

The progress of 2019 novel coronavirus event in China

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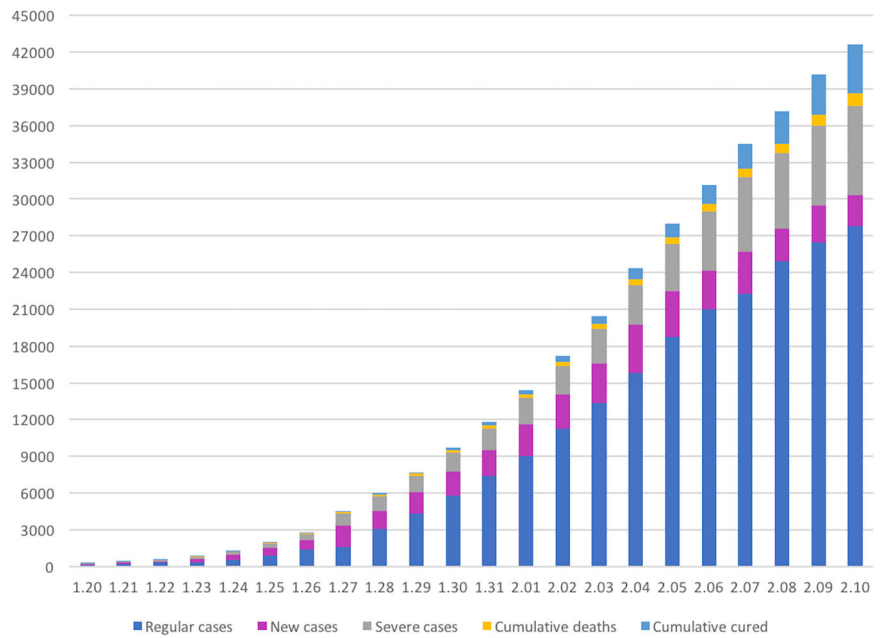
It has been more than 1 month since the first 2019-nCoV infected person was diagnosed. So far, 42 638 people have been diagnosed as 2019-nCoV pneumonia, which also known as Wuhan pneumonia, among them, 7333 are severe cases, 1016 patients died, and only 3996 patients have been cured in the mainland of China (Hong Kong, Macao, and Taiwan were excluded).¹ All 31 provincial-level regions and the Xinjiang Production Corps have the confirmed cases.¹ Hubei province, where believed to be the origin of Wuhan pneumonia outbreak, suffers the most, with 31 728 confirmed cases and 974 death cases.² The trend of cumulative cases is soaring, including 24 other countries outside of China had confirmed cases. With a remarkable notice that the total number of cases has far exceeded the number during severe acute respiratory syndrome (SARS) period. The first case of 2019-nCoV pneumonia was linked to wild animal trading in the Huanan seafood market in the city of Wuhan, the capital of Hubei province.³ Zhou et al⁴ found the initial source of 2019-nCoV probably originated from the Chinese horseshoe bat since the novel coronavirus was 96% identical to a bat coronavirus at a whole genome level. This coronavirus, which has not been identified in humans previously, had been detected from patients in Wuhan⁵ and it was the first case for human infection with 2019-nCoV from wild animals.⁶ Recently, Wu et al⁷ estimated 75 815 individuals would be infected in Wuhan, with an uncertainty range from 37 304 to 130 330 by using the susceptible-exposed-infectious-recovered model. While the variation of the virus is still under surveillance.

Coronaviruses are a huge family of viruses, of which severe acute respiratory syndrome coronavirus (SARS-nCoV) and Middle East respiratory syndrome coronavirus (MERS-nCoV), and so on have already known by humans.⁸ The 2019-nCoV has an incubation period of 3 to 7 days in general, with a maximum of 14 days.⁹ The most common symptoms at the onset of illness are fever, cough, and

myalgia or fatigue.^{9,10} While a few patients might have stuffiness, pharyngalgia, or diarrhea.⁹ By far, the main sources of infection are 2019-nCoV infected humans, however, the asymptomatic infection might also be a source of infection.⁹ These patients are not easy to be detected among the population when initially infected but might have headache, fever, dyspnea, fatigue, and so on later.¹¹ This type of coronavirus has been proved could spread from person to person through the respiratory tract and contact transmission.^{9,12} Zhang et al¹³ pointed out the digestive system might also be a potential route of 2019-nCoV infection based on bioinformatics analysis. Wu et al⁷ found R_0 , the basic reproduction number is around 2.68 with 2.47 to 2.86 of 95% credible interval, by applied Markov Chain Monte Carlo methods, where transmission characteristics appear to be similar of SARS.¹⁴ Mild and occult cases could be the major concerns for disease prevention.^{15,16} The World Health Organization (WHO) recommends wearing a medical mask when leaving homes¹⁷ and ethanol and the high temperature had been proved could prevent disease occurrence.⁹ The event has been determined as a Public Health Emergency of International Concern by WHO.¹⁸

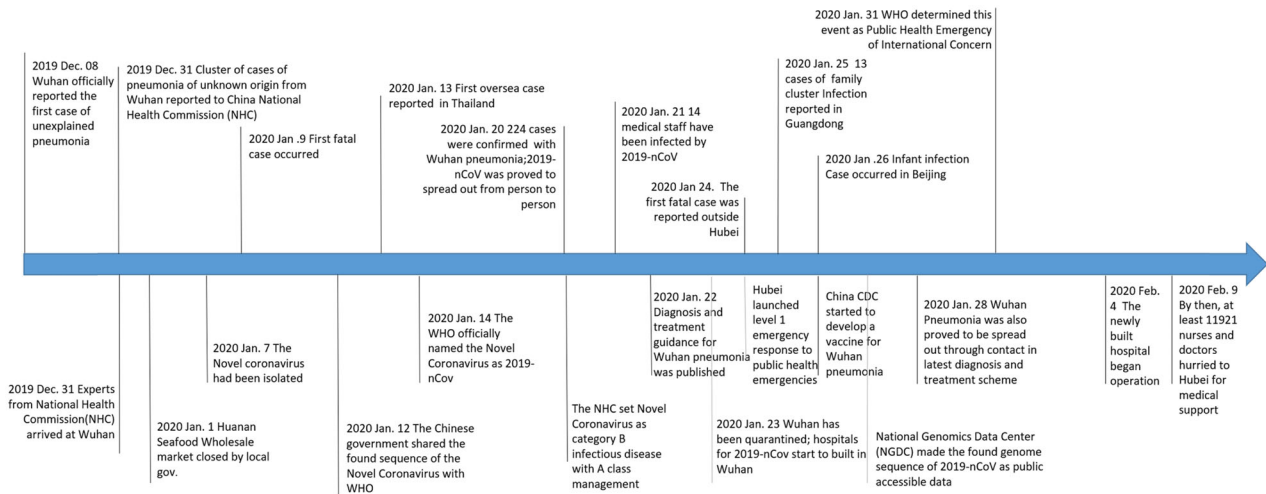
Humans are generally susceptible to coronavirus.⁹ The youngest infected patient is only 1 month after birth.¹⁹ Death cases were mostly found in the elderly and who already have chronic conditions.^{10,20} The confirmed case is defined as either positive of novel coronavirus nucleic acid by real-time fluorescent reverse transcription-polymerase chain reaction detection of respiratory or blood specimens or highly homologous to any known novel coronaviruses through virus gene sequencing of respiratory or blood specimens. Only when body temperature returns to normal for more than 3 days, respiratory symptoms significantly improved and two consecutive tests negative of the nucleic acid of respiratory pathogens, with at least 1 day on sampling interval, people could be allowed to discharge from hospital⁹ (Figure 1).

FIGURE 1 The trend of 2019-nCoV pneumonia cases



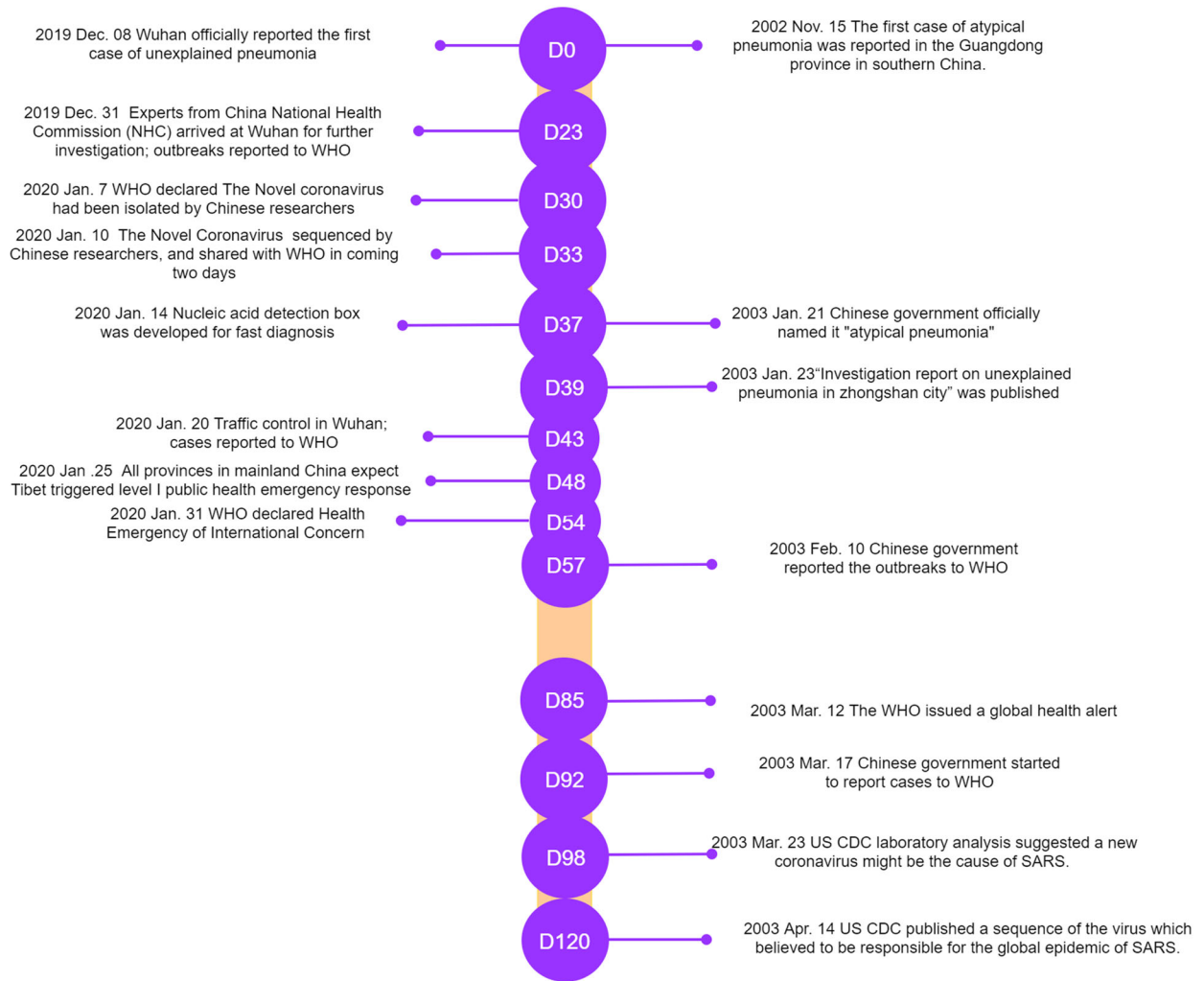
The Chinese government has taken emergency measures to support population prevention and clinical treatment after the outbreak and made remarkable progress in responding to disease control comparing with SARS time (Figure 3).^{8,21} The National Health Commission has set 2019-nCoV pneumonia as a category B infectious disease with A-class management on 20 January.²² Provincial Bureau of health from Shanghai, Anhui, Zhejiang, and so on have organized medical teams, mainly including medical staff from the respiratory department, infections department and

critical care medication, hurried to Wuhan for medical support.²³ “Huo Shen Shan” had been established for the centralized treatment of Wuhan pneumonia patients by reference to the model of Xiao Tang Shan hospital in Beijing during the SARS period. Although the cure rate has been rising up, compared with the fast-growing cases and fatality rate from the updated collected data, it is still required to improve (Table 1). Through the efforts of scientists, Chinese Center for Disease Control and Prevention (CDC) has obtained the full-length genome of 2019-nCoV from



Note: Information were sorted up from China Central Television (CCTV) network: <http://news.cctv.com>

FIGURE 2 The key nodes in 2019-nCoV pneumonia event



Note: Information were sorted up from US-CDC: <https://www.cdc.gov/about/history/sars/timeline.htm> , CNN: <http://edition.cnn.com/2003/HEALTH/04/24/timeline.sars/> , Nat Med: <https://doi.org/10.1038/s41591-020-0771-1> and an Official Account: <https://xueqiu.com/1364012634/140071762>

FIGURE 3 The comparison between 2019-nCoV and severe acute respiratory syndrome event development

clinical specimens and found the sequence of the genome has significant differences from any known coronavirus,²⁴ which is most related to the nucleotide sequence of bat-SL-CoVZC45 with 85% sequence similarity.^{24,25} All the found genome sequence of 2019-nCoV has been published as open data for scientific research as disease prevention and control.²⁵ CDC is also conducting the medication screening for Wuhan pneumonia and developing a vaccine for 2019-nCoV. University of Queensland, GeoVax Labs Inc, and other world-class research teams have also been joining in the research of vaccine development.^{26,27} The Ministry of Health Disease Control Bureau also takes psycho crisis intervention and assistance for the population in need. Figure 2 showed the key nodes in the Wuhan pneumonia event, including government measures.

It has turned out to be urgent for epidemiologists, virologists, biologists, clinical doctors, and pharmaceutical researchers working together to battle against coronavirus outbreak. Human beings should engrave this zoonotic disease in mind for better dealing with "One-Human-Environmental-Animal-Health."²⁸ We believe this novel coronavirus could be wiped out under the joint efforts of scientists around the world soon.

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TABLE 1 The updated cases of 2019-nCoV pneumonia

Date	Cumulative cases	Regular cases	New cases	Severe cases	Cumulative deaths	Cumulative cured	Fatality rate	Cure rate
1.20	291	139	77	44	6	25	2.062%	8.591%
1.21	440	155	149	102	9	25	2.045%	5.682%
1.22	571	303	131	95	17	25	2.977%	4.378%
1.23	830	335	259	177	25	34	3.012%	4.096%
1.24	1287	527	444	237	41	38	3.186%	2.953%
1.25	1975	858	688	324	56	49	2.835%	2.481%
1.26	2744	1383	769	461	80	51	2.915%	1.859%
1.27	4515	1602	1771	976	106	60	2.348%	1.329%
1.28	5974	3041	1459	1239	132	103	2.210%	1.724%
1.29	7711	4310	1737	1370	170	124	2.205%	1.608%
1.30	9692	5799	1982	1527	213	171	2.198%	1.764%
1.31	11 791	7392	2102	1795	259	243	2.197%	2.061%
2.01	14 380	9048	2590	2110	304	328	2.114%	2.281%
2.02	17 205	11 244	2829	2296	361	475	2.098%	2.761%
2.03	20 438	13 358	3235	2788	425	632	2.079%	3.092%
2.04	24 324	15 836	3887	3219	490	892	2.014%	3.667%
2.05	28 018	18 749	3694	3859	563	1153	2.009%	4.115%
2.06	31 161	21 021	3143	4821	636	1540	2.041%	4.942%
2.07	34 546	22 274	3399	6101	722	2050	2.090%	5.934%
2.08	37 198	24 894	2656	6188	811	2649	2.180%	7.121%
2.09	40 171	26 436	3062	6484	908	3281	2.260%	8.168%
2.10	42 638	27 815	2478	7333	1016	3996	2.383%	9.372%

Note: Fatality rate = $\frac{\text{cumulative deaths}}{\text{cumulative cases}}$; cure rate = $\frac{\text{cumulative cured cases}}{\text{cumulative cases}}$; cumulative cases = regular cases + new cases + severe cases + cumulative deaths + cumulative cured.

The above data only represented cases in mainland of China, Hong Kong, Taiwan, and Macau were excluded. Data were collected from National Health Commission of the People's Republic of China. Available from http://www.nhc.gov.cn/xcs/yqtb/list_gzbd.shtml

CONFLICT OF INTERESTS

The authors declare that there are no conflict of interests.

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