Short Communication

Geographic Correlation between the Number of COVID-19 Cases and the Number of Overseas Travelers in Japan, Jan–Feb, 2020

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SUMMARY: Since the coronavirus disease 2019 (COVID-19) emerged in Wuhan, China, in December 2019, it has rapidly spread worldwide, and the number of cases is also increasing in Japan. The number of COVID-19 cases in Japan in the early stages was not uniform, and cases were largely concentrated in several prefectures. There was a strong, positive correlation between the distribution of COVID-19 cases and the number of foreign travelers as well as Chinese travelers, at prefectural level, with coefficients of 0.68 (P < 0.0001) and 0.60 (P < 0.0001), respectively. Moreover, phylogenetic tree analysis revealed that all the registered SARS-CoV-2 detected from January 23 to February 29, 2020, belonged to Chinese lineage, while those detected in March 2020 belonged to American and European lineages. Only 14 (20.3%) were infected outside Japan; however, the majority of the cases (79.7%) were infected domestically. In conclusion, a higher number of COVID-19 cases were identified in prefectures with more Chinese travelers, supporting the importance of enforcing policies that restrict the entry of overseas travelers to control COVID-19 spread. These findings highlight the risk of secondary transmission in the community caused by apparent or silently imported cases.

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sightseeing buses, 6 during the quarantine operation on the Diamond Princess cruise ship, and the remaining 5 during social events (e.g., parties or festivals). According to the Japan National Tourism Organization (6), the number of overseas travelers at prefectural level from January to November 2019 was highest in Tokyo, Osaka, Hokkaido, Kyoto, and Okinawa prefectures. Likewise, the highest number of travelers from China were in Tokyo, followed by Osaka, Hokkaido, Chiba, Kyoto, and Aichi (Fig. 1B and C).

We examined the geographic correlations between the number of COVID-19 cases at prefectural level in Japan and the number of overseas travelers using Pearson’s correlation test. There was a strong, positive correlation with the total number of foreign travelers, indicated by a coefficient of 0.68 ($P < 0.0001$), as well as with Chinese travelers, indicated by a coefficient of 0.60 ($P < 0.0001$) (Fig. 1). Analysis using Spearman’s rank correlation test also corroborated the positive correlation of the high number of overseas foreign travelers and that of Chinese travelers with the number of COVID-19 cases in each prefecture (coefficient of 0.57, $P < 0.0001$ and coefficient of 0.65, $P < 0.0001$, respectively). These results indicate that in prefectures more frequently visited by overseas and Chinese travelers, the number of COVID-19 cases was higher than that in prefectures less frequently visited by such travelers.

To support the transmission path of COVID-19 from overseas travelers to Japan, we performed a phylogenetic tree analysis of 27 complete genomes of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) detected in Japan from January 20 to March 12, 2020. The data were retrieved from the Global Initiative on Sharing All Influenza Data (GISAID) EpiCoV™ database (www.gisaid.org), excluding the data on viruses detected during the outbreak on the Diamond Princess cruise ship during February and March 2020. In addition, the strains from China [15], Italy [1], France [1], Brazil [1], Canada [1], and the US [1] from December 2019 to March 2020 were included in the analysis for comparison. The analysis was conducted using MEGA v.6.0 (7), using a maximum-likelihood method.

Phylogenetic tree analysis revealed that all of the registered SARS-CoV-2 detected in Japan from January 20 to February 29, 2020, belonged to Chinese lineages, clades B (L), B (O), and A (S) in the GISAID classification (8,9), whereas those detected in March 2020 belonged to American and European lineages, clades B.1 (G), B.1 (GH), B.1.1 (GR), and B.1.36 (GH) (Fig. 2). Although the results of the phylogenetic analysis did not encompass all 69 cases, and it was not possible to distinguish between the primary imported cases and secondary local infections using information from the database, this analysis supported the idea that the early stages of the COVID-19 outbreak in Japan highlight an independent introduction mediated by strains of Chinese origin.

To date, 16,851 cases have been reported in Japan (as of May 31, 2020), excluding those from the COVID-19 outbreak on the cruise ship (10,11). Initially, border control measures in Japan were only applied to those who had arrived from Hubei Province as from February 1. Eventually, the ban was extended to those visiting from Zhejiang Province as from February 13. Eventually, entry from the whole of China was restricted as from March 16, 2020. Furthermore, from January to February, reverse transcription polymerase chain reaction testing was performed only on patients with fever ($\geq 37.5°C$), respiratory symptoms, a travel history related to the banned areas in China, or a history of close contact with COVID-19-positive patients.
These measures allowed for the entry of SARS-CoV-2 and secondary transmission in the community. In Italy, community transmission began in the north, where Chinese travelers tended to visit (12,13). In contrast, Taiwan promptly stopped Chinese travelers to prevent community transmission (14). As border screening is not fully effective, stopping the entry of travelers from infected countries is essential in preventing COVID-19 community transmission (4,15). It is challenging to balance maintenance of the economy and control of infection rates, and strong policies are needed to control highly contagious diseases such as COVID-19.

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