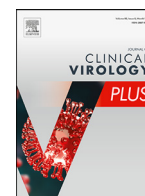




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## Short communication

## Duration of COVID-19 PCR positivity for Omicron vs earlier variants

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## ARTICLE INFO

## Keywords:

COVID-19  
SARS-CoV-2  
Vaccination  
Prior infection

## ABSTRACT

There have been reports that the Omicron variant of SARS-CoV-2 is milder and may resolve more quickly than earlier variants of SARS-CoV-2, like the Delta variant. Due to a dearth of studies on duration of PCR positivity for the Omicron variant, we studied this question in a cohort of routinely tested employees that work in a large laboratory. We found that there was no difference in duration of PCR positivity among those infected with the Omicron variant of SARS-CoV-2 versus earlier variants of SARS-CoV-2. That suggests in a clinical study that the increased infectiousness of Omicron might likely be due to factors related to viral and host cell interactions, rather than viral load or duration of infectivity, which has been suggested in immune escape studies.

The Omicron variant of SARS-CoV-2 can partially evade the humoral immune system and may have a shorter incubation period than ancestral strains Jansen et al. [1]. Most of the viral studies of SARS-CoV-2 infection that defined duration of infectiousness were conducted prior to *en masse* vaccinations and the emergence of new SARS-CoV-2 variants [2]. We aimed to assess if the duration of nasal PCR positivity was different for the Omicron variant of SARS-CoV-2 versus earlier variants.

In March 2020, Curative, a COVID-19 testing company, began routinely screening its workforce with a SARS-CoV-2 polymerase chain reaction (PCR)-based test, which was Food and Drug Administration-authorized SARS-CoV-2 [3]. The workforce has been undergoing daily screening. In Fall 2021, the workforce was mandated to be vaccinated for COVID-19. The first case of the Omicron variant of SARS-CoV-2 in the United States was detected on 1 December 2021 and quickly became the prevalent strain of SARS-CoV-2 [4].

We aimed to assess the duration of PCR positivity before and after 1 December 2021 among infected employees, when the Omicron variant of SARS-CoV-2 became the dominant strain [4]. Infection was defined as at least 2 positive sequential nasal PCR tests. Clearance was defined as at least 2 negative sequential PCR tests. All employee samples were sent for sequencing. Analyses were performed on SQL (IBM, Armonk, NY).

The study of de-identified electronic medical record data was determined by the Advarra institutional review board (Pro00054560) to be exempt from review.

In the cohort, demographic characteristics were similar between groups. All employees were vaccinated (Table 1). We identified 770

Table 1

Characteristics and duration of PCR positivity among a cohort of employees routinely tested for SARS-CoV-2.

Variable	Value	
	Before Dec 1 (N = 36)	On or after Dec 1 (N = 734)
Duration of PCR positivity	12.9 (SD: 6.8)	14.3 (SD: 7.0)
Age (years)	33.6 (SD: 12.6)	31.6 (SD: 9.1)
Female	66.7%	63.5%
Heritage		
Asian	2.8%	1.5%
Black or African American	5.6%	12.1%
White	22.2%	16.8%
Other/Prefer not to share	69.4%	69.6%
Hispanic	16.7%	20.8%

infections. There were 36 infections that occurred before 1 December 2021 (pre-Omicron period). Those were PCR positive for an average of 12.9 days (Standard deviation [SD]: 6.8). There were 734 infections that occurred after 1 December 2021 (Omicron period). Those were PCR positive for an average of 14.3 days (SD: 7.0). Durations of infection between the pre-Omicron period and Omicron period were not significant.

In a study by Puhach et al. that assessed viral burden, the mean nasopharyngeal viral copy values and the infectious viral load among infections caused by the Delta and Omicron variants of SARS-CoV-2 were similar [5]. PCR positivity generally lasts longer than the period an individual is infectious [2]. Infectiousness is predicted by an individual's viral load, duration of infection, and viral characteristics, like a virus'

Abbreviations: SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; PCR, polymerase chain reaction; COVID-19, coronavirus disease 2019.

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<https://doi.org/10.1016/j.jcvp.2022.100085>

Received 16 May 2022; Accepted 20 May 2022

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ability to bind to and enter a host cell [6][1,5]. Given our findings and those of Puhach et al., the increased infectiousness of Omicron might likely be due to factors related to viral and host cell interactions, rather than viral load or duration of infectivity.

### Funding

None

### Declaration of Competing Interests

NK is a consultant for Curative. AR is employed by Curative. JDK is an independent consultant and serves as the Medical Director of Curative.

### Acknowledgements

None.

### References

- [1] L. Jansen, B. Tegomoh, K. Lange, K. Showalter, J. Figliomeni, B. Abdalhamid, et al., Investigation of a SARS-CoV-2 B.1.1.529 (Omicron) variant cluster - Nebraska, *MMWR Morb. Mortal Wkly. Rep.* 70 (5152) (2021) 1782–1784, doi:[10.15585/mmwr.mm705152e3](https://doi.org/10.15585/mmwr.mm705152e3).
- [2] T. Jefferson, E.A. Spencer, J. Brassey, C. Heneghan, Viral cultures for coronavirus disease 2019 infectivity assessment: a systematic review, *Clin. Infect. Dis.* 73 (11) (2021) e3884–e3e99, doi:[10.1093/cid/ciaa1764](https://doi.org/10.1093/cid/ciaa1764).
- [3] N. Kojima, F. Turner, V. Slepnev, A. Bacelar, L. Deming, S. Kodeboyina, et al., Self-collected oral fluid and nasal swab specimens demonstrate comparable sensitivity to clinician-collected nasopharyngeal swab specimens for the detection of SARS-CoV-2, *Clin. Infect. Dis.* 2 (73) (2021) e3106–e3109, doi:[10.1093/cid/ciaa1589](https://doi.org/10.1093/cid/ciaa1589).
- [4] J.M. Baker, J.Y. Nakayama, M. O'Hegarty, A. McGowan, R.A. Teran, S.M. Bart, et al., SARS-CoV-2 B.1.1.529 (Omicron) Variant Transmission Within Households - Four U.S. Jurisdictions, November 2021-February 2022, *MMWR Morb. Mortal Wkly. Rep.* 71 (9) (2022) 341–346, doi:[10.15585/mmwr.mm7109e1](https://doi.org/10.15585/mmwr.mm7109e1).
- [5] O. Puhach, K. Adea, N. Hulo, P. Sattonnet, C. Genecand, A. Iten, et al., Infectious viral load in unvaccinated and vaccinated patients infected with SARS-CoV-2 WT, Delta and Omicron, *Nat Med* (2022), doi:[10.1038/s41591-022-01816-0](https://doi.org/10.1038/s41591-022-01816-0).
- [6] Y. Cao, J. Wang, F. Jian, T. Xiao, W. Song, A. Yisimayi, et al., Omicron escapes the majority of existing SARS-CoV-2 neutralizing antibodies, *Nature* 602 (7898) (2022) 657–663, doi:[10.1038/s41586-021-04385-3](https://doi.org/10.1038/s41586-021-04385-3).