

Two Studies now suggest the circulating Monkeypox Virus has been manipulated in a Biolab

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By The Exposé

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TWO STUDIES NOW SUGGEST THE CIRCULATING MONKEYPOX VIRUS HAS BEEN MANIPULATED & EDITED IN A BIOLAB

Recently we revealed how a study published by Portugal's Institute for Health had found abnormal mutations among the alleged circulating monkeypox virus suggesting it had been manipulated and edited in a biolab. Now a second study has been published adding weight to this theory.

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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.

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.

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

Multi-country outbreak of Monkeypox virus: genetic divergence and first signs of microevolution

Monkeypox | Genome Reports



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May 23

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Source

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 sequenced viruses released so far tightly cluster together.

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.

But while the virus closely resembles those exported from Nigeria in 18/19, it is still vastly different with over 50 single nucleotide polymorphisms (SNPs), which are genetic variations.

- **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, 2022](#): 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).

Richard Neher, a computational evolutionary biologist at the University of Basel has publicly claimed in the mainstream media that –

“Based on normal evolutionary timelines, scientists would expect a virus like monkeypox to pick up that many mutations over perhaps 50 years, not four. That is somewhat remarkable.”

Now a second study has been published that has found something in the alleged genome of the virus that shouldn't be there.

The authors of the study are Jean-Claude Perez and [Valère Lounnas](#) of the European Molecular Biology Laboratory. Their study is titled '[May 2022: Peculiar Evolution of the Monkeypox Virus Genomes](#)'.

The scientists compared the evolution of 14 monkeypox virus genomes with the aim of discovering mutations or other viral evolutions (recombination) that may explain the sudden impact of this very low-level circulating epidemic.

By chance, what the scientists discovered is that the alleged circulating monkeypox virus contains a '30-T long sequence in the centre of the monkeypox genome, between the DNA-dependent RNA and the cowpox A-type inclusion protein.

Monkeypox virus isolate MPXV_USA_2022_MA001, complete genome

GenBank: ON563414.3

[Gene 128941..132435](#) /note="A25R RNA polymerase subunit (RP0132) (Cop-A24R) RNA polymerase, 132 kDa subunit similar to [Vaccinia virus strain Copenhagen A24R](#)"

[gene complement \(133217..133444\)](#) /note="A-type inclusion protein (Cop-A25L), A26L" "MDP_FIV_STMT_KKQ_ER_KL_VK_RL_RQ_EL_TQ_LH_ED_LK_RV_RE_SD_KN_DS_TT_RE_SL_MK_QR_AK_VI_EV_EK_EL_ER_YF_DD_NR_LE_E"

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132481 tattatcggg ttcgggtattg ttactcgaga atagagttcg ttatgctcct gatattcggg
132541 aatctgtgga gtttcaggtt ttggtggaag tgtaactgct acttgggtgg atactgaagg
132601 atatttcaga gagttgtgga tggtcgggtt cgacatccac cgatgggtgc acgccactaa
132661 tcggttcggt aacgtctgtg gatggaggtg ctacttctac agaacctgta gcctcagttg
132721 tcaacggaga tacatattca atgcgcggaa atgtataatt tggtaatggt ttctcatgtg
132781 gatcttaaga agaagaggta agatatctac gaaagatacc gatcacgttt ctagtctctt
132841 tttgtagaac tttaaactttt tctttctcag catctagttg atattccgac ctcttcacgt
132901 ttgcgatggg ttacctcgcg agtttttaca agcgatttca cgttccagat cacgttcagc
132961 ctccatacgt ctctccctct ctctatcgag tttatcagag cagtctttct gaaggcgatc
133021 gaactccata aatttctcca acgctttgat tgtttccata gatctccgaa gtttagcttc
133081 taggacggcg attctttttt tttttttttt tttttttttt ttcgaattca cggggtacaa
133141 ccgtttccat taccaccatc tctatgtttc ttttctagat cggcaatctt tctcaacatt
133201 tcatccccat accttttca
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gene complement -          agtt tctctgagtc tattgtcgtc gaaatatcgt tccagctcct
133261 tttcgacctc aataacttta gcacgttggt tcatcaagct ctctcttgta gtactatcat
133321 ttttatctga ttccctgaca cgtttaagat ctctcatgta ttgagtcagc tcttgacgca
133381 atctcttaac taacttctc tcttgcttct tcgctcatagt acttacaatc actatgggat
133441 ccat
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Why is that strange? Well according to the scientists it is because this is never encountered fully inside a sequence. The scientists claim that whilst they may be common findings at the termination of a genome, for instance at the end of the monkey encephalitis virus, it is almost never encountered fully inside a sequence.

You can read the full study for yourself [here](#).

We allegedly have a circulating monkeypox virus in several first-world countries at the same time for the first time in history, and this alleged virus has over 50 mutations that have occurred in the space of 4 years instead of the 50 years it should have taken. And now we know it contains something that just shouldn't be there.

Are we really to believe that if this virus exists that it has occurred naturally? If you buy into germ theory then this whole thing reeks of viral manipulation in a biolab.

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