BRIEF REPORT

Transmission Potential of the Omicron Variant of Severe Acute Respiratory Syndrome Coronavirus 2 in South Korea, 25 November 2021–8 January 2022

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Our study indicates sustained transmission (effective reproduction number, 1.3; serial interval, 4.2 days; regional doubling times, 3.3–11.4 days) of the severe acute respiratory syndrome coronavirus 2 Omicron (B.1.1.529) variant (N = 2351) in South Korea (25 November 2021–8 January 2022), implicating insufficient protection through vaccination and supporting nonpharmaceutical control measures.

Keywords. COVID-19; Korea; Omicron; reproduction number; SARS-CoV-2.

Since its first identification on 24 November 2021, the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) Omicron (B.1.1.529) variant has been detected in 149 countries [1]. In South Korea, the first 2 Omicron cases were identified on 25 November 2021 and on 7 December 2021; the first local outbreak was identified in Michuhol-gu, Incheon Metropolitan City (population 2.9 million) [2]. Six weeks after attempting a transition to "living with COVID-19," coronavirus disease (COVID-19) infection-control measures were reinstated by the South Korean government on 18 December 2021, with stricter social distancing rules, such as banning gatherings of >4 fully vaccinated individuals [2]. On 13 December 2021, the Korea Disease Control and Prevention Agency reported 269 new infections (total n = 894), with a sharp increase in Omicron infections [2]. By 24 January 2022, Omicron accounted for >50% of all sequenced cases in

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South Korea, and replaced the Delta (B.1.617.2) variant as the dominant SARS-CoV-2 variant [2].

In late December 2021, South Korea, the United Kingdom, and Thailand shortened the standard 6-month COVID-19 booster-dose interval to 3 months to prepare for the impending Omicron wave [3]. Despite 85% of South Korea's 51 million population having been fully vaccinated, an unprecedented spike in COVID-19 cases was reported as of 1 February 2022 (>10 000 cases reported daily), and the epidemiology and transmission potential of Omicron is unclear. We investigated the transmission potential and epidemiological characteristics of Omicron in South Korea by analyzing the nationwide Omicron case data from 25 November 2021 to 8 January 2022.

METHODS

Modeling Methods

Individual-level data, including sex, age, diagnosis date, symptom-onset date, and autochthonous (local transmission)/ imported case, of confirmed SARS-CoV-2 Omicron cases that were reported to the Korea Disease Control and Prevention Agency and Central Disease Control Headquarters, were analyzed. Symptom-onset dates were available for only 1116 of the 2351 Omicron cases. Therefore, we used empirical distribution of reporting delays from symptom onset to diagnosis to impute the missing dates of symptom onset for the remaining 1235 cases [4]. The epidemic curve is often described by the reporting dates, but dates of symptom onset are more suitable for analyzing the epidemic curve to reduce systematic or random error and artificial trends, such as a weekend drop, in surveillance data [5]. We reconstructed 300 epidemic curves by the symptom-onset dates and obtained the mean incidence curves of local and imported cases [4, 6]. The last 5 data points were excluded to adjust for reporting delays in the real-time analysis.

The frequency of doubling of the cumulative incidence was calculated, assuming

$$2C(t_{d_i}) = C(t_{d_{i+1}})$$

where t_{d_i} and $C(t_{d_i})$ are the times at which the cumulative incidence doubled and the cumulative number of cases at the time t_{d_i} ($i = 0, 1, 2, 3, ..., n_d$), respectively. We assume $t_{d_0} = 0$ and $C(t_{d_0}) = C_0$, and n_d denotes the total number of times that the cumulative incidence doubles. Therefore, the sequence of doubling times is derived as

$$d_j = \Delta t_{d_i} = t_{d_i} - t_{d_{i-1}}$$

where $j = 1, 2, 3, ..., n_d$. Additionally, we incorporated parameter uncertainty into our analysis and obtained a

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95% confidence interval (CI) using parametric bootstrapping with a Poisson error structure around the harmonic mean of the doubling times [7].

We estimated the effective reproduction number R_t using the incidence curves for imported and local cases. We initially calibrated the daily number of new local infections using a generalized growth model [8], which characterizes the ascending number of cases in an epidemic using the growth rate (r) and the deceleration of growth parameter (p) (Supplementary Methods) [8, 9], and thereby simulates the progression of incident cases at calendar time t_i . We estimated the reproduction number using the following renewal equation:

$$R_{(t_i)} = \frac{I_i}{\sum_{j=0}^{i} (I_{i-j} + \alpha J_{i-j})\rho_i},$$

assuming γ -distribution with a mean of 4.41 (standard deviation, 3.17) days for the generation interval (ρ_i) [7]. The local and imported incidence at calendar time t_i are denoted by I_i and J_i , respectively, whereas the parameter α ($0 \le \alpha \le 1$) is defined as the relative contribution of imported cases to secondary disease transmission. We estimated the R_t from 300 simulated curves by assuming a Poisson error structure, and derivegrd uncertainty bounds around the R_t curve [7].

To estimate the serial interval, we identified 202 infector-infectee pairs for whom the date of symptom onset of both the infector and infectee was available. The transmission pair was defined as including an infector who had a laboratoryconfirmed infection and an infectee who reported a single epidemiological link with that infector. Using the onset dates of transmission pairs, the Epicontact R library was utilized to analyze pairwise contact between individuals and to estimate the serial interval [10]. The maximum-likelihood estimation of the normal distribution was performed to estimate the distribution of the serial interval. Furthermore, we applied the correction of the estimates of serial interval to address possible sampling bias during the early exponential growth phase of the epidemic (Supplementary Methods) [11].

This study was conducted in accordance with the Declaration of Helsinki and was exempt from ethical approval due to a waiver that was granted by the Institutional Review Board of Soongsil University (SSU-202202-HR-381-1).

RESULTS

During the study period (25 November 2021–8 January 2022), 1276 imported and 1075 local Omicron cases were detected in South Korea (Figure 1A). Among the local cases, 30 (3%) were epidemiologically linked with imported cases and 845 (79%) with local cases; 200 (18%) cases were not epidemiologically linked.

The 5 major transmission networks of Omicron infection clusters in South Korea are shown in Figure 1B; the characteristics of each cluster, as of 8 January 2022, are summarized in Table 1. The first Omicron infection cluster was associated with a church in Michuhol-gu, Incheon, South Korea (n = 61), and coincided with the country's first confirmed Omicron cases comprising a couple who returned from Nigeria and were diagnosed on 24 November 2021 [2]. Another cluster outbreak, associated with the United States Forces Korea Air Base in Gunsan, North Jeolla province (n = 35), that led to community transmission was subsequently identified. Three other Omicron infection clusters are shown in Figure 1B.

Analysis of the 202 infector–infectee transmission pairs indicated that the mean serial interval fitted to a normal distribution was 4.2 (95% CI, 3.8–4.5) days (Supplementary Table 1). The mean effective reproductive number as of 8 January 2022 was approximately 1.3 (95% CI, 1.2–1.4), with a growth rate (r) of 0.3 (95% CI, .2–.4) and deceleration of growth parameter (p) of 0.9 (95% CI, .8–1.0); this indicates the subexponential growth dynamics of the Omicron variant in South Korea (Supplementary Figures 1 and 2).

During the study period, the harmonic mean of the arithmetic means of doubling times, which were estimated from the cumulative incidence, ranged from 3.3 (95% CI, 2.7–4.4) days in Busan to 11.4 (95% CI, 7.5–15.9) days in North Jeolla province, and was 4.0 (95% CI, 3.9–4.1) days for South Korea. The harmonic means of the doubling times in Busan, Seoul, Gyeonggi province, and North Gyeongsang province were <4.0 days (Figure 1C).

DISCUSSION

In February 2022, a surge of SARS-CoV-2 Omicron cases was reported worldwide, even in countries with relatively high COVID-19 vaccine coverage; the basic reproduction number in the absence of control measures was >8 [12]. Our study quantifies the transmission potential of Omicron in South Korea and explains the recent unprecedented national surge in COVID-19 cases. Using reconstructed onset dates for the first reported cases, we estimated an effective reproduction number of 1.3, which is lower than previous estimates in other settings (1.9–3.2) [13, 14], but clearly indicates sustained Omicron transmission in South Korea. The serial interval of Omicron infections was estimated as 4.2 days (Supplementary Figure 3), which is longer than that of previous estimates (2.8–2.9 days) in South Korea [15, 16] but shorter than that in Spain (4.8 days) [17].

Furthermore, 1370 of the 2351 (58%) Omicron infections occurred in individuals who had received at least 2 vaccine doses, and this finding concurs with reports of Omicron's immune escape contributing to the lower efficacy of COVID-19 vaccines as well as a greater replication rate compared with the Delta



Figure 1. Epidemiological characteristics of the severe acute respiratory syndrome coronavirus 2 Omicron variant in South Korea. *A*, Epidemic curve of the daily Omicron cases based on the reporting date (N = 2351). *B*, The Omicron variant's transmission network in South Korea: transmission networks associated with the daycare in Daegu (n = 152; a), the daycare in North Jeolla province (n = 152; b), the kindergarten in North Jeolla province (n = 101; c), the church in Incheon (n = 61; d), and the United States Forces Korea (USFK) air base in North Jeolla province (n = 35; e). *C*, Harmonic mean of the arithmetic means of the estimated doubling time for the Omicron variant in South Korea, between 25 November 2021 and 8 January 2022, for each administrative division.

Table 1. Demographic Characteristics of the 2351 Omicron Cases and the Major Outbreak Clusters in South Korea

Characteristic	Total	Major Cluster Outbreaks				
		Daycare in Daegu	Daycare in North Jeolla Province	Kindergarten	Church	USFK Air Base
Overall, No.	2351	152	152	101	61	35
Imported	1276 (54.3)	0 (0)	1 (0.7)	0 (0)	2 (3.3)	0 (0)
Pandemic period	25 Nov 2021– 8 Jan 2022	24 Dec 2021– 5 Jan 2022	5 Dec 2021– 4 Jan 2022	16-30 Dec 2021	25 Nov– 16 Dec 2021	24 Dec 2021– 3 Jan 2022
Sex						
Male	1165 (49.6)	61 (40.1)	71 (46.7)	46 (45.5)	33 (54.1)	20 (57.1)
Female	1186 (50.4)	91 (59.9)	81 (53.3)	55 (54.5)	28 (45.9)	15 (42.9)
Age group, y						
≤7	181 (7.7)	46 (30.3)	22 (14.5)	48 (47.5)	10 (16.4)	0 (0)
8–19	281 (12.0)	23 (15.1)	4 (2.6)	5 (5.0)	6 (9.8)	6 (17.1)
20–39	1129 (48.0)	40 (26.3)	50 (32.9)	22 (21.8)	24 (39.3)	16 (45.7)
40–59	565 (24.0)	42 (27.6)	42 (27.6)	17 (16.8)	15 (24.6)	11 (31.4)
60–74	170 (7.2)	1 (0.7)	24 (15.8)	9 (8.9)	6 (9.8)	2 (5.7)
≥75	25 (1.1)	0 (0)	10 (6.6)	0(0)	0(0)	0 (0)
Clinical features, asymptomatic	459 (19.5)	11 (7.2)	25 (16.4)	29 (28.7)	9 (14.8)	6 (17.1)
COVID-19 vaccination status						
1 dose	72 (3.1)					
2 doses	1249 (53.1)					
3 doses	121 (3.5)					

Data are presented as No. (%) unless otherwise indicated.

Abbreviations: COVID-19, coronavirus disease 2019; USFK, United States Forces Korea.

variant [18]. Insufficient prevention of symptomatic Omicron infections among otherwise healthy individuals who had received 3 doses of COVID-19 messenger RNA vaccines has been demonstrated, and emphasizes the need for nonpharmaceutical control measures [18].

Imported cases accounted for more than half of the reported cases (1276/2351 [54%]), and thus contributed significantly to infection transmission in the early phase of the Omicron wave. These findings validate the international travel-related interventions that were implemented by the Korean government to control the outbreak.

This study had some limitations. First, we could not account for unreported cases of asymptomatic or mild Omicron infections. Second, our results were based on a statistical reconstruction of epidemic curves using symptom-onset dates [11]. Third, given the relatively high COVID-19 vaccine coverage and low prevalence of COVID-19 in the pre-Omicron era in South Korea, our estimate of transmissibility is nongeneralizable to resource-limited countries. Nonetheless, the findings highlight the importance of maintaining nonpharmaceutical control measures in South Korea to mitigate the impact of the Omicron variant.

Supplementary Data

Supplementary materials are available at *Open Forum Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

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Patient consent. This study did not include factors necessitating patient consent.

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