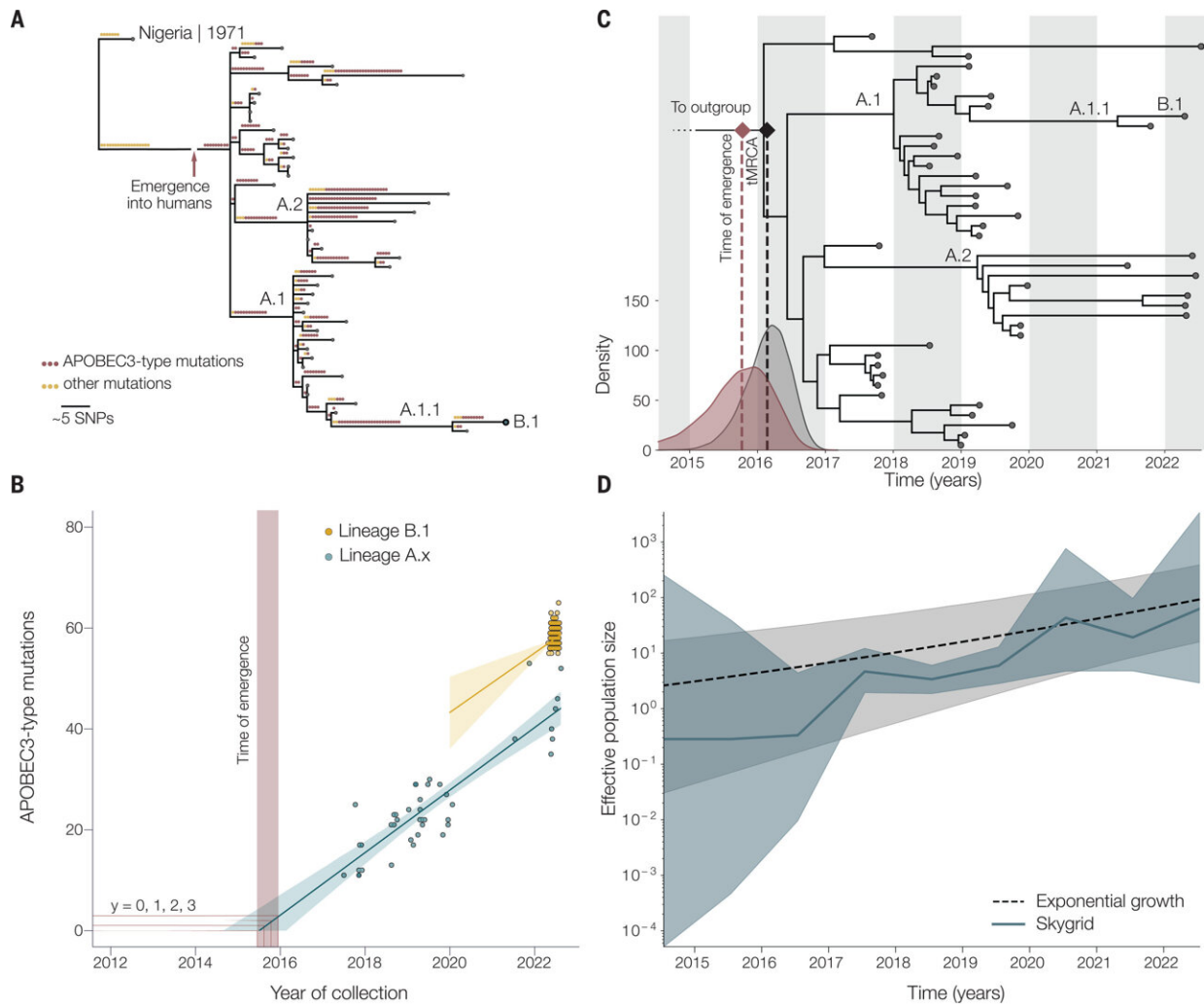


# Researchers find evidence of mpox circulating in humans since 2016

November 3 2023, by Bob Yirka



Estimating the time of MPXV emergence into the human population from the accumulation of APOBEC3-type mutations. (A) MPXV genomes sampled from human infections from 2017 to 2022, with an outgroup sequence from an outbreak in Nigeria in 1971. Mutations along each branch are indicated with

circles colored by whether it is putatively APOBEC3 edited (TC→TT and GA→AA; red) or whether it is another mutation type (yellow). (B) APOBEC3 mutations from MPXV genomes sampled since 2017. The reconstructed most recent common ancestor (MRCA) of the panel A phylogeny is used as the root in the root-to-tip plot, and the y intercept is used as a proxy for time of emergence, which is inferred by fitting a Bayesian regression to the sequence dates from panel A. (C) Maximum clade credibility (MCC) phylogeny of MPXV clade IIb with absolute time shown on the x axis. (D) Estimated effective population size of the outbreak using a nonparametric coalescent Skygrid model with 11 change points over a period of 8.5 years. Credit: *Science* (2023). DOI: 10.1126/science.adg8116

A large international team of medical researchers and epidemiologists has found evidence that monkeypox (mpox) has been circulating in humans since 2016. In their study, [reported](#) in the journal *Science*, the group used Bayesian evolutionary analysis of the mpox virus to show that its genomic history includes years of change due to human infections.

Mpox was first identified in the 1950s after an illness struck a group of research monkeys in Denmark. Twenty years later, the first case was detected in a human in Africa. Over the following decades, several cases of the disease were seen in humans and all were attributed to the [virus](#) jumping from other mammals.

Then, in 2017, an [outbreak](#) occurred in Nigeria and by 2022, it had spread across the globe, demonstrating that the virus had evolved to jump from human to human. In this new effort, the research team took a closer look at the [genome](#) of the virus behind mpox to learn more about its [evolutionary history](#), particularly how it relates to human infections.

The researchers sequenced the genome of the mpox virus to learn more about its evolutionary history. They found that the clade IIb was the one

that had spread around the world. They also noted that it looked different from other strains that had been seen before in Africa.

They found a mutation that had led to the production of an enzyme called APOBEC3, which was found to cause further mutations that alter genome base pairs. It was also found to have come about due to infections in humans. That allowed the team to trace the evolutionary history of the virus as it infected humans—they found such [mutations](#) going back to approximately 2016, which strongly suggests that the virus has been transmittable between humans since that year.

The research team concludes that there is a strong likelihood of multiple cases of small mpox outbreaks that have not been recognized, allowing the virus to spread under the radar. They further suggest stronger surveillance methods be established because the virus is still mutating rapidly and could become deadlier.

**More information:** Áine O'Toole et al, APOBEC3 deaminase editing in mpox virus as evidence for sustained human transmission since at least 2016, *Science* (2023). [DOI: 10.1126/science.adg8116](https://doi.org/10.1126/science.adg8116)

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