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## Short Communication

## Importation of SARS-CoV-2 infection leads to major COVID-19 epidemic in Taiwan

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## ABSTRACT

**Objective:** COVID-19 has recently become a pandemic affecting many countries worldwide. This study aims to evaluate the current status of COVID-19 in Taiwan and analyze the source of infection.**Methods:** National data regarding SARS-CoV-2 infection were obtained from Taiwan.

CDC at the end of April 2020. These data were subjected to analysis of the current status and correlation between indigenous and imported COVID-19 cases. A phylogenetic tree was created to analyze the phylogeny of Taiwanese SARS-CoV-2 isolates.

**Results:** The first case of SARS-CoV-2 infection in Taiwan was detected on January 21, 2020. Epidemiological data indicate that by April 30, there were a total of 429 COVID-19 confirmed cases with the death rate of 1.3%. Most cases were identified as imported (79.9%; 343/429), with the majority originating from the United States of America (22.1%) and the United Kingdom (17.6%). Results from phylogenetic tree analyses indicate that the Taiwanese SARS-CoV-2 isolates were clustered with the SARS-CoV-2 isolates from other countries (bootstrap value 98%) and sub-clustered with bat SARS-like coronaviruses (bootstrap value 99%).**Conclusion:** This study suggests that the importation of SARS-CoV-2 infection was the primary risk-factor resulting in the COVID-19 epidemic in Taiwan.© 2020 The Author(s). Published by Elsevier Ltd on behalf of International Society for Infectious Diseases. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Emerging diseases pose a threat to global health and have the potential to become fatal. In December 2019, an atypical pneumonia induced by a novel coronavirus was first reported Wuhan, China (Huang et al., 2020). This novel coronavirus was initially named 2019-novel coronavirus (2019-nCoV). The name is now severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), and the disease is coronavirus disease 2019 (COVID-19) (Coronaviridae Study Group of the International Committee on Taxonomy). Since the first reported case, there has been a rapid increase in the number of cases, with outbreaks being reported in

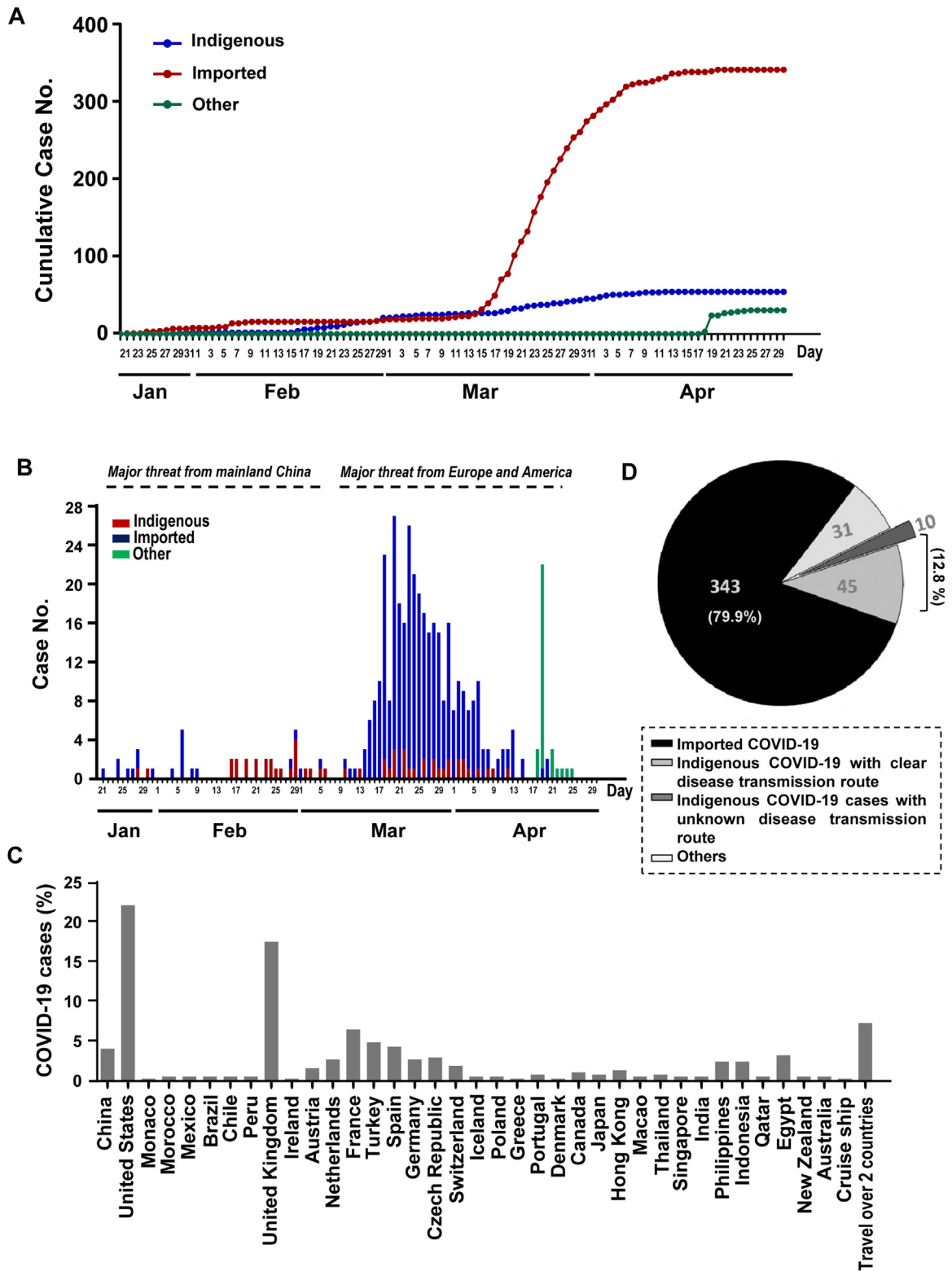
countries all over the world. SARS-CoV-2 has gradually spread to Europe, America, and Asia via travelers and has caused a COVID-19 pandemic since March (WHO, 2020b). The World Health Organization (WHO) declared the outbreak as a Public Health Emergency of International Concern on January 30, 2020, and an official pandemic on March 11, 2020. As of April 30, 2020, more than 3.2 million cases of COVID-19 have been reported in 185 countries and territories, resulting in more than 229,000 deaths (WHO, 2020b).

Coronaviruses are non-segmented enveloped viruses with a single-stranded, positive-sense RNA genome. Coronaviruses are known to infect a variety of animals, with some strains being capable of infecting humans. In recent decades, the severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) have caused regional outbreaks, leading to high mortality in human infections (Peeri et al., 2020). In 2003, there was an outbreak of SARS-CoV in

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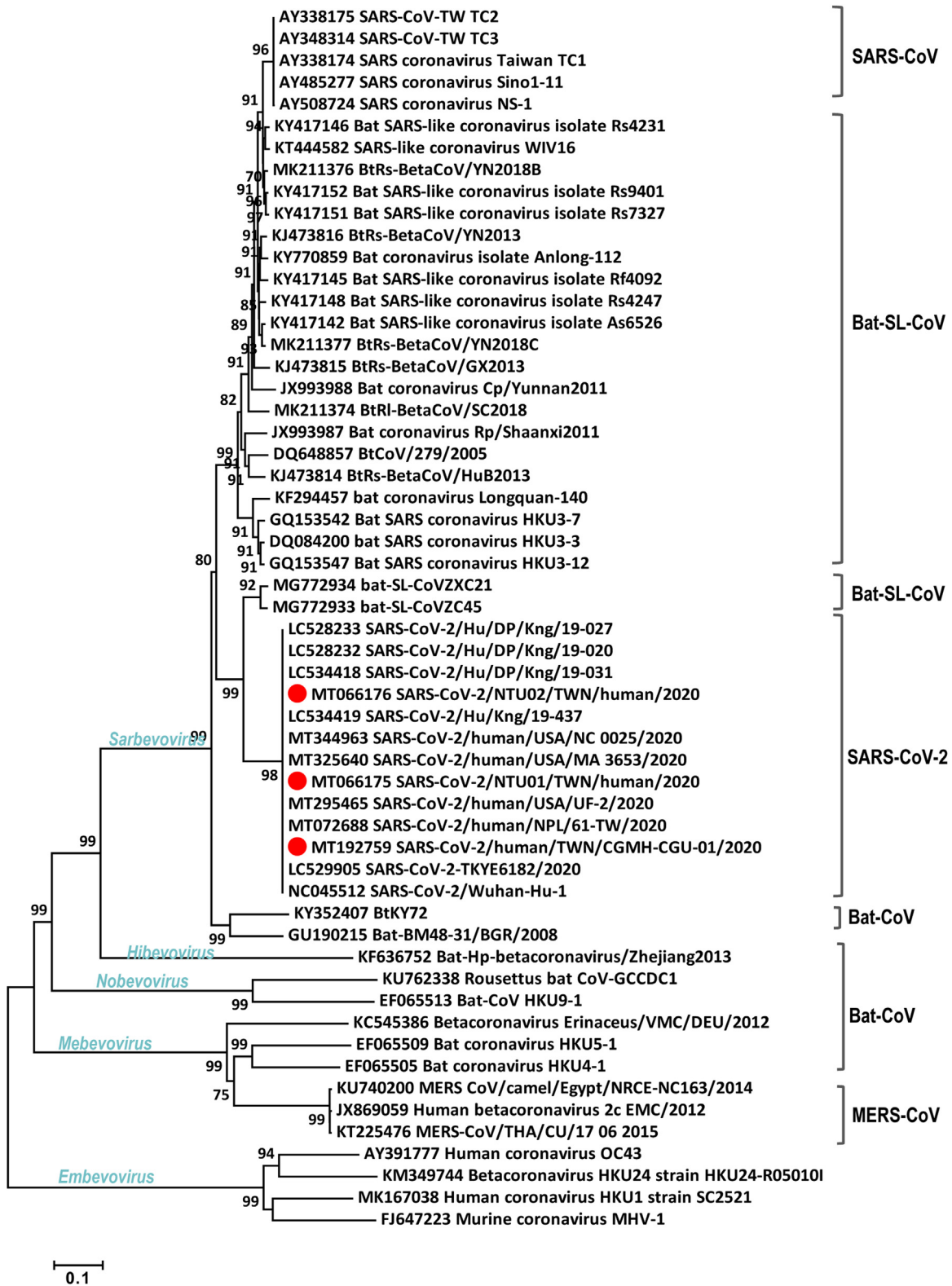
**Figure 1.** Current status of COVID-19 epidemics in Taiwan.

(A) Accumulated cases of COVID-19 from indigenous, imported and other undefined sources are shown. (B) Daily COVID-19 laboratory-confirmed cases from indigenous, imported, and other undefined sources are indicated. (C) Percentage of COVID-19 importation from the infectious-source-identified countries (D) COVID-19 case numbers from imported, indigenous with clear transmitted source, indigenous with unknown transmitted source, and other undefined cases are shown.

Taiwan with 664 SARS probable cases and 346 laboratory-confirmed cases (Taiwan CDC).

Taiwan is an island in the Pacific Ocean, located beside mainland China. International travel has a significant role in

transmitting emerging or re-emerging infectious diseases in Taiwan (Wang et al., 2020). In recent decades, the interactions between Taiwan and China have become frequent and close. Through this close interaction, SARS-CoV-2 infection was initially



**Figure 2.** Phylogenetic analysis of full-length genomes of SARS-CoV-2 viruses. The phylogenetic tree was constructed based on the nucleotide sequence of the full-length genome (~29 kb). The filled red circles indicate Taiwanese SARS-CoV-2 isolates. The analysis was performed using the MEGA 6 software and neighbor-joining method. Bootstrap support values > 70 are shown (1,000 replicates).

detected in Taiwan on January 21, 2020 (Taiwan CDC) (Figure 1A&B). The first case was a 50-year-old woman who was detected by a fever-screen station in Taoyuan International Airport, as she arrived from Wuhan, China. Since then, several sporadic COVID-19

cases have been detected in Taiwan between January and March 2020 (Figure 1A&B). Data indicate that imported COVID-19 cases have dramatically increased since the middle of March (Figure 1A). Before mid-March, the incidence of COVID-19 importation

**Table 1**  
Clinical characteristics of SARS-CoV-2 infection.

Disease Type	Clinical Manifestations	COVID-19 RT-PCR Nucleic Acid Detection
Asymptomatic cases	No clinical symptoms and no apparent chest imaging findings.	Positive
Mild cases	The clinical symptoms are mild and no pneumonia manifestation can be found in imaging.	Positive
Moderate cases	Patients have symptoms like fever and respiratory tract symptoms, etc. and chest imaging shows mild pneumonia manifestation.	Positive
Severe cases	Suspected respiratory infection symptoms, plus any of the following: (1) RR $\geq$ 30 breaths/min; (2) At rest, SpO <sub>2</sub> $\leq$ 93%; (3) PaO <sub>2</sub> /FiO <sub>2</sub> $\leq$ 300 mmHg (1 mmHg = 0.133 kPa);(4) Chest imaging show the lesions significantly progressed > 50% within 24–48 h.	Positive
Critical cases	Rapid progress of disease, plus any of the following: (1) Respiratory failure that requires mechanical ventilation; (2) Shock; (3) Complicated with other organ failure that requires monitoring and treatment in ICU.	Positive

RT-PCR (reverse transcriptase-polymerase chain reaction); RR (respiratory rate); SpO<sub>2</sub> (blood oxygen saturation levels); PaO<sub>2</sub> (arterial partial pressure of oxygen); FiO<sub>2</sub> (oxygen concentration); ICU (intensive care unit). These data were referenced with previous publications (2020, Gao et al., 2020).

averaged 0.58 per day. After that, the rate of COVID-19 importation increased to an average of 10.57 per day (Figure 1B). We further investigated the source of these COVID-19 importations. Our results indicated that the imported COVID-19 cases were mainly from the United States of America (22.1%), the United Kingdom (17.6%), and France (6.5%) (Figure 1C). In addition to imported cases, there were a few indigenous COVID-19 cases reported. According to the Taiwan CDC, by the end of April, there were 429 COVID-19 laboratory-confirmed cases with a fatality rate of 1.39%. Among these cases, 343 (79.9%) and 55 (12.8%) were identified as imported and indigenous, respectively (Figure 1D). The remaining cases (7.2%) remain questionable, as their source of infection was not clearly defined. Accordingly, we suggest that the constant importation of SARS-CoV-2 infection is the major risk factor that led to the COVID-19 epidemic in Taiwan.

The source of infection from the indigenous cases was also traced. Results indicated that most indigenous cases (81.8%; 45/55) had a contact history or exposure to SARS-CoV-2 infected patients, SARS-CoV-2 contaminated devices, or the environment directly or indirectly (Figure 1D). There were ten (18%) indigenous COVID-19 cases that remained unclear as to their possible source of infection (Figure 1D). We further addressed the phylogeny of the SARS-CoV-2 isolated in Taiwan. Results demonstrated that three Taiwanese isolates, collected in the early phase of the COVID-19 epidemic, were similar to SARS-CoV-2 isolates from other countries with a bootstrap value of 98% (Figure 2). It was also noted that SARS-CoV-2 was sub-clustered with Bat SARS-like strains isolated from China (Bat-SL-CoVZXC21 and Bat-SL-CoVZC45) (bootstrap value 99%) (Figure 2), indicating that SARS-CoV-2 might have evolved from Bat SARS-like viruses. However, the source and origin of SARS-CoV-2 still remain controversial, and further studies are required.

To reduce the effects of COVID-19 importation to Taiwan, Taiwan CDC implemented relevant prevention strategies. The international airport reinforced fever-screening of arriving passengers, questioning their travel history, and conducting health assessments. Travelers coming from COVID-19 affected countries were required to fill out a “Novel Coronavirus Health Declaration and Home Quarantine Notice.” Finally, foreign nationals were prohibited from entering Taiwan since March 19, 2020, in response to COVID-19 pandemics.

The COVID-19 spectrum of illness severity has been divided into four types: mild, moderate, severe, and critical Gao et al., 2020; WHO, 2020a). The WHO reported that fever, fatigue, and dry cough are considered the main clinical manifestations of COVID-19 patients. Other symptoms may include runny nose, myalgia, pharyngalgia, stuffy nose, and diarrhea; however, these are relatively less common (WHO, 2020b). In severe cases, COVID-19 may become fatal due to respiratory failure, shock,

and organ failure. The clinical features of COVID-19 are shown in Table 1.

With this novel coronavirus causing a pandemic, more and more evidence indicates that most of the COVID-19 cases may not develop severe manifestations, with some cases even remaining asymptomatic; nevertheless, these individuals still can transmit the virus to others. Asymptomatic infections are identified as individuals testing positive for the detection of SARS-CoV-2 nucleic acid using RT-PCR (Gao et al., 2020) (Table 1); however, these individuals do not display the typical clinical symptoms, and there are no apparent abnormalities on imaging, including lung X-ray film and computed tomography (CT). The Taiwan CDC indicates that around 60–70% of COVID-19 patients belonged to asymptomatic or mild cases (Taiwan CDC). Similar findings were observed in our hospital (Kaohsiung Medical University Hospital), indicating that most SARS-CoV-2 infected patients were asymptomatic.

The reasons for a majority of COVID-19 infections displaying “none-to-mild symptoms” remain unclear. It has been proven that SARS-CoV-2 invades cells by using angiotensin-converting enzyme 2 (ACE2) as its receptor (Zhou et al., 2020). Expression of a lower level of ACE2 or weaker binding capacity between SARS-CoV-2 and ACE2 should be an essential factor that leads to the absence of any clinical manifestations for asymptomatic infections. Also, host major histocompatibility complex (MHC) is proposed to play a role to mildly initiate and regulate the SARS-Cov-2 induced immunopathogenesis (Nguyen et al., 2020). It is suggested that more clinical samples should be collected, and a comparative examination of ACE2, as well as MHC typing, should be carried out.

Here, we reported the current status of the COVID-19 epidemic in Taiwan. We found that the importation of SARS-CoV-2 infection was the major risk factor correlating with the outbreak, causing a threat to Taiwan.

### Ethical approval

Approval was applied for and received from the Institutional Ethics Committee of the Kaohsiung Medical University, Taiwan. All procedures were conducted according to committee regulations.

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### Declaration of competing interest

There is no competing interest.



### Author contributions

CYL and WHW prepared and revised the manuscript. ANU and CYL helped to analyze the data. YHC, SPT, and PLL revised and edited the manuscript. MLY and SWF conceived the study and revised the draft.

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