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Letter to the Editor

The incubation period of the SARS-CoV-2 B1.1.7 variant is shorter than that of other strains

Dear editor

We read with great interest, the article by Yumeng Gao et al., who reported that SARS-CoV-2 was contagious during the incubation period, with a median incubation period of 10 days.[1] However, no studies have so far reported the incubation period of the B.1.1.7 variant that was reported to have a substantial transmission advantage over other lineages.[2] Here, we report that the incubation period of the B.1.1.7 variant is shorter than other strains.

In mid-March 2021, a cluster of B.1.1.7 variant cases occurred in downtown Matsuyama, Ehime Prefecture, Japan with approximately 200 positive cases reported as of March 31. As patients infected with the B.1.1.7 variant were hospitalized for isolation under national regulations, we were able to obtain a detailed medical history; most were infected in restaurants and bars open late at night. The medical histories imply that the incubation period of the B.1.1.7 variant may be shorter than that of other strains. Since February 2020, a retrospective investigation at a public health center in Japan reported a high risk of clusters occurring in '3C' environments (closed spaces, crowded places, and close-contact settings).[3] In this study, the main sites of infection were bars and late-night restaurants, which are 3C environments. Therefore, we also investigated the effect of 3C environments on the incubation periods of the B.1.1.7 variant and other strains.

This retrospective observational study enrolled patients with symptomatic novel coronavirus infection admitted to either of two medical institutions in Ehime Prefecture, Japan. The study included patients admitted in March 2021 with novel coronavirus infections caused by the B.1.1.7 variant and patients infected with other SARS-CoV-2 strains admitted between March 1, 2020 and January 31, 2021. The B.1.1.7 variant was detected by real-time PCR tests for the N501Y mutation,[4] and confirmed by the whole-genome sequences of the strain.[5] The study included only patients whose age, sex, source of infection, date of exposure, and date of onset were clearly documented. In March 2021, 57 patients infected with the B.1.1.7 variant were admitted. Of these, 27 were excluded because of missing data, such as unknown source or date of exposure, and the remaining 30 were included in the study (Fig. 1A). There were 149 patients infected with other strains admitted between March 1, 2020 and January 31, 2021. Of these, 107 were excluded because of missing data such as unknown source or date of exposure, indeterminable or asymptomatic cases, or inability to communicate; the remaining 42 patients were included (Fig. 1B). Of the 30 and 42 patients infected with the B.1.1.7 variant and other strains, respectively, 28 and 20 were infected in 3C environments, respectively.

Poisson regression analysis was used to examine the relationship between the incubation period of the B.1.1.7 variant and those of other strains. Almost all patients infected with the B.1.1.7 variant were infected in 3C environments. We postulated that the amount of virus is greater in 3C environments than in other environments, shortening the incubation period. Therefore, we also used Poisson regression analysis to examine the relationship between incubation periods among those infected in 3C environments using R (ver. 4.0.0). The variables evaluated in the analysis were sex, age, presence of the mutant strain, and incubation period. This study was approved by the Ethics Committee of Ehime Prefectural Central Hospital, Ehime, Japan.

The analysis included 30 patients infected with the B.1.1.7 variant strain in March 2021, of whom 28 were infected in bars and late-night restaurants (3C environments). The mean age of the 30 patients infected with the B.1.1.7 variant was 32.4 years, and the mean (median) incubation period was 3.53 (3.0) days. The mean age of the 42 patients infected with other strains was 56.2 years, and the mean (median) incubation period was 5.71 (5.0) days. Of the patients infected with other strains, 20 were infected in 3C environments, such as bars and late-night restaurants, and the other 22 were infected at workplaces or in households. The mean age of the 20 patients infected in 3C environments was 53.2 years, and the mean (median) incubation period was 4.30 (4.0) days. Poisson regression analysis showed that the incubation period of the B.1.1.7 variant was 0.66 times shorter than that of other strains (95% CI: 0.38, 0.71) (Table 1A). Among the patients infected in 3C environments, the incubation period of the B.1.1.7 variant was 0.63 times shorter than that of other strains (95% CI: 0.504, 0.797) (Table 1B). After adjusting for age and sex, the incubation period of the B.1.1.7 variant was 0.62 times shorter than that of other strains in 3C environments (95% CI: 0.47, 0.82) (Table 1C).

This study had several limitations. First, almost all of the patients infected with the B.1.1.7 variant were infected in 3C environments, such as restaurants or bars. It is possible that they were exposed to more virus particles in closed, unventilated, crowded environments. It is not clear whether the incubation period is affected by the site of exposure. However, when incubation periods were compared among similar 3C environments, the incubation period of the B.1.1.7 variant was significantly shorter than that of other strains. Second, factors such as the patient's underlying diseases and smoking status were not analyzed because these data were not fully available. Third, this was a retrospective observational study, which may have introduced recall bias because we collected self-reported information on the dates and sites of patients' exposure. However, to obtain the most accurate information possible, when the patients were admitted to a medical institution after the public health center interview, we reinterviewed each patient to confirm the dates of exposure and onset.

In conclusion, our study demonstrated the incubation periods of the B.1.1.7 variant were shorter than other strains. In order to contain outbreaks caused by variant strains, stronger measures will

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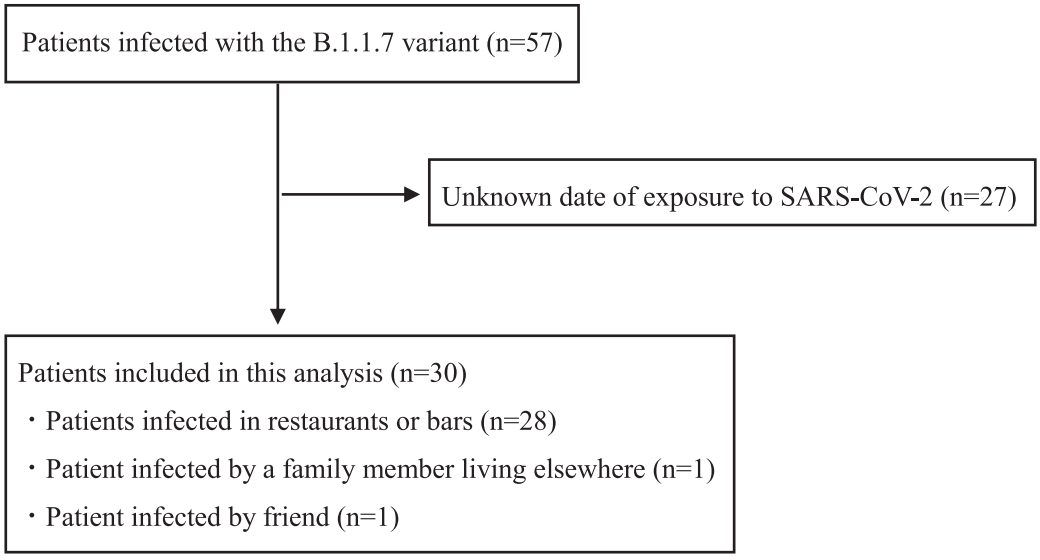

Figure 1B: Flowchart of the selection of COVID-19 patients infected with other strains.

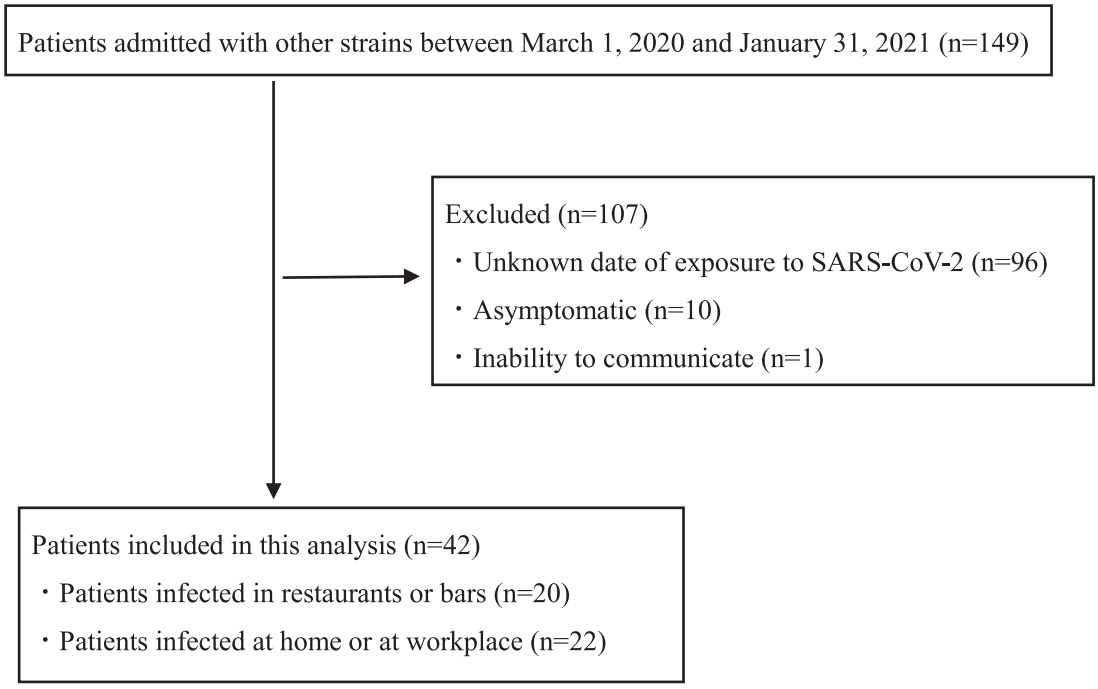

Fig. 1. (A) Flowchart of the selection of COVID-19 patients infected with the B1.1.7 variant. (B) Flowchart of the selection of COVID-19 patients infected with other strains.

be necessary, such as lockdown, and vaccination will be essential to end the epidemic.

Declaration of Competing Interest

There are no conflicts of interest to declare.

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Table 1
Poisson regression analysis of the relationship between the incubation period of the B.1.1.7 variant and that of other strains.

A. Poisson regression analysis of the relationship between the incubation period of the B.1.1.7 variant and that of other strains.			
	Coefficient (β)	SE	*P*-value
(Intercept)	1.79	0.190	$<2 \times 10^{-16}$
Male	−0.00952	0.105	0.364
Age	−0.00108	0.00282	0.00173
B.1.1.7 variant	−0.411	0.131	0.00173
B. Poisson regression analysis of the relationship between the incubation period of the B.1.1.7 variant and that of other strains in 3C environments.			
	Coefficient (β)	SE	*P*-value
(Intercept)	1.74	0.0646	$<2 \times 10^{-16}$
B.1.1.7 variant	−0.456	0.117	9.62×10^{-05}
C. Poisson regression analysis of the relationship between the incubation period of the B.1.1.7 variant and that of other strains in 3C environments after adjusting for age and sex			
	Coefficient (β)	SE	*P*-value
(Intercept)	1.81	0.210	$<2 \times 10^{-16}$
Age	−0.00685	0.00317	0.829
Male	−0.0473	0.113	0.674
B.1.1.7 variant	−0.476	0.140	0.000645

Authorship statement

All authors care for the patients and collected the patients' data. YH wrote the draft and others revised. All authors approved the submission of the current manuscript and meet the ICMJE authorship criteria.

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