

Omicron's BQ.1.1 and XBB sub-variants: a global problem and management strategies

Subvariantes BQ.1.1 y XBB de ómicron: un problema global y estrategias de manejo

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To the Editor,

In response to the statement by the World Health Organization Technical Advisory Group on SARS-CoV-2 Virus Evolution (TAG-VE) regarding the current "soup" variants, BQ.1.1 and XBB, and their health implications¹⁻³, the published studies are limited but highlight 3 works mentioning that the BQ.1.1 variant is a descendant of the Omicron subvariant BA.5 and BQ.1. The BQ.1.1 variant has one of the highest numbers of immune-evasive mutations in regions coding for key antigenic sites of the Spike protein, including p.K444T, p.N460K, and p.R346T. This strain has a global rate of 65% (GISAID)¹⁻³. The subvariant XBB*, on the other hand, is a recombination of sublineages BA.2.10.1 and BA.2.75, with a global prevalence of 1.3%. It is a hybrid subvariant with seven key mutations enabling immune evasion¹⁻³. Clinically, its distinctive characteristics have not been reported.

Considering this, and the importance of early clinical identification to reduce mortality, it can be achieved with an examination of the oral cavity, which has enabled differentiation among SARS-CoV-2 variants, even Omicron subvariants, each with unique features⁴. In light of new immune-evasive variants, trained immunity must be reactivated, for which we have the immunoregulator OM-85, which promotes phagocytosis and reduces viral expression, and has been foundational in Omicron management in the Sierra Sur of Oaxaca⁴. In the case of the XBB variant, we suggest calcium dobesilate, which blocks the binding of heparan sulfate to ACE2, or LP pirfenidone, which

downregulates ACE2⁵, thereby inhibiting SARS-CoV-2 entry into the cell. Currently, there are new viral receptors to consider, such as GPR78, exotoxins, and xylosyl transferases that, through docking, interact with SARS-CoV-2⁶. Carboplatin and gemcitabine are effective in such cases. Instead of viewing this as a global health issue, it is necessary to pursue innovative treatments, particularly those based on early diagnosis.

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Conflicts of interest

None declared.

Ethical disclosures

Protection of human and animal subjects. The authors declare that no experiments were performed on humans or animals for this study.

Confidentiality of data. The authors declare that no patient data appear in this article. Furthermore, they have acknowledged and followed the recommendations as per the SAGER guidelines depending on the type and nature of the study.

Right to privacy and informed consent. The authors declare that no patient data appear in this article.

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References

1. World Health Organization. TAG-VE statement on Omicron sublineages BQ.1.1 and XBB. (Consultado el 20-11-2022.) Disponible en: <https://www.who.int/news/item/27-10-2022-tag-ve-statement-on-omicron-sublineages-bq.1-and-xbb>.
2. Wong C. Subvariant 'soup' may drive wave. *New Sci.* 2022;256:11.
3. Callaway E. COVID 'variant soup' is making winter surges hard to predict. *Nature.* 2022;611:213-4.
4. Domínguez-Rodas J, López de la Mora DA, Dávalos NO, Ramírez-García SA, Rincón AR, Guzmán LR, et al. Detección clínica y descripción de las características socio-demográficas de la variante SARS-COV-2 omicron en población de la sierra sur de Oaxaca. *Cir Cir* 2022;90:567-472.
5. Seifirad S. Pifenidone: a novel hypothetical treatment for COVID-19. *Med Hypotheses.* 2020;144:110005.
6. Achom A, Das R, Pakray P. An improved Fuzzy based GWO algorithm for predicting the potential host receptor of COVID-19 infection. *Comput Biol Med.* 2022;151:106050.