

# Monkey Pox Update: “War Game” Scenario Planning. “The Controlled Media Have No Shame”. Dr. Robert Malone

By [Dr. Robert Malone](#)

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[Who is Robert Malone](#) 31 May 2022

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Will the blatant fearporn ever stop? The controlled media have no shame.




If Ronald Reagan were still with us, I suspect we would be hearing “[There you go again](#)” replays. First came the coordinated media blast of public health-related fearporn. For example, the image from Jake Tapper’s CNN broadcast program “[The Lead](#)” of May 20, 2022 (above) which appears to me to be a case of smallpox, not monkeypox. Another example involves the self-explanatory paired images below.

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## Rare Monkeypox Cases Reported from US, First Time In Nearly 20 Years: All You Need To Know About It



Rare Monkeypox Cases Reported from US, First Time In Nearly 20 Years


**Monkeypox is a rare but potentially serious viral illness that is characterized by flu-like symptoms such as fever, chills, cold and cough, headache, swelling of the lymph nodes, etc.**

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What is shingles? (with pictures)

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### What is shingles? (with pictures)



You may have heard of chickenpox, but have you heard of shingles?

Shingles—also known as herpes zoster—is a disease caused by a reactivation of the [chickenpox](#) virus.

Shingles is a serious disease and [1 in 10 people](#) have nerve pain (which can be severe) caused by shingles which can sometimes last for months or even years.

Shingles causes a blistering rash and can only develop if you've had chickenpox before.

### What causes shingles and who is at risk?

And of course the Bill and Melinda Gates – funded GAVI text which is quite blatant, claiming 10% mortality, which I covered in my [prior substack article](#) concerning Monkeypox and fearporn.

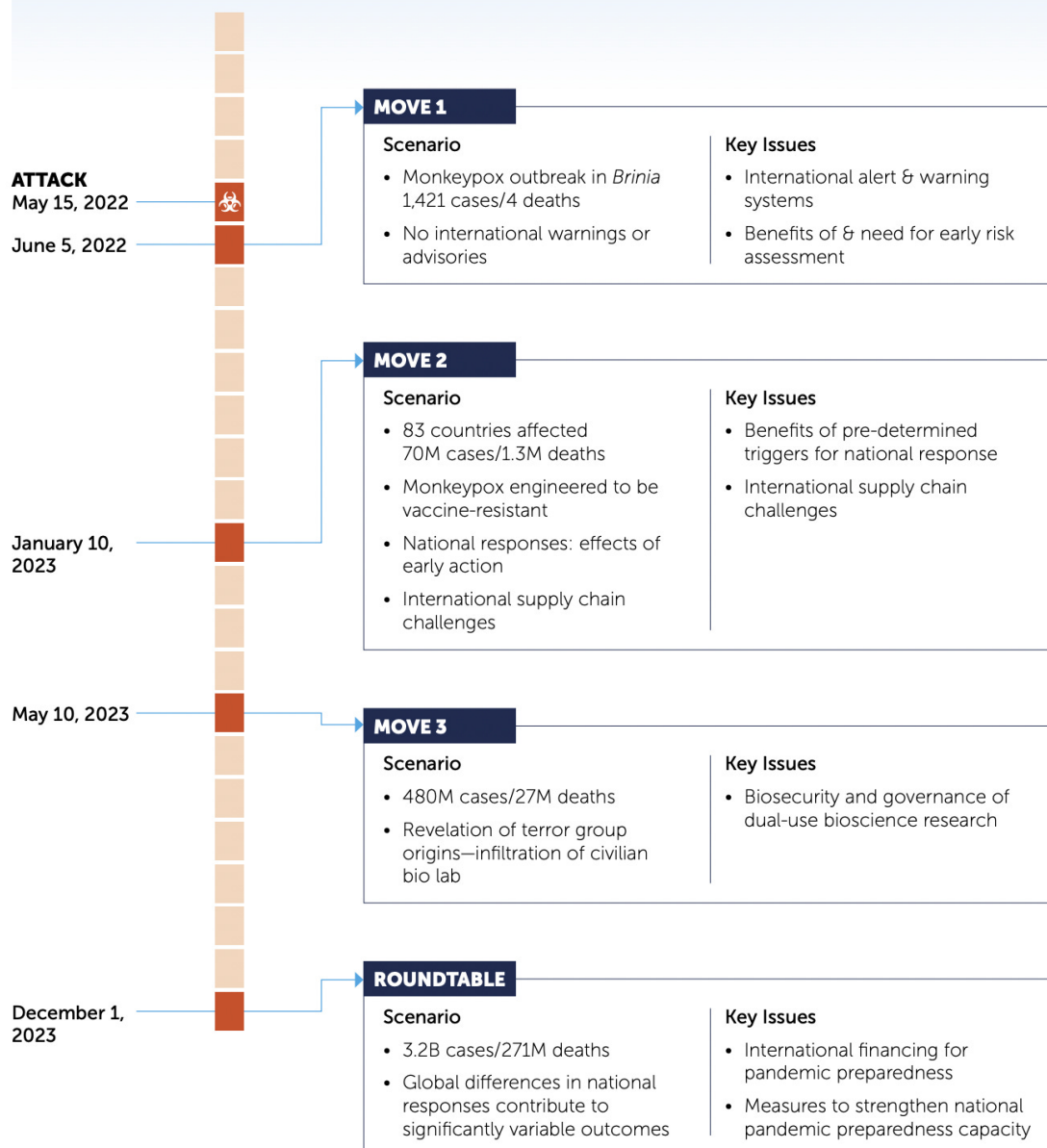
I almost cannot believe that I am writing this, but since my original substack article on this topic, we had the reveal of an [Event 201-style wargame exercise](#) modeled around a bioterror-related release of an engineered Monkeypox virus “caused by a terrorist attack using a pathogen engineered in a laboratory with inadequate biosafety and biosecurity provisions and weak oversight.”

With amazing (coincidental?) prescience, the “table top exercise” of March 2021 (one year and three months into the Covidcrisis) models a Monkeypox bioterror attack initiated on May 15, 2022.

Note the date of the CNN/Jake Tapper fearporn piece – May 20, 2022. The modeling deployed in the scenario upon which the “exercise” was based predicts 3.2 billion cases and 271 million deaths by December 01, 2023.

Of course, the predictive accuracy of the simplistic public health models such as that used to support this scenario have repeatedly proven to be absolutely horrid, and these types of models should be either relegated to the trash heap (or ongoing dumpster fire) as unscientific speculation which is all too frequently weaponized by the fearporn peddlers such as CNN, MSNBC, NYT, Washington Post. By now we all know the usual USG and WEF-controlled media players.

Figure 1. Scenario Design Summary



As the Italian's like to say:

*Niente e lasciato al caso.*

Nothing happens by chance.

As we now know, the amazing foresight of this modeled date immediately preceded a seminal WHO meeting which has just concluded, in which international health regulation (IHR) modifications which would grant the WHO unprecedented powers to bypass national constitutions (proposed on January 23, 2022 by the US HHS) were actively considered but tabled for a future meeting (~November 2022?) largely due to African nation concerns regarding infringement of national sovereignty. The stated purpose of the “exercise” was remarkably well aligned with the stated objectives and topics proposed by US HHS in the submitted IHR modifications:

- To establish a new global biosecurity entity dedicated to reducing emerging biological risks that can accompany certain technology advances. Its mission will

be to reduce the risks of catastrophic consequences due to accidents, inadvertent misuse, or deliberate abuse of bioscience and biotechnology by promoting stronger global biosecurity norms and developing tools and incentives to uphold them.

- To explore the possibility of establishing a new Joint Assessment Mechanism to investigate high consequence biological events of unknown origin. This new mechanism would operate at the “seam” between existing mechanisms—including World Health Organization (WHO) outbreak investigation capabilities and the United Nations Secretary-General’s Mechanism for investigating alleged deliberate bioweapons use—thereby strengthening UN system capabilities to investigate pandemic origins.
- To advocate for establishing a catalytic, multilateral financing mechanism for global health security and pandemic preparedness. The goal is to accelerate sustainable biosecurity and pandemic preparedness capacity-building in countries where resources are most needed.

So, do we have yet another example of a “[Plandemic](#)”? All I can say is ~

“Oh! What a tangled web we weave, when first we practice to deceive” (Sir Walter Scott, *Marmion*)

Or perhaps the more appropriate quote would be ~

The Italians having a Proverb, “He that deceives me once, its’ his fault; but if twice, its’ my fault.” – Anthony Weldon, *The Court and Character of King James* (1651)

In my prior substack entitled “[Monkey Pox, Truth versus Fearporn](#)”, I concluded the essay with the following caveat:

Unless there has been some genetic alteration, either through evolution or intentional genetic manipulation, it is not a significant biothreat, and has never been considered a high threat pathogen in the past.

Which brings us to [this](#) May 23, 2022 report from the Portuguese National Institute of Health.

## 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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Just to set the stage, the outbreak seems to be tightly associated with a point of origin at what appear to have been [two large European dance party events](#) (“Raves”), in the Canary Islands (“Gay Pride event in the Canary Islands, which drew some 80,000 people”) and “a Madrid sauna”.

The Canary Islands event was the 20th anniversary of “[Maspalomas Gay Pride](#)”, which took place from May 05 to May 15 (the precise date of the [previously modeled Monkeypox bioweapon release](#)). The organizers anticipated “a huge parade with over 100,000 participants, boat trips, pool parties and more!”. So, basically, pretty much a perfect opportunity for a Monkeypox super spreader event, whether intentional or inadvertent. Donning my “cynical skeptic” tinfoil hat for a moment, if one was looking for an opportunity to seek a pathogen into a highly mobile international population, mindful of the early history of HIV-based AIDS, this would be just what the doctor (Mengle...) ordered.

Multiple cases were soon detected in Portugal, and to their great credit, INSA Portugal got busy and promptly did the deep sequencing necessary to enable building a phylogenetic map of the Monkeypox variant associated with the outbreak.

Based on their findings, they have rapidly disclosed both their data as well as a series of startling hypothesis regarding the origin of the currently circulating Monkeypox (West African Clade) Monkeypox. Cutting to the chase, having reviewed their data and paper, I now have to conclude that one of the many “working hypotheses” concerning the origin of this particular virus must be that it is the product of laboratory-based manipulation – precisely as previously [modeled by the Nuclear Threat Initiative \(NTI\):Bio/Munich Security Conference](#) . True story. Truth continues to be stranger than fiction.

The authors briefly (and elegantly) summarize the study purpose and methods as follows:

Following the ([First draft genome sequence of Monkeypox virus associated with the suspected multi-country outbreak, May 2022 \(confirmed case in Portugal\) 184](#)), we now release 9 additional genome sequences of Monkeypox virus causing a multi-country outbreak. These sequences were obtained from clinical specimens collected from 9 patients on May 15th and 17th, 2022 through high throughput shotgun metagenomics using Illumina technology (see details bellow), with depth of coverage throughout Monkeypox genome ranging from 38x to 508x (mean of 201x).

The rapid integration of the newly sequenced genomes into the Monkeypox genetic diversity, also including the sequence released by USA\* (Gigante et al, [Monkeypox virus isolate MPXV\\_USA\\_2022\\_MA001, complete genome - Nucleotide - NCBI 156](#)).

They then proceed to raise the following main observations:

- 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, 183](#): 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).

- As also mentioned by Rambaut ([Discussion of on-going MPXV genome sequencing 228](#)), 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).

Those not versed in academic science talk may be shaking their head by this point, and probably getting ready to post a comment along the lines of “Why don’t you just tell us that this means in simple language?”

So, at the risk of oversimplification:

1. Looks like the Monkeypox outbreak comes from a single original virus source. Following the teachings of the “[Multiple working hypothesis](#)” model for arriving at scientific “truth” (which was a core part of my education as a young scientist), a) this could be (for example) a “natural” single jump event from some infected animal into a single human somewhere in the world (who presumably had some relationship to the [Maspalomas Gay Pride](#) event). Or b) it could have come from an intentional release of a viral isolate. Mixed news – could be good or bad
2. The authors have confirmed that this new outbreak virus maps to the “(less disease-causing) West African group (clade) of Monkeypox viruses. Good news
3. This single source virus could have come from West Africa or could have come from United Kingdom, Israel or Singapore (consistent with either hypothesis a or b). Mixed news – could be good or bad
4. Despite the sequences indicating that the virus is most closely related to those isolated in 2018-2019, it is significantly different. This could be due to natural evolution or due to laboratory engineering/gain of function “research” (consistent with hypotheses a) and b). Generally bad news. Basically, the authors are indicating that they believe that genome of this virus is either evolving more rapidly than one would expect from a double stranded DNA poxvirus, (left unsaid, or somebody has been messing around with it).
5. The authors speculate that the pattern of mutations are consistent with the effects of a natural cellular protein with the abbreviated name of 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 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. Mixed news – could be good

or bad. Still does not differentiate between hypothesis a) or hypothesis b).

6. Here is the rub. While APOBEC3 is associated with cellular resistance (yet another form of “innate immunity” - isn’t molecular virology and cell biology amazing!) 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.
7. 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.

In conclusion, the preponderance of current evidence is pointing towards a hypothesis for the origin of this outbreak which is increasingly consistent with prior “war game” scenario planning, remarkably akin to that which occurred during Event 201, which posits emergence of an engineered Monkeypox virus into the human population during mid-May of 2022.

Draw your own conclusions, and do your own diligence.

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