conducted in Thailand, a country that has not ratified the Nagoya Protocol. In addition, many of the countries included in this work have not ratified the Nagoya Protocol, or do not yet have functioning systems to implement it. Several countries where sampling was conducted currently lack stable governmental institutions due to conflict or operate under autonomous local control systems. In such cases, the local authorities or control groups confirmed that no special permits were applicable. Furthermore, in some regions, the current political administrations do not recognize agreements made by previous governments under the Nagoya Protocol and instead have their own independent systems of regulation and oversight. The study was formally reviewed and received ethical exemption approval from our institute in Japan, as environmental fecal samples are not considered to involve animal experimentation. This exemption applies to all countries where sampling took place, and local authorities confirmed that the approach was consistent with their regulations. Across all sampled countries, we have conducted participatory surveillance for over 15 years, supported by strong, long-standing collaborations and data-sharing agreements with local communities and volunteers, the LGBTQ community, and marginalized communities; moreover, many authors of this study are citizens of the countries and members of the LGBTQ community and marginalized local communities where sampling was conducted. In addition, we have submitted all the sequencing data obtained in this study to public repositories which can be accessed by researchers worldwide. We have updated our acknowledgements and ethical statements to more clearly reflect our commitment to transparency in all contributions and to a formal declaration of adherence to established standards of integrity. All procedures were carried out within the framework of our broader wastewater and environmental waste surveillance program, initiated in 2018.

In summary, the anomalies identified by the correspondents were the result of an accidental sequence upload error to GISAID. We take full responsibility for this mistake and are taking corrective steps to rectify the public record.

We thank the authors again for their careful attention and constructive feedback, which will help strengthen the scientific value and accuracy of our work. We are committed to ensuring that the revised sequence data and manuscript are corrected, transparent, and aligned with global influenza surveillance standards.

References

1. Chen, R. & Holmes, E. C. Avian influenza virus exhibits rapid evolutionary dynamics. *Mol. Biol. Evol.* **23**, 2336–2341, https://doi.org/10.1093/molbev/msl102 (2006).
2. Kim, G. et al. Effects of host and pathogenicity on mutation rates in avian influenza A viruses. *Virus Evol.* **8**, veac013. https://doi.org/10.1093/ve/veac013 (2022).
3. Department of Environment, Science and Innovation, Queensland (2023) East Asian—Australasian Flyway, Wetland*Info* website, accessed 23 2025. Available at: https://wetlandinfo.des.qld.gov.au/wetlands/ecology/components/biota/fauna/fauna-taxon/birds/eaa-flyway.html (2025).
4. BirdLife International Flyways (2025) accessed 23 August 2025. Available at: https://datazone.birdlife.org/about-our-science/flyways (2025).
5. The flyways. RED KNOTS. Accessed 2025. Available at: https://www.theredknotsproject.org/the-flyways2 (2025).

6. Internal Displacement Monitoring Centre (2023) Globale report of Internal displacement accessed 23 2025. Available at: https://api.internal-displacement.org/sites/default/files/publications/documents/IDMC_GRID_2023_Global_Report_on_Internal_Displacement_LR.pdf (2025).
7. Kasianov, N. et al. Exploring avian influenza viruses in Yakutia—the largest breeding habitat of wild migratory birds in Northeastern Siberia. *Viruses* **17**, 632 (2025).
8. Hoye, B. J., Munster, V. J., Nishiura, H., Klaassen, M. & Fouchier, R. A. Surveillance of wild birds for avian influenza virus. *Emerg. Infect. Dis.* **16**, 1827–1834 https://doi.org/10.3201/eid1612.100589 (2010).
9. Report of the Meeting of the ad hoc Group meeting on guidelines for the implementation of avian influenza 7 surveillance in small-scale poultry keepers in resource-limited settings / April 2025 accessed 23 August 2025. Available at: https://www.woah.org/app/uploads/2025/05/202505-report-ahg-ai-surveillance-in-small-scale-poultry-keepers-1.pdf#:~:text=The%20Group%20recommended%20integrating%20HPAI%20surveillance%20with,fowl%20cholera%20and%20virulent%20infectious%20bursal%20disease (2025).
10. Yong, D. L. et al. The state of migratory landbirds in the East Asian flyway: distributions, threats, and conservation needs. *Front. Ecol. Evol.* **9**, 2021https://doi.org/10.3389/fevo.2021.613172 (2021).
11. Liang, J. et al. Impacts of changing climate on the distribution of migratory birds in China: Habitat change and population centroid shift. *Ecol. Indic.* **127**, 107729 https://doi.org/10.1016/j.ecolind.2021.107729 (2021).
12. Christina Troup, Bird migration – International arrivals, Te Ara – the Encyclopedia of New Zealand, https://teara.govt.nz/en/map/7218/the-east-asian-australasian-flyway (2025).
13. Migrating birds know no boundaries. 2025 accessed 23 August 2025. Available at: https://datazone.birdlife.org/articles/migrating-birds-know-no-boundaries (2025).
14. 40,000 km between Japan and Australia! The migratory route of the white-throated needletail 2025 accessed 23 2025. Available at: https://healthist.net/en/biology/2450/ (2025).
15. Qu, R. et al. Disentangling the drivers and host-mediated global spread of H7 influenza A virus. *Nat. Commun.* **17**, 6076 (2026).
16. Li, Y. et al. Mapping global avian influenza risk patterns through waterbird activity entropy. *Nat. Commun.* **17**, 3606 (2026).

Author contributions

All authors contributed equally to the conceptualization, methodology, formal analysis, investigation, writing—original draft preparation, and writing—review and editing.

Competing interests

The authors declare no competing interests.

Additional information

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