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A similar observation can be made for bivalent vaccine boosters containing the spike of omicron variants BA.5, in addition to wildtype SARS-CoV-2. Wildtype SARS-CoV-2 is neutralised most effectively, even though a broadening of the immune response towards newer omicron variants also occurs, but in a much lesser magnitude.⁶ If this broadening of the immune response offers long-lived improved protection from infection, especially by emerging omicron variants, remains to be seen.

But the insights gained through studies of neutralising antibodies do not seem to translate into higher mortality. Priming with wildtype SARS-CoV-2 through three vaccine doses upholds efficacy against the most important outcomes of vaccination, severe disease, and death in the case of an omicron infection,⁷ potentially aided by upheld T-cell immunity. And priming with pre-omicron variants of SARS-CoV-2, before an infection with the first omicron variants BA.1 or BA.2, reduced the risk of re-infection, rather than promoted it.⁸

Considering that infections with omicron variants were associated with less, albeit still considerable, serious adverse outcomes than the ancestral delta variant,⁹ it appears to be a beneficial population strategy to maintain high memory B-cell immunity against ancestral strains. The action of immune imprinting, by upholding high neutralising antibody titres against ancestral SARS-CoV-2 strains in the population, might help eradicate ancestral strains, in favour of attenuated strains circulating in consecutive waves. A novel (hypothetical) strain derived from the delta variant that shares the predisposition to cause lethal outcomes might be the worst-case scenario going forward in the pandemic in regions with high population-immunity. And immune imprinting might help protect us from this prospect.

We agree with Hoffmann and colleagues that overcoming immune imprinting might be needed to optimise vaccine efficacy against reinfection with omicron variants emerging today and in the future. We

can learn from the observation that the response towards newer omicron variants is enhanced in magnitude and breadth through previous infection,¹⁰ which exposes the immune system to wider range of non-neutralising epitopes. The frequency of vaccination and the time intervals between them also play an important role. Alternative strategies, such as mucosal vaccines, might also help in broadening the immune response.

Meanwhile, it should be considered that immune imprinting might be offering a wall of protection from even more severe variants derived from ancestral strains.

SC reports once being a part of a clinical advisory board of BioNTech in 2020. SH and SC received study support from Roche diagnostics.

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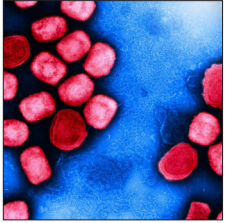
New nomenclature for mpox (monkeypox) and monkeypox virus clades



In May, 2015, WHO recommended best practices for naming new infectious diseases to avoid offense or economic effect for any ethnic, regional, or

other groups.¹ Although mpox (formerly known as monkeypox) is not new, WHO has endorsed mpox as the new name for this re-emerging disease and backed the

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scientific community to agree on neutral nomenclature for variants of viruses.

The first report of mpox that led to the discovery of the global outbreak was made to WHO on May 13, 2022. The outbreak spread to 110 countries² and was declared a public health emergency of international concern. The Director-General of WHO called on member states to ensure respect for human rights and to address stigma and discrimination.³ As of Jan 31, 2023, there were 85 549 confirmed cases of mpox reported by 110 countries, including 89 deaths.²

Mpox is caused by the species monkeypox virus (MPXV), genus *Orthopoxvirus*, discovered in 1958 in a primate research facility in Denmark, with the first human case reported in 1970.⁴ Two virus clades were identified: the Congo Basin (or central African) clade and the west African clade.⁵ Although stigma became a concern during outbreaks in Africa,⁶ the 2022 global outbreak reignited discussion with proposals to rename virus clades.⁷

Although the nomenclature of virus variants is the remit of scientists, reaching consensus quickly was important. On Aug 8, 2022, WHO convened an ad-hoc expert meeting to discuss characteristics of MPXV clades and propose names for them. Participants included orthopoxvirologists, evolutionary biologists, and other scientists from (1) WHO collaborating centres on orthopoxviruses at the US Centers for Disease Control and Prevention and the Russian State Research Centre of Virology and Biotechnology; (2) the WHO Technical Advisory Group on SARS-CoV-2 Virus Evolution; (3) the WHO Advisory Committee on Variola Virus Research; (4) the Poxviridae study group of the International Committee on the Taxonomy of Viruses; (5) research and public health institutes in Africa and around the world; and (6) public virus-sequence databases.

The meeting reviewed the phylogeny and characteristics of MPXVs and proposed a neutral naming convention.⁷ MPXV phylogeny shows two distinct clusters corresponding to the previously recognised clades. Consensus was reached for nomenclature of a Roman numeral for each clade with lowercase Latin characters for subclades; the Congo Basin clade became Clade I and the west African clade became Clade II, encompassing two phylogenetically distinct subclades, IIa and IIb.⁸

There are appreciable genetic differences between Clades I and II, showing nearly twice the divergence as that between subclades IIa and IIb. Nonetheless, both subclades include genomes from the 1960s and 1970s and appear to have evolved separately from a most recent common ancestor dating back hundreds of years. Neither subclade is descended from the other.⁵ Although the current global outbreak is related primarily to Clade IIb, new cases related to Clade IIa continue to be reported, requiring the tracking of numerous clades and lineages.

To distinguish emerging lineages, nomenclature that encodes genealogical relationships between variants was proposed. Lineage labels would follow the convention used for SARS-CoV-2, with an uppercase Latin character followed by a period, and a number representing the *n*th descendant of the Latin character (eg, Clade IIb.A.1).⁹ The assignment of virus lineage will help to identify epidemiological links within and across geographic regions and support the understanding of evolutionary dynamics.

Parallel discussions considered changing the disease name in the WHO International Classification of Diseases (ICD). WHO issued a public call for new name suggestions for monkeypox in August, 2022. Over 200 proposals received on the ICD platform were reviewed with criteria such as rationale, appropriateness, current usage, scientific accuracy, pronounceability, translatability, potential for confusion, and the guidance for the naming of new diseases. Consultations involved the ICD Medical and Scientific Advisory Committee, the Classification and Statistics Advisory Committee with representation from WHO member states, and the WHO Family of International Classifications. The review recommended the use of mpox as a synonym or inclusion name for monkeypox. The new name was proposed by a men's health community organisation, endorsed by WHO after all suggestions were considered,¹⁰ and is being phased in as a synonym to become the preferred term of the ICD after December, 2023. Discussions on terminology in other languages will continue throughout 2023, providing member states with a choice of preferred term in their language for national usage and statistics. Mpox is now included in ICD-10 and ICD-11, effective as of January, 2023.¹⁰ WHO encourages all member states and stakeholders to follow these recommendations on mpox and its virus clades.

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All other authors declare no competing interests. The working group thanks African scientists who advocated for new clade names for MPXV, and front-line health workers and advocates at Rézo, a Montreal community based organisation for gay, bisexual, queer, cis, and trans men who have sex with men, who led a grassroots movement to rename mpox. DU chaired the ad-hoc experts meeting on MPXV clades and variants, which involved authors AA, JB, KK, EJL, MRM, TdO, JO, AR, and RFL, and experts Ifedayo Adetifa, Oluwatoni Akinola, Olajumoke Babatunde, Sylvie Briand, Clarissa Damaso, Inger Damon, Drew Endy, Delia Enria, Mariano Esteban, Bradley Hersh, Christina Hutson, Yu Li, Abdi Mahamud, Sandy Mak, Peter Mala, Colin McInnes, Jean-Vivien Mombouli, Richard Neher, Nnaemeka Ndodo, Mark Perkins, Mike Ryan, Jilian Sacks, Soumya Swaminathan, Henda Triki. We thank Meng Zhang, Co-Chair of the ICD Classification and Statistics Advisory Committee, all participants in these discussions, and Maria Van Kerkhove for ongoing support. The findings and conclusions in this Comment are those of the authors and do not necessarily represent the views of their respective institutions.

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Peer review at *The Lancet Infectious Diseases* in 2022



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With this issue of *The Lancet Infectious Diseases* the editorial team would like to thank the 1152 peer reviewers who provided reports for articles in the journal. We are especially grateful to the reviewers who have assessed fast-track articles, for example, containing essential information relating to COVID-19 or mpox. Furthermore, we particularly appreciate the peer reviewers who have assessed several articles.

As in previous years, we have assessed some of the demographics of our peer reviewers, although we only have data for the first 6 months of 2022 that is comparable to previous years, as we have switched to a more detailed assessment in the middle of the year. Of invited reviewers who have reported their gender, 40% were women, which is slightly higher than in the previous year. However, we do not have data on more than a third of invited reviewers. By contrast, we have

data for 97% of reviewers who submitted a report and, in this group, 36% were women and 0.4% gender-diverse or non-binary, similar to the previous year. 21% of reviewers who submitted a report are from a low-income or middle-income countries. Both the gender and country data are similar to the previous year and we are continually working on broadening our peer reviewer base to make sure it reflects the diversity of our readership and of the people and regions affected by the infectious diseases that we cover.

Without the expertise and input of our peer reviewers the journal would not be possible and we are grateful for their support.

I declare no competing interests.

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