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Short Communication

# Breakthrough infections with the SARS-CoV-2 Delta variant: vaccinations halved transmission risk



RSPH

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# ABSTRACT

Objectives: The SARS-CoV-2 Delta variant (B.1.617.2) is associated with increased infectivity. Data on breakthrough SARS-CoV-2 Delta variant infections in vaccinated individuals and transmission risk are limited. The aim of this study was to provide estimates of transmission risk in Delta variant breakthrough infections. Study design: A matched case-control study was performed. Methods: To analyse onward transmission of fully vaccinated individuals infected with B.1.617.2, we compared 85 patients (vaccination group [VG]) with an age- and sex-matched unvaccinated control group (CG; n = 85). Results: Transmission of B.1.617.2 was significantly reduced (halved) in the VG. The number of infected contacts to total number of contacts per infected person was  $0.26 \pm 0.40$  in the VG vs  $0.56 \pm 0.45$  in the

CG (P = .001). Similarly, fully vaccinated contacts were less likely to be infected by fully vaccinated infected persons (IPs) than by unvaccinated IPs (20.0% vs 37.5%), although this association was not significant.

Conclusions: Fully vaccinated contacts had 50% less transmissions than unvaccinated individuals. These findings must be verified in larger sample populations, and it is especially important to investigate the role of vaccination status of close contacts.

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#### Introduction

The SARS-CoV-2 Delta (B.1.617.2) variant of concern (VoC) has rapidly become the dominant variant in numerous countries and now accounts for more than 95% of cases in Germany.<sup>1</sup> It was first reported in India in early October 2020 and increasingly displaced other SARS-CoV-2 variants, such as Alpha (B.1.1.7), Beta (B.1.351) and Gamma (P.1). In addition to other authors, Liu et al.<sup>2</sup> identified the spike mutation P681R as a significant determinant for enhanced viral replication fitness of the Delta variant compared with the Alpha variant. Thus, the R0 (the initial reproduction

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number in an immune-naïve population) of the ancestral COVID-19 strain (wild type), the Alpha variant and the Delta variant were reported as 2.4–2.6, 4–5 and 5–8, respectively.<sup>3</sup>

Initial data show that (full) vaccination protects against infection with the Delta variant, but vaccine effectiveness seems to be reduced.<sup>4</sup> However, it is unclear whether complete vaccination influences onward transmission in the case of so-called breakthrough infections. Preliminary results found no difference in viral load between unvaccinated and vaccinated individuals with breakthrough infections.<sup>5</sup> In contrast, Chia et al. demonstrated that the viral load of B.1.617.2 decreased more rapidly in vaccinated than in unvaccinated infected individuals (preliminary data).<sup>6</sup> In terms of breakthrough B.1.617.2 infections after AstraZeneca vaccination, Chau et al. described asymptomatic or mild diseases, which were associated with higher cycle threshold (Ct) values, prolonged polymerase chain reaction (PCR) positivity and low levels of vaccineinduced neutralising antibodies.<sup>7</sup> However, the effect of vaccination

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is not only via neutralising antibodies but also cellular immunity. Thus, a robust T-cell response also correlates with clinical protection and is probably involved in immunity to COVID-19 even with a reduction in antibodies.<sup>8</sup>

Accurate assessment of breakthrough infections and the risk of ongoing transmission from vaccinated infected individuals to other (vaccinated) persons is essential in successfully fighting this pandemic. So far, however, no corresponding studies on vaccineinduced protection in terms of the Delta variant are available. To date, methods analysing onward transmissions or transmission risks have been highly respectively. Ct values are frequently used as a marker of infectivity, resp. viral load. Other possibilities are monitoring, cohort studies or the tracking of close contacts according to the legal regulations for the control of infectious diseases, as has been done by the German Public Health Departments on the basis of the Infection Protection Act. Close contact individuals in Germany are defined as those who had contact with an infected person (IP) for >10 min at <1.5 m, without face masks or direct physical contact, within a timeframe ranging from 2 days before symptom onset in the IP to 10–14 days after symptom onset.<sup>9</sup>

To analyse vaccine-induced protection in terms of Delta variant breakthrough infections, real-world data from the largest German public health department, which is based in Cologne, were used. Data for the transmission of B.1.617.2 infection to close contacts were compared between fully vaccinated IPs in the vaccination group (VG) and IPs in the unvaccinated control group (CG).

## Methods

A total of 679 B.1.617.2 infections were reported to the public health department in Cologne between 19 April (occurrence of the first B.1.617.2 case) and 24 July 2021; 116 of these infections were in fully vaccinated individuals, defined as  $\geq$ 14 days after receipt of all recommended COVID-19 vaccine doses.

Of the 116 fully vaccinated individuals, 47 had been vaccinated with Pfizer BNT162b2 (55.3%), three had been vaccinated with Moderna mRNA-1273 (3.5%), six had been vaccinated with Astra Zeneca AZD1222 (7.1%), 24 had been vaccinated with Johnson & Johnson Ad26.COV2.S (28.2%) and 5 had been vaccinated with a combination vaccine (5.9%). The last vaccination took place on average 56.8  $\pm$  40.2 days before infection, with a range of 16–176 days.

From the 116 fully vaccinated individuals, only patients for whom complete contact tracing was possible were included (n = 85 [VG]). Individuals for whom complete contact tracing was not possible or who were incompletely vaccinated were excluded.

We selected a control population (CG) from the Cologne Health Department's registry. The CG included patients with PCRconfirmed COVID-19 during the same observation period who had not yet received any vaccination. Each patient in the VG was randomly matched 1:1 with a B.1.617.2-positive patient without vaccination (CG). Age and sex were chosen as matching criteria, as they may influence immune response on vaccination and transmissibility.

# Data analyses

We considered the total number of contacts per IP and the total number of infected contacts per IP to determine the infected contacts relative to the total number of contacts per IP. In addition to descriptive statistics (age and sex), differences between VG and CG were assessed using an unpaired *t*-test or a chi-squared test. Linear regression (backwards elimination) was used to examine the influence of vaccination (yes = 0, no = 1), age (in years), sex (male = 1, female = 2), symptoms (present = 1, not present = 2) and vaccination interval (in days) on the number of infected contacts relative to the total number of contacts per IP. A *P* value below 0.05 was considered significant. All calculations were performed with SPSS version 27.0.

## Results

In both the VG and CG, 45.9% were female. On average, vaccinated individuals were aged  $35.8 \pm 17.7$  years; this did not differ from the CG (age:  $34.8 \pm 16.0$  years). In the VG group, 138 close contacts (range per IP 0-9) were identified, compared with 95 close contacts in the CG (range per IP 0-7). The number of total and infected contacts, as well as the number of infected contacts in relation to the total number of contacts per IP, are shown in Table 1. There was a trend towards a higher number of total contacts per IP in the VG, but these contacts were significantly less infected. The total number of infected contacts per IP and the number of infected contacts in relation to the total number of contacts per IP were higher in the unvaccinated CG. The number of infected contacts in relation to the total number of contacts per IP increased in the unvaccinated group ( $\beta = 0.350$ ; P < .001) and with age ( $\beta = 0.454$ ; P < .001). This model was able to explain 30.8% (corr.  $R^2$ ) of the variance. Sex, symptoms and vaccination interval (in days) were excluded in the final model (see table S1 in the supplementary material).

Of the 138 close contacts in the VC, 80 (58.0%) were fully vaccinated, whereas only 23 (24.2%) of 95 close contacts in the CG were fully vaccinated (P < .001; see Table 1). Fully vaccinated

Table 1

Total contacts, total infected contacts and relation to the total number per infected persons (IPs); total fully vaccinated contacts and infected fully vaccinated contacts in total and in relation to total number in vaccination group (VG) vs control group (CG).

| Variable  | Group (n) | Mean | Standard deviation | P-value <sup>a</sup> |
|---|-----------|------|--------------------|----------------------|
| Number of contacts per IP <sup>b</sup>                                      | VG (85)   | 1.62 | 1.85               | 0.056                |
|   | CG (85)   | 1.12 | 1.57               |                      |
| Number of infected contacts per IP <sup>c</sup>                             | VG (57)   | 0.47 | 0.76               | 0.001                |
|   | CG (42)   | 1.17 | 1.23               |                      |
| Number of infected contacts to total number of contacts per IP <sup>c</sup> | VG (57)   | 0.26 | 0.40               | 0.001                |
|   | CG (42)   | 0.56 | 0.45               |                      |
| Number of fully vaccinated contacts per IP                                  | VG (57)   | 1.40 | 1.32               | < 0.001              |
|   | CG (42)   | 0.55 | 0.92               |                      |
| Number of infected, fully vaccinated contacts per IP                        | VG (42)   | 0.38 | 0.62               | 0.270                |
|   | CG (15)   | 0.60 | 0.74               |                      |
| Number of infected, fully vaccinated contacts in relation to total number   | VG (38)   | 0.29 | 0.43               | 0.360                |
| of fully vaccinated contacts per IP   | CG (13)   | 0.41 | 0.48               |                      |

<sup>a</sup> Calculated with unpaired *t*-test.

<sup>b</sup> Persons who did not indicate close contacts were also integrated in order not to distort the number.

<sup>c</sup> Only taken into account if close contacts were indicated.

contacts in the VG had an infection rate of 20.0% (n = 16) compared with 37.5% (n = 9) in the CG. The total number of fully vaccinated contacts infected, and the total number of fully vaccinated contacts infected in relation to the total number of vaccinated contacts per IP did not differ significantly.

# Discussion

Based on real-world studies, SARS-CoV-2 vaccines have reassuring safety and can effectively reduce fatal outcomes, severe cases, symptomatic cases and infections.<sup>10</sup> In addition, a follow-up of 6 months after the application of BNT162b2 showed a favourable safety profile, but with a gradual decline in efficacy.<sup>11</sup> However, few and inconsistent data exist regarding the transmission of the SARS-CoV-2 Delta variant between fully vaccinated individuals. Such knowledge is essential for the implementation of effective infection control measures. Most studies are currently looking at the occurrence of breakthrough infections and the clinical course. However, the results are very heterogeneous. Two studies reported substantially lower viral loads in BNT162b2-infected patients who were vaccinated compared with those who were not vaccinated.<sup>12,13</sup> In contrast, Ioannou et al. showed comparable viral loads among vaccinated and nonvaccinated healthcare workers infected with variant B.1.1.7, suggesting suboptimal protection of SARS-CoV-2 vaccines against new variants compared with wild-type SARS-CoV-2.14

Most studies focus on the risk of infection or infectivity, and little is known about the transmission risk of close contacts in terms of the SARS-CoV-2 Delta variant. Therefore, to our knowledge, this is the first study based on epidemiological data to investigate the ongoing transmission of B.1.617.2 from fully vaccinated IPs to close (vaccinated) contacts. The results of the present study show a significant reduction in transmission of more than 50% in vaccinated compared with unvaccinated IPs.

Similarly, fully vaccinated contacts were less likely to be infected by fully vaccinated IPs than by unvaccinated IPs (20.0% vs 37.5%), although this association was not significant.

## Strength and limitations

A strength of this study is the systematic and complete recording of the data by the Cologne Public Health Department. IPs were digitally recorded and interviewed via telephone to determine the route of infection, symptoms and medical history, including vaccination. In each case, VoC analysis was carried out via PCR, provided that sufficient sample material was available. Accordingly, the proportion of B.1.617.2 infections was complete compared with other surveys, which often assume estimated values. In addition, all close contacts in Cologne were also tracked during quarantine, both digitally and by telephone. PCR testing was carried out when symptoms occur.

This study is limited by its small number of IPs and fully vaccinated close contacts. In addition, deviations in PCR tests and sequencing in various Cologne laboratories are possible because a unified method is not present. Although the ct values were recorded, they were only available at one test time in IPs; therefore, ct values were not taken into account in the context of this analysis and among new variants.

## Conclusions

In conclusion, fully vaccinated individuals who are infected with B.1.617.2 can transmit the infection to close contacts; however, they had a >50% reduced transmission rate compared with the unvaccinated CG. These findings must now be verified in larger sample populations. It will be especially important to investigate the role of

vaccination status of close contacts and to also consider the decreased efficacy of the vaccine over time.

## Author statements

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Ethical approval

None sought.

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Competing interests

None declared.

## Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.puhe.2022.01.005.

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