The Rise and Fall of SARS-CoV-2 Variants

A Ascensão e Queda das Variantes de SARS-CoV-2

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Dear Editor.

As the pandemic evolves, Portugal and countries worldwide are facing the threat of the emergence of new SARS-CoV-2 variants, which represent potential game-changers in this fight. One of the most recently detected variants was the Mu variant (B.1.621). It was classified on August 30 by the World Health Organization as a variant of interest for presenting mutations that are shared with some of the variants of concern and that suggest a potential property of immunological escape.1 This lineage carries several Spike protein mutations, some common with other variants of concern, while others are new. Indeed, experimental studies demonstrated that the Mu variant could escape humoral immunity acquired from infection from previous strains or vaccines.² At that point, further studies were required to assess the biological and epidemiological roles of the substitution pattern found.

However, the scientific community's interest quickly faded in parallel with the favorable epidemiological evolution of the new variant. In terms of cases sequenced, the global prevalence rate has been increasing since January, peaked in mid-July and then declined, being consistently below 0.2% (spectrum). In Portugal, it was reported firstly at the end of May, and, until now, a total of 24 cases were sequenced; a decreasing trend was observed, representing 0% of sequenced cases since August.3 Thus, the Mu threat seems to have been quelled. However, its emergence reminds us that the tracking of SARS-CoV-2 variants is crucial. The first Italian cluster of the SARS-CoV-2 B.1.621 lineage was associated with a traveler from Colombia, which underlines that surveillance of SARS-CoV-2 genomic evolution is essential to limit the spread of new lineages to different countries.4

At the moment, a new Delta sublineage (AY.4.2) is arising in England and was classified as 'variant under investigation' on October 22nd by the UK Health Security Agency.5 It contains two mutations in the Spike protein, already found in other lineages and has been suggested that it might be 10% to 15% more transmissible than the original Delta variant.5 The first cases emerged in late June and represent up to now less than 1% of cases sequenced worldwide.3 In Portugal, nine cases were sequenced, and the respective epidemiological contexts are under investigation.3 Further studies concerning the ability to escape immunity are needed.

As countries gradually resume pre-pandemic activities, risk assessments should continue to be conducted systematically, updating the global lists of variants to support priority setting for surveillance and research, and ultimately guide response strategies.

AUTHORS CONTRIBUTION

TPS: Conducted the research and wrote the first draft of the letter; approved the final draft of the manuscript.

AA, MP: Participated in the writing, reviewing and editing of the letter; approved the final draft of the manuscript.

RD: Conceived the idea and participated in the writing, reviewing and editing of the letter; approved the final draft of the manuscript.

COMPETING INTERESTS

The authors have declared that no competing interests

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- 1. Unidade de Saúde Pública. Agrupamento de Centros de Saúde Tâmega III. Vale de Sousa Norte, Pacos de Ferreira, Portugal,
- 2. EPIUnit. Instituto de Saúde Pública. Universidade do Porto. Porto. Portugal.
- 3. Laboratório para a Investigação Integrativa e Translacional em Saúde Populacional. Porto. Portugal.
- 4. Unidade de Investigação Clínica. Administração Regional de Saúde Norte. Porto. Portugal
- 5. Faculdade de Psicologia e Ciências da Educação. Universidade do Porto. Porto. Portugal
- 6. Departamento de Saúde das Populações, Instituto de Ciências Biomédicas Abel Salazar, Universidade do Porto, Porto, Portugal,
- 7. Serviço de Pneumologia. Centro Hospitalar de Vila Nova de Gaia/Espinho. Vila Nova de Gaia. Portugal

Autor correspondente: Teresa Silva. atpsilva@arsnorte.min-saude.pt

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