SARS-CoV-2 Variants' temporal and Viral Load Distributions In Immunocompromised Patients

Karen ZAFILAZA[1], Valentin LEDUCQ[1], Romain COPPEE [2] , Eve TODESCO[1], Cathia SOULIE[1], Anna-Maria FRANCO YUSTI[2], Antoine FAUCHOIS[2], Charlotte CHARPENTIER[2], Antoine BRIDIER-NAHMIAS[2], Diane DESCAMPS[2], Anne-Geneviève MARCELIN[1], Vincent CALVEZ[1], Valentine FERRE[2], Stéphane MAROT[1] for the EMERGEN Study group

[1]Sorbonne Université, INSERM, Institut Pierre Louis d'Epidémiologie et de Santé Publique (iPLESP), AP-HP, Hôpital Pitié-Salpêtrière, Service de virologie, Paris, France
[2]Université de Paris, INSERM, UMR1137, IAME, Service de Virologie, Hôpital Bichat-Claude Bernard, AP-HP, Paris, France

BACKGROUND

Since the beginning of COVID-19 pandemic, the general population has become widely immune and protected from severe symptoms, despite the regular arise of new variants. However, immunocompromised patients still have worse clinical outcomes, higher mortality and rarely develop effective immunity through vaccination or infection.

➔ We studied the **temporal distribution** of infections, **viral loads** as well as the **viral genetic diversity** among an immunocompromised patient cohort, between January 2021 and September 2022.

METHODS

- **478 immunocompromised patients and 234 health care worker controls** (HCW) from two large hospitals in Paris diagnosed with SARS-CoV-2 infection by **RT-qPCR** were enrolled.
- **Whole Genome Sequencing** was performed according to the ARTIC protocol on the **Oxford Nanopore** platform.
- Viral genomes were used to **determine lineage** and mapped to Wuhan-Hu-1 reference to **produce a phylogenetic tree.**
- Differences in temporal distribution of infections and viral loads were assessed using nonparametric statistical tests.

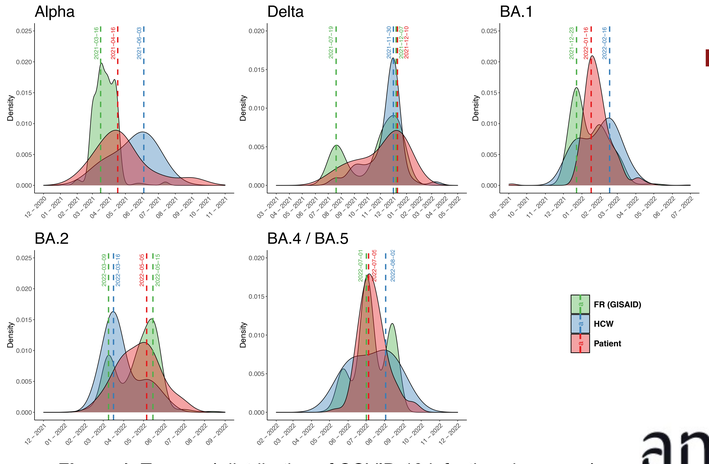


Figure 1. Temporal distribution of COVID-19 infections in general population, hospitalized immunocompromised patients and health care workers, according to different variants

No temporal or genetic differences between the strains infecting immunocompromised patients and HCW.

Lower Viral Load of Omicron subvariants at the time of infection.

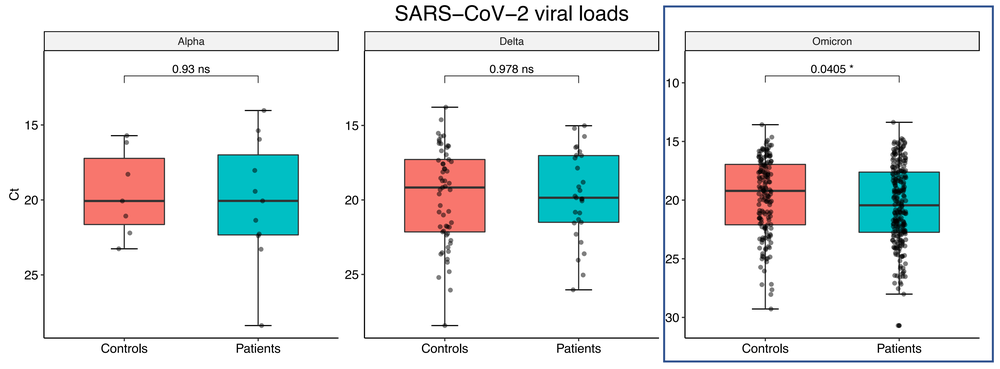


Figure 2. SARS-CoV-2 viral loads between immunocompromised patients and controls according to different variants

RESULTS

- **The temporal distribution of COVID-19 infections were similar** between immunocompromised patients and HCW **except with BA.2** for which HCW appear to be infected earlier (p<0,001) (**Fig.1**)
- **Viral loads** of immunocompromised patients infected with Omicron variants were **significantly lower** (p=0,04). No differences in viral load are observed for Alpha and Delta variants. (**Fig. 2**)
- SARS-CoV-2 infecting immunocompromised patients and those infecting healthy individuals are distributed in a similar way. There was no significant genetic difference between viral genomes from patients and HCW within the different lineages (**Fig. 3**)

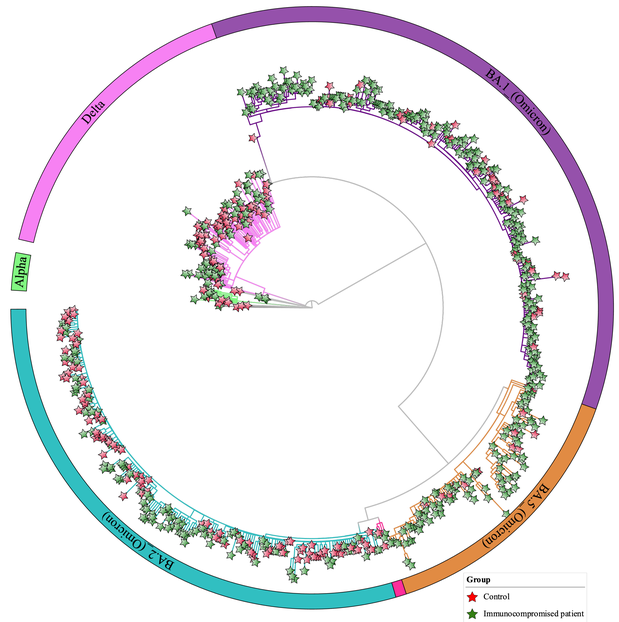


Figure 3. Phylogenetic tree (IQTree, 1000 bootstraps) of immunocompromised patients and HCW viral's genome

CONCLUSIONS

- There were **no genetic or temporal distribution differences** at the time of infection except for BA.2. These findings suggested that immunocompromised patients are infected by the same strains circulating in the general population.
- For **Omicron BA.2**: temporal distribution suggests that HCW were infected before immunocompromised patients.
- **Viral loads were lower** in immunocompromised patients infected with **Omicron** variants.
- An earlier peak of Omicron viral load and a testing of Immunocompromised patients hospitalized once severe symptoms have appeared could imply a testing in these patients once the replicative phase over.

ADDITIONAL KEY INFORMATION

Funded by ANRS | MIE EMERGEN consortium
Author Contact Information : karen.zafilaza-ext@aphp.fr