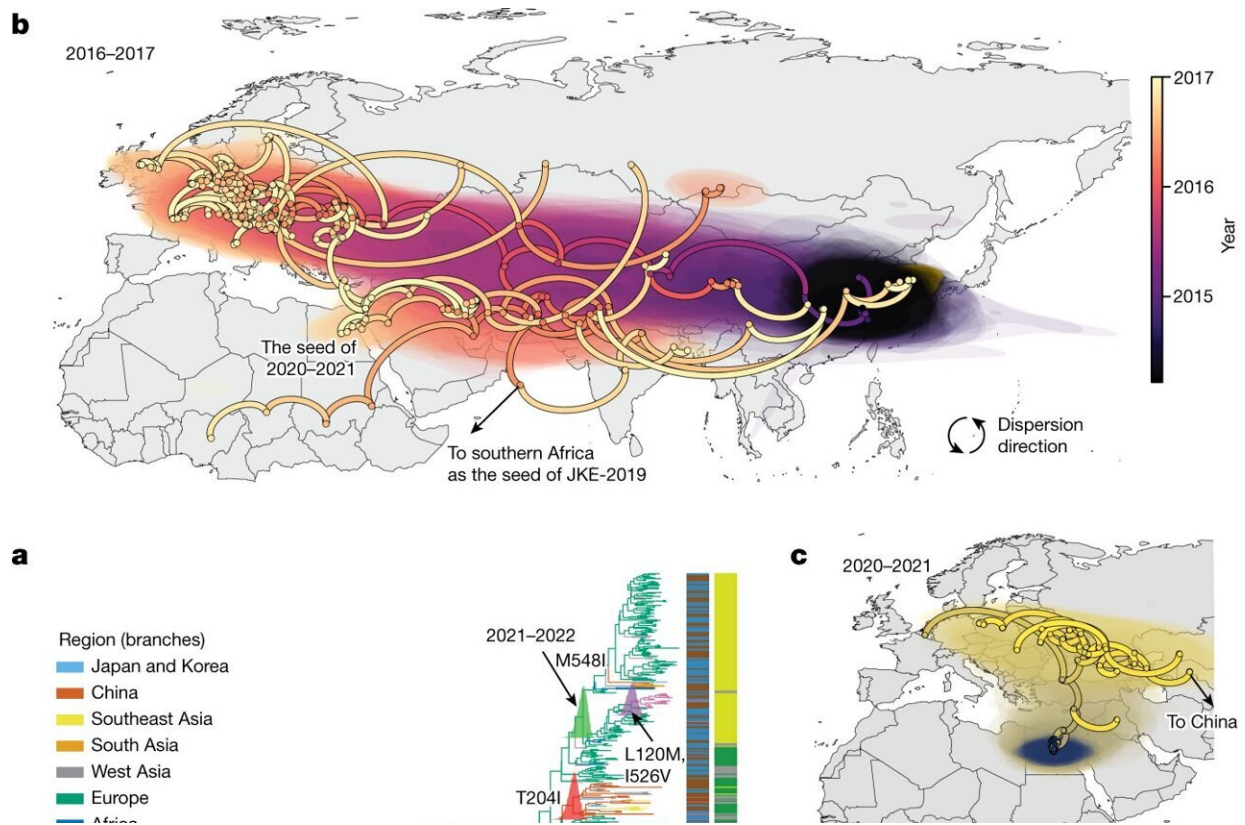


Current bird flu epidemic found to have originated in Europe and Africa

October 19 2023, by Bob Yirka



Evolution of clade 2.3.4.4b HA genes and early migration patterns of resurgent HPAI. a, Maximum clade credibility tree with branches colored by discrete geographic region. Color bars indicate host and subtype. The posterior distribution of the tMRCA is shown as bar charts on specific nodes. b, Continuous phylogeographic reconstruction of the spread of H5N8 from mid-2014 to 2017. c, Early spread of H5N8 from 2017 to mid-2020 before the 2020–2021 resurgence. d, Early spread of H5N1 from mid-2020 to 2021 before the 2021–2022 resurgence. Circles represent nodes in the maximum clade

credibility phylogeny, colored by the inferred time of occurrence. Arcs indicate direction of dispersion (counterclockwise) between nodes. An interval of 80% HPD is depicted by shaded areas, illustrating the uncertainty of the phylogeographic estimates. Credit: *Nature* (2023). DOI: 10.1038/s41586-023-06631-2

An international team of biologists, public health specialists and infectious disease experts reports that the current near-global bird flu epidemic has its roots in Europe and Africa. In their study, [published](#) in the journal *Nature*, the group analyzed bird flu data from multiple animal health databases.

Going back to 2020, infectious disease experts have found a new strain of the H5N1 [bird flu virus](#) in both wild and domestic birds. Since that time, infections have spread to every place on Earth except Oceania and Antarctica. Thus far, it is the worst [bird flu](#) outbreak in Europe's history and has killed record numbers of birds in many other countries. It has also been found to jump to other animals, including humans—to date, it has killed 458 people.

Fortunately, while the virus can leap from birds to humans, it has not yet evolved the ability to jump between people. In this new effort, the research team sought to find the origins of the new outbreak by analyzing information in databases of statistics about animals, including bird deaths, around the globe.

The data came from two massive databases, one maintained by the World Organization for Animal Health and another by the United Nation's Food and Agriculture Organization. The team also obtained [genetic information](#) from several entities that have been tracking bird deaths due to bird flu from multiple sites around the world.

The researchers found that a major shift has occurred with bird flu—where once new strains almost always originated in Asia, the new variant came from Africa and Europe. They found that it was a new variant of H5N1, the strain that originated in China back in mid-1990s. Genetic analysis showed that the new version of the variant had originated in north Africa as H5N8. As it moved to Europe, it evolved to H5N1, where it become more virulent, resulting in massive bird losses. Since that time, it has spread to most of the rest of the world.

The researchers suggest that the evolutionary path of the virus represents a major shift in bird flu evolution—one that will require a new approach by officials and health experts hoping to quash the [outbreak](#) before the virus adapts to jump between humans, and before the next new strain arrives.

More information: Ruopeng Xie et al, The episodic resurgence of highly pathogenic avian influenza H5 virus, *Nature* (2023). [DOI: 10.1038/s41586-023-06631-2](#)

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