

Genetic sequencing points to endemic origin of monkeypox virus outbreak in Nigeria

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Scientists working to control a human outbreak of monkeypox virus (MPXV) in Nigeria performed genetic sequencing of patient samples, revealing that the outbreak likely originated from a source within the country. Their results emphasize the value of local surveillance for the early detection of viral spillovers and the need for advanced genetic characterization to help determine the origins of outbreaks.

"Based on our findings, it appears that the index case of the current outbreak in Nigeria was not imported, but probably originated from a spillover event or events involving reservoir hosts," said Gustavo Palacios, Ph.D., who heads the Center for Genome Sciences at the U.S. Army Medical Research Institute of Infectious Diseases. USAMRIID and a multinational team of collaborators published their analysis in a letter posted online this week in the journal *The Lancet Infectious Diseases*.

According to the World Health Organization, 172 suspected and 61 confirmed MPXV cases, including one death, were reported in different parts of Nigeria between Sept. 4 and Dec. 9, 2017. Prior to this outbreak, only ten such cases had been reported in the region between 1971 and 1978. Due to this lapse and the recent cases in the Congo Basin, the origin of the latest Nigerian outbreak needed to be identified, as did whether the outbreak was a result of a local zoonotic spillover event or importation from another endemic country.

The research effort was supported by the Institut Pasteur in Dakar (IPD)

in Senegal and the U.S. Defense Threat Reduction Agency. Sequencing equipment was provided to IPD, where the sequencing was conducted, by the Targeted Acquisition of Reference Materials Augmenting Capabilities (TARMAC) initiative and the Defense Biological Product Assurance Office (DBPAO) through a task order award to the National Strategic Research Institute. Outbreak control teams were composed of staff from the Bayelsa State Ministry of Health, Niger Delta University Teaching Hospital, Nigeria Field Epidemiology and Laboratory Training Program, and the Nigeria Centre for Disease Control.

According to Bruce Goodwin, director of the DBPAO, the sequencing capability established at IPD under the TARMAC initiative allowed for a significantly improved response time—less than two months from sample receipt to results that could be used by public health professionals working to control the outbreak. This effort demonstrates the importance of in-country sequencing capacity coupled with the appropriate protocols and support to produce actionable data. The data produced from this event was used to validate existing DBPAO assays, a process under TARMAC that ensures DBPAO is able to detect diseases of biodefense relevance.

Monkeypox virus was first identified in 1958 and has caused sporadic human outbreaks in central and western Africa, with a mortality rate between one and ten percent. Recently, MPXV outbreaks have occurred in Sudan (2005), the Republic of Congo and Democratic Republic of Congo (2009), and the Central African Republic (2016).

According to Palacios, genetic analysis of the virus's "family tree" indicates that the isolates described in the letter grouped most closely to a genome isolated from a human case in Ihie, Abia State, Nigeria in 1971, which is relatively close to the epicenter of the current [outbreak](#).

More information: Ousmane Faye et al. Genomic characterisation of

human monkeypox virus in Nigeria, *The Lancet Infectious Diseases* (2018). [DOI: 10.1016/S1473-3099\(18\)30043-4](https://doi.org/10.1016/S1473-3099(18)30043-4)

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