

# Severe reinfection with South African SARS-CoV-2 variant 501Y.V2: A case report.

Noémie Zucman<sup>1,2\*</sup>, Fabrice Uhel<sup>1\*</sup>, Diane Descamps<sup>2-4</sup>, Damien Roux<sup>1,2,4</sup>, Jean-Damien Ricard<sup>1,2,4</sup>

1. AP-HP, Hôpital Louis Mourier, Médecine Intensive Réanimation, DMU ESPRIT, F-92700, Colombes, France.
2. Université de Paris, UFR de médecine Paris Nord, F-75018 Paris, France
3. AP-HP, Hôpital Bichat Claude Bernard, Virologie, 75018 Paris, France
4. IAME, INSERM UMR 1137, F-75018 Paris, France

\*NZ and FU contributed equally

*Corresponding author:*

Dr Fabrice Uhel, Réanimation médico-chirurgicale, Hôpital Louis Mourier, AP-HP, 178 rue des Renouillers, 92700 Colombes, France. Phone: +33 147 606 193. Mail: [fabrice.uhel@aphp.fr](mailto:fabrice.uhel@aphp.fr)

Dear editor,

The rapid acquisition of herd immunity appears to be the only way out of the COVID-19 pandemic. However, the strength and duration of immunity against this coronavirus are still uncertain. Reinfections have been described but remain rare albeit probably underestimated (31 confirmed cases worldwide as of January 2021), and in most cases less severe than the initial infection [1,2]. However, major concern is arising from the recent description of variants carrying mutations providing SARS-CoV-2 with selective advantages. Three emerging variants of concern (VOC) are currently associated with a new rise in the incidence and mortality related to COVID-19. There are well-grounded fears that these VOC could cause reinfections or post-vaccination infections. As a matter of fact, we read with interest the article by Harrington et al. describing a case of reinfection with SARS-CoV-2 Variant VOC-202012/01 [3].

We here report a case of severe SARS-CoV-2 reinfection with South African variant 501Y.V2, four months after recovering from a first episode of COVID-19. In September 2020, a 58-year old immunocompetent male with a history of asthma presented with mild fever and dyspnea. SARS-CoV-2 infection was diagnosed by real-time RT-PCR on a nasopharyngeal swab. Symptoms resolved within a few days and the patient tested negative twice in December 2020. In January 2021, 129 days after onset of the first infection, he presented to hospital for recurrent dyspnea and fever. SARS-CoV-2 RT-PCR was positive again, and viral genome sequencing identified D80A, E484K and N501Y mutations in the spike region, characterizing the 501Y.V2 lineage B.1.351 variant. Seven days later, the patient developed a severe acute respiratory distress syndrome requiring intubation and mechanical ventilation. He was treated with dexamethasone and tocilizumab. Antibody testing was positive for IgG against SARS-CoV-2. The patient was negative for HIV, and showed no biological evidence for immunological disorder. He is still in critical condition at the time of submission. The strain responsible for the first episode of COVID-19 was not available for sequencing. However, the

occurrence of the primary infection one month before emergence of the 501Y.V2 strain in South Africa and three months before its first description in France rules out the hypothesis of a persistent viral shedding from the first infection.

This is, to our knowledge, the first description of reinfection with the South African SARS-CoV-2 VOC 501Y.V2 causing severe COVID-19, four months after a first mild infection. Whether SARS-CoV-2 infection confers immunity against recurrent infections remains controversial. Experimental reinfections in rhesus macaques and follow-up of patients infected during the first wave suggest that adaptive immunity confers acceptable protection against reinfection for at least six months [4,5]. However, cases of SARS-CoV-2 reinfections despite detectable serum levels of neutralizing antibodies have been reported, some of which being more severe than the first occurrence [6]. The emergence of variants with increased virulence is a new matter of concern. The 501Y.V2 variant, initially detected in South Africa, has rapidly spread worldwide as of December 2020 [7]. It is characterized by eight mutations in the spike protein-coding sequences, including three in the receptor-binding domain (K417N, E484K and N501Y) that may account for its increased transmissibility [8]. This variant has not been reported to be responsible for more severe disease or worse outcomes so far [9]. However, the impact of 501Y.V2 mutations on the effectiveness of vaccines developed based on earlier SARS-CoV-2 strains is still unknown.

Our case illustrates that the 501Y.V2 SARS-CoV-2 variant can also be responsible for severe reinfections after a first mild infection with non-VOC SARS-CoV-2. Further investigation is urgently needed to assess cross immunity against VOC 501Y.V2, and to monitor vaccine effectiveness against new variants.

## NOTES

### *Collaborators:*

Benoit Visseaux, IAME, INSERM UMR 1137, AP-HP, Hôpital Bichat - Claude Bernard, Virologie, F-75018 Paris, France

Laurent Abel, Paul Bastard, Université de Paris, Laboratoire de génétique humaine des maladies infectieuses, INSERM U1163, Institut Imagine, Hôpital Necker Enfants Malades, F-75015 Paris, France

Frédéric Rieux-Laucat, Université de Paris, Laboratoire Immunogénétique des maladies auto-immunes pédiatriques, INSERM UMR 1163, Institut Imagine, F-75015 Paris, France

Luce Landraud, Université de Paris, IAME, INSERM UMR 1137, F-75018 Paris, AP-HP, Laboratoire de Microbiologie Hygiène, Hôpital Louis Mourier, F-92700, Colombes, France

Sébastien Besset, Santiago Freita-Ramos, Isabelle Priour, Charles Verney, Coralie Gernez, Médecine Intensive Réanimation, AP-HP, Hôpital Louis Mourier, DMU ESPRIT, F-92700, Colombes, France.

## Potential conflicts of interest

D.R. reports personal fees from Astellas, outside the submitted work. J.-D.R. reports travel expenses from Fisher & Paykel. D.D. reports personal fees from Viiv Healthcare, Gilead-Sciences, and Janssen-Cilag, outside the submitted work; None of the other authors has any potential conflict or funding source.

## References

1. Babiker A, Marvil C, Waggoner JJ, Collins M, Piantadosi A. The Importance and Challenges of Identifying SARS-CoV-2 Reinfections. *J Clin Microbiol* **2020**; :JCM.02769-20.
2. Lee J-S, Kim SY, Kim TS, et al. Evidence of Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection After Recovery from Mild Coronavirus Disease 2019. *Clin Infect Dis* **2020**; :ciaa1421.
3. Harrington D, Kele B, Pereira S, et al. Confirmed Reinfection with SARS-CoV-2 Variant VOC-202012/01. *Clinical Infectious Diseases* **2021**; Available at: <https://doi.org/10.1093/cid/ciab014>. Accessed 22 January 2021.
4. Stokel-Walker C. What we know about covid-19 reinfection so far. *BMJ* **2021**; 372:n99.
5. Deng W, Bao L, Liu J, et al. Primary exposure to SARS-CoV-2 protects against reinfection in rhesus macaques. *Science* **2020**; 369:818–823.
6. Tillett RL, Sevinsky JR, Hartley PD, et al. Genomic evidence for reinfection with SARS-CoV-2: a case study. *Lancet Infect Dis* **2021**; 21:52–58.
7. WHO | SARS-CoV-2 Variants. World Health Organization, Available at: <http://www.who.int/csr/don/31-december-2020-sars-cov2-variants/en/>. Accessed 22 January 2021.
8. Tegally H, Wilkinson E, Giovanetti M, et al. Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa. *Epidemiology*, 2020. Available at: <http://medrxiv.org/lookup/doi/10.1101/2020.12.21.20248640>. Accessed 24 January 2021.
9. Eurosurveillance editorial team. Updated rapid risk assessment from ECDC on the risk related to the spread of new SARS-CoV-2 variants of concern in the EU/EEA - first update. *Euro Surveill* **2021**; 26.

Accepted Manuscript