



## Study Finds Latest Monkeypox Outbreak is Result of Biolab Manipulated Virus, Released Intentionally?

### Description

**A new study published by Portugal's National Institute of Health has uncovered evidence that the virus responsible for the Monkeypox outbreak allegedly sweeping across Europe, America and Australia, has been heavily manipulated in a lab by scientists, and further evidence suggests it has been released intentionally.**



Monkeypox illness usually begins with a fever before a rash develops one to five days later, often beginning on the face then spreading to other parts of the body. The rash changes and goes through different stages before finally forming a scab which later falls off. An individual is contagious until all the

scabs have fallen off and there is intact skin underneath.

The disease has always been extremely rare and was first identified in humans in 1970 in the Democratic Republic of the Congo in a 9-year-old boy. Since then, human cases of monkeypox have been reported in 11 African countries. It wasn't until 2003 that the first monkeypox outbreak outside of Africa was recorded, and this was in the United States, and **it has never been recorded in multiple countries at the same time.**

**Until now.**

**Suddenly, we are being told that cases of monkeypox are now being recorded in the USA, Canada, the UK, Australia, Sweden, the Netherlands, Belgium, France, Spain, Italy and Germany, all at the same time.**

According to the UK Health Security Agency, **172 cases of monkeypox have been identified in England as of the week ending 29th May 2022** (*ER: we are truly sceptical*), and they have now [released new guidance](#) advising anyone with the virus to abstain from sex whilst they have symptoms, and to use a condom for at least eight weeks once the infection has cleared.

But there's something extremely strange about this outbreak, as if the fact we're allegedly witnessing an outbreak across first-world countries all at the same time for the first time in history wasn't strange enough.

We don't believe in coincidences, but there are many people that do. But we imagine those will do will struggle to comprehend this one.

**Back in March 2021, the Nuclear Threat Initiative (NTI) partnered with the Munich Security Conference to conduct [a tabletop exercise](#) on reducing high-consequence biological threats.**

The [exercise](#) examined gaps in national and international biosecurity and pandemic preparedness architectures—exploring opportunities to improve prevention and response capabilities for high-consequence biological events.

Here's the [scenario](#) that they conducted:

***A monkeypox outbreak that began on May 15th 2022, resulting in 3.2 billion cases and 271 million deaths by December 1st 2023.***

**Are we really to believe it's just a coincidence that we're now witnessing an actual monkeypox outbreak, with the first cases being reported to the World Health Organisation on May 13th 2022?**

The Munich Security Conference exercise revealed that the engineered monkeypox virus was developed illicitly at the fictional country of Anica's leading institute of virology by lab scientists working alongside an Arnican terrorist group. This terrorist group then released the "highly contagious and deadly" pathogen at a crowded train station in neighbouring fictional country Brinia.

Now, a new scientific study published by Portugal's National Institute of Health (NIH) suggests the real-world monkeypox outbreak may be the result of something eerily similar.

The study was published May 23rd 2022 and can be accessed in full [here](#).

Scientists from the NIH collected **clinical specimens from 9 monkeypox patients between May 15th and May 17th 2022** and analysed them.

The scientists concluded that the multi-country outbreak of monkeypox that we're now allegedly witnessing is **most likely the result of a single origin** because all sequences viruses released so far tightly cluster together.

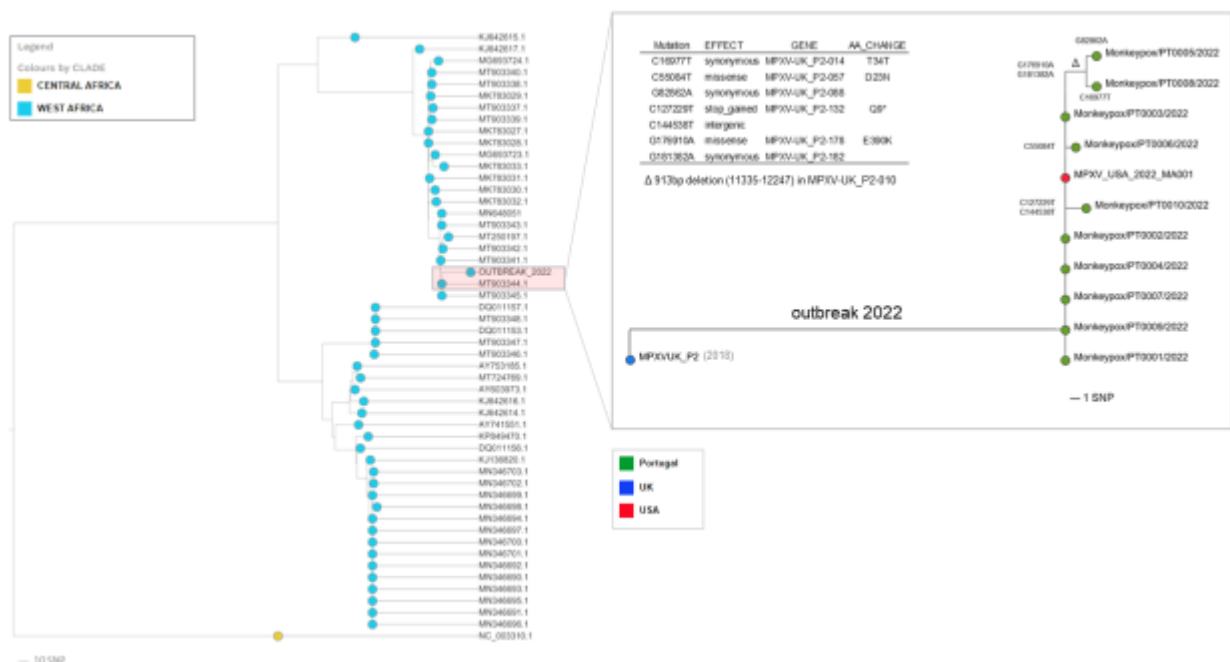


Figure 1: Draft phylogenetic analysis of Monkeypox viral sequences, highlighting the diversity within the outbreak cluster.

They also concluded that the virus belongs to the West African clade of monkeypox viruses. However, they found it is most closely related to monkeypox viruses that were **exported from Nigeria to several countries in 2018 and 2019, namely the UK, Israel and Singapore**. This is our first clue that this latest outbreak may be the result of an engineered virus leaking from a lab.

The next piece of evidence that this virus has leaked from a lab comes with the finding that whilst the virus **closely resembles** those exported from Nigeria in 18/19, **it is still different with over 50 single nucleotide polymorphisms (SNPs), which are genetic variations**. The scientists state **this is far more than one would expect**. This strongly indicates that somebody, somewhere has been playing with this virus in a lab.

- **The multi-country outbreak most likely has a single origin**, with all sequenced viruses released so far\* tightly clustering together (Figure 1).
- **Confirmation of the phylogenetic placement unveiled by the first draft sequence** [Isidro et al, 185](#) : the outbreak virus belongs to the West African clade and is most closely related to viruses (based on available genome data) associated with the exportation of monkeypox virus from Nigeria to several countries in 2018 and 2019, namely the United Kingdom, Israel and Singapore (1, 2).
- Still, **the outbreak virus diverges a mean of 50 SNPs from those 2018-2019 viruses** (46 SNPs from the closest reference MPXV\_UK\_P2, MT903344.1) ([📄 Table 1\\_2022-05-23.zip](#) (15.0 KB)), which is **far more than one would expect considering the estimated substitution rate for Orthopoxviruses** (3).

The final findings of the study are written in a way that is hard to get your head around, as follows:

- As also mentioned by Rambaut ([Discussion of on-going MPXV genome sequencing 231](#)), one cannot discard the **hypothesis that the divergent branch results from an evolutionary jump** (leading to a hypermutated virus) caused by APOBEC3 editing (4)
- We have already detected the **first signs of microevolution within the outbreak cluster, namely the emergence of 7 SNPs** ([📄 Table 2\\_2022-05-23.zip](#) (10.9 KB)), leading to 3 descendant branches (Figure 1) including a further sub-cluster (supported by 2 SNPs) involving 2 sequences (PT0005 and PT0008). Notably, these two sequences **also share a 913bp frameshift deletion** in MPXV-UK\_P2-010 gene coding for an Ankyrin/Host Range (Bang-D8L); D7L protein (MT903344.1 annotation). Gene loss events were already observed in the context endemic Monkeypox circulation in Central Africa, being hypothesized to correlate with human-to-human transmission (5).
- This microevolution scenario also suggests that **genome sequencing might provide enough resolution to track the virus dissemination in the context of the current outbreak** (which could seem implausible for a dsDNA virus).]

But thankfully, someone who has managed to get their head around the above is none other than **Dr Robert Malone**, and he has provided an easy to understand breakdown of what the Scientists are attempting to declare above:

“The authors speculate that the pattern of mutations is consistent with the effects of a natural cellular protein with the abbreviated name: **APOBEC3**. For those who want to dive into the molecular virology of **APOBEC3**, [here is a nice 2015 J Immunology review](#).

For those seeking the “Cliff Notes” abridged version, see [Wikipedia](#). For the obsessives or aficionados, note that APOBEC3 is associated with a specific pattern of base changes- (C?U). On the basis of their hypothesis regarding the potential role for APOBEC3, I infer

that the authors must have detected a statistically significant fraction of C?U changes in the current isolates relative to the 2018-2019 isolates.#

Here is the rub. While **APOBEC3 is associated with cellular resistance** (*yet another form of “innate immunity”*) **to HIV** (*and presumably other retroviruses*), **a quick PubMed search reveals that Poxviruses are resistant to the mutational effects of APOBEC3!**

For example, see this [2006 paper published in “Virology”](#). Frankly, whether through lack of curiosity or fear of attack from government-controlled media and journals, the failure of the authors to even mention this Virology article is a major oversight at best.

My inference and interpretation?

On the basis of this sequence analysis report from the INSA team cited above, to me, this is looking more like a laboratory manipulated strain than a naturally evolved strain. **Bad news.**

Furthermore, **this double-stranded DNA virus, infections by which have historically been self-limiting, appears to be evolving** (during the last few days!) **to a form that is more readily transmitted from human to human.**

**Bad news.”**

This newly published scientific study has essentially uncovered a mass of evidence pointing to the latest monkeypox outbreak being the result of a heavily manipulated virus that has leaked from a lab.

Couple this with the Munich Security Conference simulation conducted in March 2021 that just so happened to revolve around a monkeypox outbreak beginning in May 2022 as the result of a bioterrorist lab leak, then it's not hard to conclude that we're either witnessing a real-life monkeypox outbreak that has been purposely released from a lab, or one hell of a coincidence. And we don't believe in the latter.

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