From SARS-CoV to Wuhan 2019-nCoV Outbreak: Similarity of Early Epidemic and Prediction of Future Trends

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Abstract:

The ongoing large-scale pneumonia outbreak in China is caused by the 2019-nCoV, a new coronavirus highly similar to SARS-CoV in the SARS outbreak. The cause and consequence of the outbreak remain largely unknown as it is still in its early stage. As many aspects of the new virus are similar to SARS in 2003, knowledge, patterns and lessons of the SARS-CoV outbreak are valuable resources for responding to the Wuhan 2019-nCoV outbreak. Using epidemiological surveys and analyses from the early stage of the SARS outbreak, we assessed and compared the characteristics of those two outbreaks and predicted the possible outcome for the current 2019-nCoV outbreak. Like the SARS-CoV, the 2019-nCoV has a high human-to-human transmission capability and healthcare workers and family members are high risk populations. Because the early outbreak stage coincides with the Chinese spring festival travel rush, it is a challenge to prevent and control the spread of the virus. In this situation, the emergence and movement of a 2019-nCoV super-spreader is difficult to identify. Using the reported case data so far (as of Jan 23, 2019), a logistic model was built and the cumulative and daily counts of the 2019-nCoV cases were predicted. The cumulative counts of 2019-nCoV cases was estimated about 2-3 times the total number of SARS, and the peak incidence is predicted to be in early or middle February. Regional migration should be limited or prohibited to prevent emergence and movement of a super-spreader. There is an urgent need to establish enhanced surveillance and implement efficient measures nationwide to control this epidemic.

Keywords: 2019-nCoV; SARS-CoV; Outbreak; Viral Super-Spreader.

Emerging infectious diseases represent a great threat for human public health worldwide[1,2]. The 2019-nCOV caused pneumonia outbreak originating in Wuhan, China, is spreading around the country and affected 32 provinces and regions of China by January 24, 2020[3,4]. Countries outside China, including Japan, the United States, Thailand, and South Korea, have also reported cases imported from Wuhan, China. With the joint efforts of Chinese scientists, health workers and related departments, the pathogen causing this epidemic was quickly identified as a new type of coronavirus 10 days after the first official report. After confirming the pathogen, specific detection methods were rapidly developed and etiological diagnoses were improved. As of January 22, 2020, it has been confirmed that the new coronavirus came from wild bats and belonged to group 2b of the beta coronavirus, which contained severe acute respiratory syndrome associated coronavirus (SARS-CoV)[5]. Although 2019-nCOV and SARS-CoV belong to the same subgroup of beta coronavirus, the similarity at the genome level is only 70%, meaning that the new virus is genetically different from the SARS-CoV (Figure 1). The rapid discovery of the causing agent and development of diagnostic reagents demonstrated that technologies have been greatly improved in the 17 years since the SARS outbreak. However, no effective antiviral medication and vaccine are available for this new virus and much about it remains to be explored. Similar to the SARS outbreak, this outbreak also happened during spring festival, the most important Chinese traditional festival, when three billions of people travel throughout the country[6]. This unexpectedly represents beneficial conditions for transmission of this highly infectious disease and a correspondingly great challenge for prevention and control of the outbreak.

Although the current technology has been greatly improved since the 2003 SARS outbreak, the

basic laws and characteristics of the occurrence and development of infectious diseases have not changed fundamentally. Therefore, the past epidemic laws and characteristics of the SARS and the painful lessons we learned in responding to epidemics is of great value for us now and in the future. Due to concerns about controlling the impact of the epidemic and the relatively less developed information exchange tools of the time, the epidemics and characteristics of the early SARS cases were not reported. However, as we had participated in the epidemiological investigations of early cases of SARS in 2003, we collected important data about its early outbreak. Using these valuable data, we analyzed the characteristics of the early SARS cases and how the outbreak progressed. By comparing the epidemic situations of the two outbreaks, we found some strikingly similar characteristics and trends, providing lessons for better responses to the present and future epidemics.

On January 2, 2003, a hospital of Heyuan city, Guangdong Province, reported 2 strange cases with severe pneumonia which were then transferred to a larger hospital for further treatment. Several days later, 7 medical staff in the department that treated this patient developed symptoms. Retrospective investigations found that a hospital in Foshan had treated a similar case on November 25, 2002 (Figure 2A). This patient developed symptoms on November 16, 2002, subsequently, 5 family members developed symptoms as well. This indicated that SARS-CoV emerged with high human-to-human transmission capability, characterized by family and medical staff infections[7,8]. The investigation of family clustering cases identified 35 clusters involving 105 patients in families with two or more family members in Guangzhou. The largest cluster derived from a female patient. A total of 91 persons were infected due to visiting or nursing the female patient, and 2 of these died (Figure 2B). This indicated that super virus spreader emerged at earliest stage of the outbreak, confirming the high infection capability of the virus[9,10]. Subsequent case investigations also showed

that SARS-CoV has the capability of multiple and continuous human-to-human transmission (Figure 2C) and at least four generations of cases were identified from one original patient. Among the cases of clusters, healthcare workers are very common victims. As of April 13, 2003, a total of 48 medical institutions had medical staff infected and 33 medical institutions in Guangzhou reported a total of 283 cases. The incidence among medical staff in the respiratory care department of a university affiliated hospital in Guangzhou was 61.7% (29 / 47), that is, more than half of the medical staff were infected during their patient medication.

For the 2019-nCoV outbreak, the first patient with unexplained pneumonia was discovered on December 12, 2019. On December 31, 2019, 27 cases of viral pneumonia were officially announced, of which 7 were in severe conditions. Respiratory infectious diseases, including influenza, SARS and Middle East respiratory syndrome (MERS), were screened and excluded. On Jan 7, 2020, only one week later, a new type of coronavirus was discovered. The detection of pathogenic nucleic acids was completed on January 10 and on January 12, WHO officially named the new coronavirus the "2019 new coronavirus" (2019-nCoV). It took less than 10 days from the first official announcement to the identification of the pathogen (Figure 2D). In contrast to SARS-CoV, the discovery of human-to-human transmission of the 2019-nCoV was relatively late. On Dec 29, 2019, an obvious human-to-human transmission case was identified but not announced, and the official conclusion said the risk of human-to-human transmission is relatively low. Five days later, clusters of cases, including 15 healthcare workers, were confirmed to be infected by patients, confirming that 2019-nCoV also have the human-to-human transmission capability (Figure 2D). Based on these results, it was concluded that 2019-nCoV also have high capability of human-to-human transmission. It remains unknown whether earlier cases also had this capability, and if so, how many victims had not been identified.

The close contacts of these unidentified cases might be new infection sources and could become super-spreaders.

The incidence and development process of SARS outbreak also has valuable implications for the 2019-nCoV outbreak. After discovering the earliest case occurred on Nov 16, 2002, the incidence remained low until Jan 2, 2003. The peak of the incidence was observed between Jan 3 and Feb 4, 2003, and the number of cases accounted for 54.7% of the total cases. According to the case number and the development characteristics of the SARS epidemic, it can be roughly divided into 4 stages: stage 1, Nov 16, 2002 to Jan 31, 2003; stage 2, Feb 1 to Mar 2, 2003; stage 3, Mar 3 to Apr 2; and stage 4, after Apr 4 (Figure 3A). Coincidentally, the SARS outbreak duration also covered the Chinese spring festival. Each year, the Chinese government will launch a 40-day spring festival transport support system, and during this period, billions of people will migrate around China. In 2003, the spring festival transport period was from Jan 17 to Feb 25 and coincided with the incidence peak (Figure 3A, purple box). The spring festival travel period in 2020 was from Jan 10 to Feb 18 which coincided with the rapid increase of 2019-nCoV cases between Jan 10 and 22, 2020 (Figure 3A, red box). Given previous trends, this is unlikely to be the incidence peak of this new virus outbreak. The daily counts of 2019-nCov cases we observed were higher than the daily counts of SARS cases during its peak in 2003, implying a possible higher number of cumulative cases. We analyzed the transportations between different large cities. High frequency transportations are mainly distributed among megacities (Figure 3B). The highest ranked cities include Beijing, Guangzhou, and Shanghai. Wuhan, the outbreak center, has a population of 10 million, is also a major hub in the spring festival transportation network (Supplementary data). The predicted number of passengers traveling during the 2020 spring festival transport is 3.11 billion, 1.7 times the 2003 total number of 1.82 billion (Figure

3C). This large-scale migration has brought favorable conditions for disease spread that is difficult to control.

Because it is now in the early stage of outbreak, we must be prepared for subsequent larger-scale outbreaks and ask how large the scale will be. Since the 2019-nCoV is highly similar to SARS-CoV, some important characteristics of SARS-CoV could be used in this prediction. By combining the reported daily counts of 2019-nCoV cases and data from SARS outbreaks, we constructed a logistic model and predicted the incidence of 2019-nCoV over time. In the 2003 SARS outbreak, a total of 8,000 cases had been reported. With this data and the present situation, we predict that the cumulative number of 2019-nCoV cases might be 2-3 times the total of SARS cases. Logistic models were fitted with these data and cumulative and daily counts of 2019-nCoV cases were predicted. As shown in Figure 4A, we also calculated the time that is needed to reach the peak of incidence under different senarios. Setting the upper limit of cumulative incidence (K) to 8000 (the total number of global SARS cases in 2003), 16000 (two times the total global SARS cases), and 24000 (three times the total global SARS cases), the peak of incidence will be reached in 22.28 days (February 2), 25.18 days (February 5), and 26.82 days (February 7) respectively. Overall, the peak incidence will appear early at the beginning of February, or latest in mid-February. This appears to be consistent with the 7-10 days incubation time of the 2019-nCoV and the spring festival transport.

Taken together, in this study, by using valuable epidemiological data from the SARS outbreak, we systematically evaluated and compared characteristics of the 2019-nCoV and SARS-CoV outbreak. The two outbreaks shared many similarities, and the ongoing 2019-nCoV outbreak situation seemed to repeat what we experienced during the SARS-CoV outbreak. Fortunately, the Chinese government are carrying out many efficient measures, including shutting down public transportation in Wuhan

and other cities, reducing population migration, and encouraging personal protection by mask. With these measures, the case number could be reduced significantly. However, due to the lack of awareness of the human-to-human transmission capability of 2019-nCoV at early stage, there is a possibility that super-spreaders do exist. These super-spreaders can be distributed in different places and are difficult to track. This represents the most important problem for this outbreak.

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Authors' contribution

J. Lu and Z. Chen participated in the prevention and control of SARS outbreak; J. Lu participated in epidemiological investigation of SARS outbreak in Guangdong. J. Lu and Z. Chen conceived and designed the study, W. Zhang performed the prediction. Y. Lu, C. Guo provide helpful suggestion and revised the manuscript. Z. Guo, C. Liao, X. Zhang, Y. Zhang, and X. Han analyzed data and prepared materials for the manuscript. Z. Chen wrote the manuscript with help from all other authors.

Figure 1

Characteristics	2019-nCoV	SARS
Lineage	Beta-coronavirus Group 2b, with >70% genetic similarity	
Source	Bat (Chrysanthemum)	Civet and bat
Latent period	2-14 days	2-7 days
Human-to-human transmission	Confirmed	
Duration time*	On-going since Dec 31, 2019	Nov 16, 2002 to July 2003
Cases	913 known cases with 17 fatalities (as Jan 23, 2020)	8, 098 cases with 774 fatalities
Current status	Mainly reported in Wuhan city. Imported cases are identified in other regions of China and foreign countries, including U.S..	No reported new cases since 2004
Symptom	Fever, cough and shortness of breath	
Treatment	No effective antiviral medication or protective vaccine	
Prevention	Reduce unnecessary exposure, hand and respiratory hygiene and safe food practices	

Figure 1 Basic Epidemiological Characteristics of 2019-nCoV and SARS-CoV Outbreak

*China annual spring festival travel rush is from Jan 17 to Feb 25 in year 2003 (the number of passenger population is 1.8 billion), and from Jan 10 to Feb 18 in year 2020 (estimated number of passenger population is 3.1 billion).

Figure 2

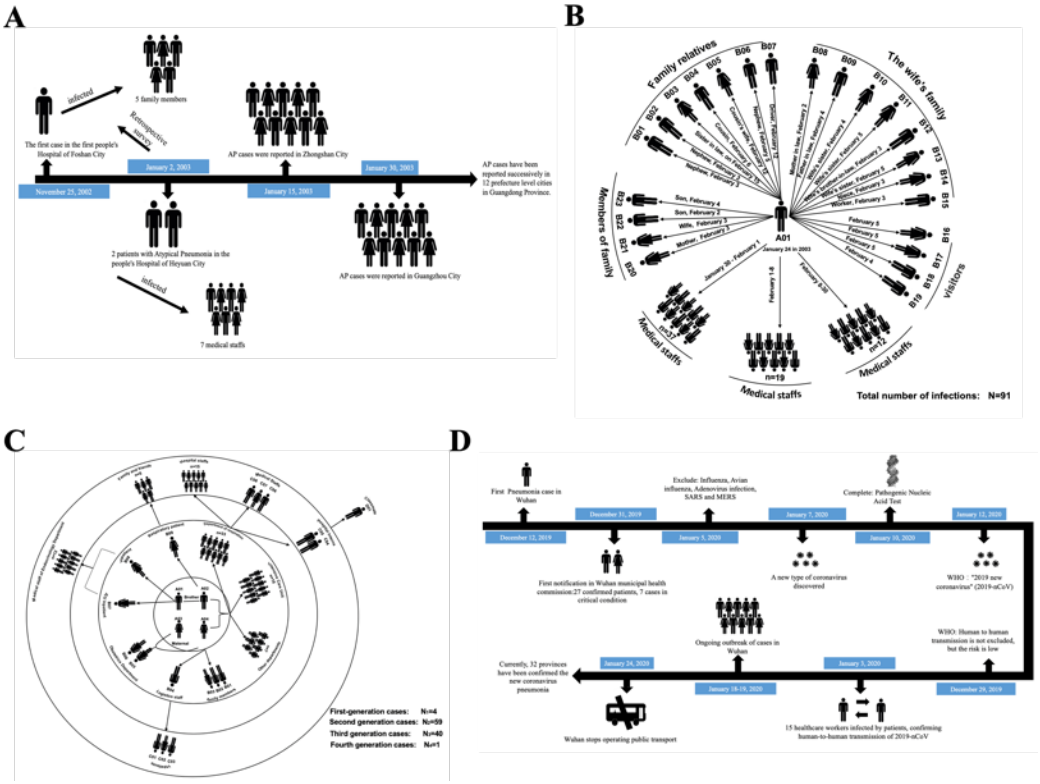

Figure 2 Identification of Early Cases and Transmission Chain of Super Virus Spreader

A, Discovery of early cases during SARS-CoV outbreak. Human-to-human transmission was observed in the first identified cases. B, the “one-to-X” human-to-human transmission clusters, 91 persons were infected by the super spreader. C, the “n-x-y” continuous human-to-human transmission cluster. Up to 4 generation of transmitted patients were observed in this cluster. D, early cases identification during the 2019-nCoV outbreak. Human-to-human transmission was not discovered in the earliest cases.

Figure 3

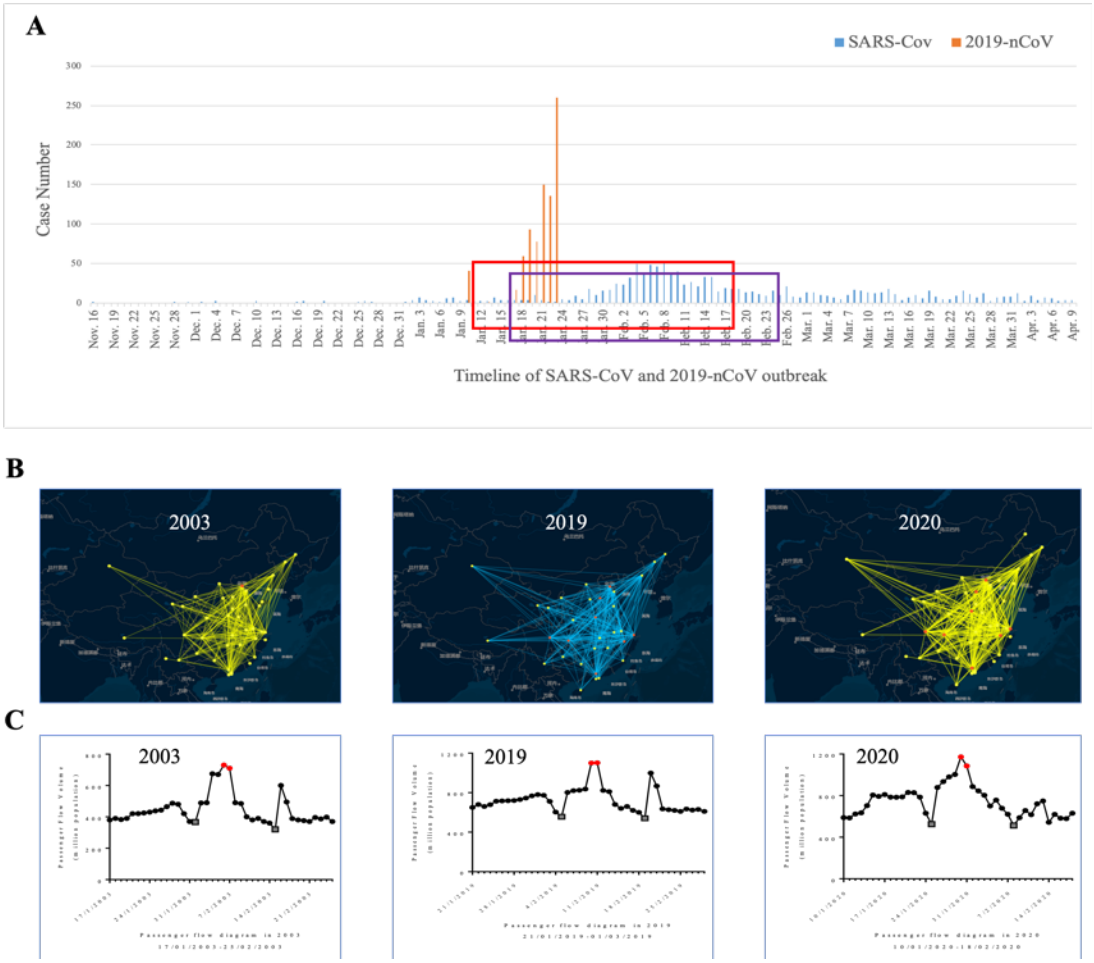

Figure 3 Coincidence of Outbreak Early Stage with spring festival Transport

A, the two outbreaks happened near Chinese spring festival, when billions of people will transmit between different places. Red box, spring festival duration of 2020 (Jan 10 to Feb 18, 2020); Purple box, spring festival duration of 2003 (Jan 17 to Feb 25, 2003); The first official report on the outbreak was Jan 2, 2003, and Dec 27, 2019. B, Population movement network during spring festival of 2003, 2019 and 2020. C, Passenger flow rush during spring festival of 2003, 2019 and 2020. Total population is 1.81, 2.91 and 3.11 billion for 2003, 2019 and 2020 respectively. Spring festival transport data of 2020 was predicted.

Figure 4

A

K	a	r	R^2	F	p	t_{max} (day)
8000	6.0174	0.2701	0.85	66.28	0	22.28
16000	6.6994	0.2661	0.85	67.34	0	25.18
24000	7.1013	0.2648	0.85	67.67	0	26.82

B

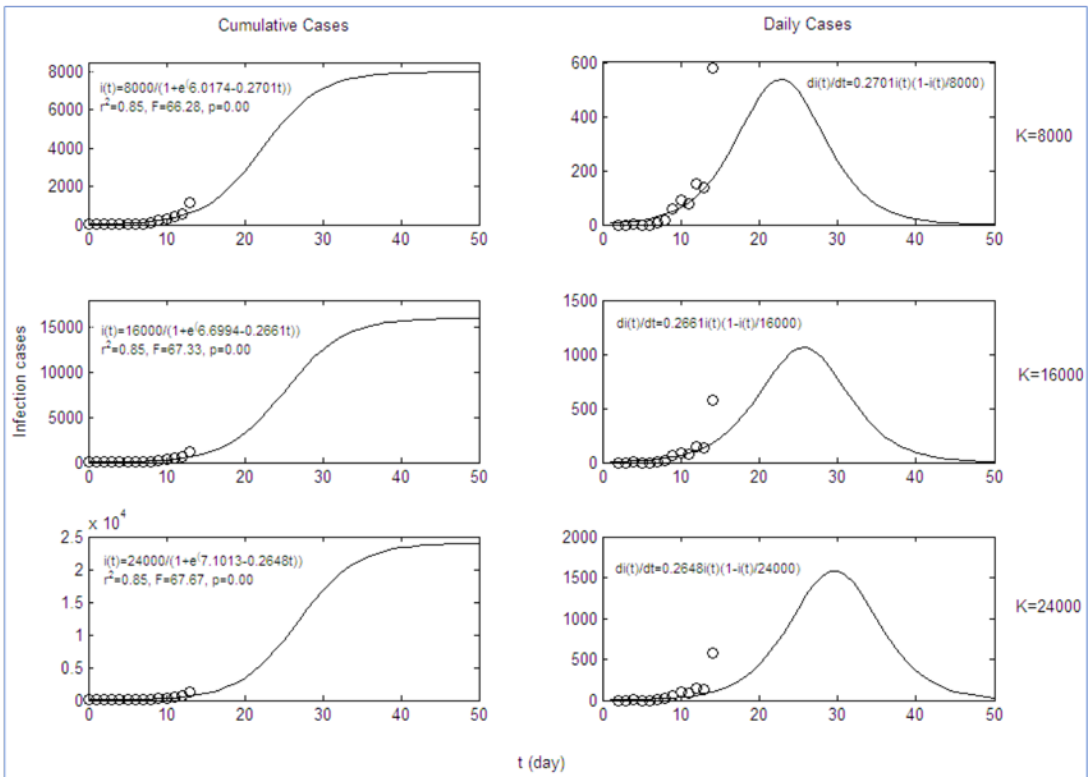

Figure 4 Logistic Model Fitting and Incidence Prediction Over Time

Fitting Logistic model to the dynamics of global infection cases of 2019-nCoV. Prediction results of cumulative case and daily cases with upper limit of cumulative cases of 8000, 16000 and 24000. t=0 denotes Jan10, 2020.

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