Covid19 Pandemic, Closing Gaps in the Responses and Transmission Chain Events

Hamid Yahya Hussain^{*1}, Bushra baderkhan¹, Mohamed Hamid¹ and Abdulla Hamid²

¹Dubai Health authority, UAE

²Faculty of Medicine, University of Baghdad, Iraq

Abstract

Background: Emerging and reemerging pathogens are global challenges for public health.1 Coronaviruses are enveloped RNA viruses that are distributed broadly among humans, other mammals, and birds and that cause respiratory, enteric, hepatic, and neurologic diseases. the high prevalence and wide distribution of coronaviruses, the large genetic diversity and frequent recombination of their genomes, and increasing human–animal interface activities, novel coronaviruses are likely to emerge periodically in humans owing to frequent cross-species infections and occasional spillover event.

Objectives: To study the short-term morbidities and mortalities and international spread time trends of the N Corona Virus 2019 outbreak, to study, to study the explosiveness and aggressiveness of the outbreak and the gaps in response.

Methodology: Outbreak events follow up and observation study over two months has been carried out through daily statistical reports issuing by world health organizations as all as different national authorities regarding (mortalities and morbidities incidents) all over the world with specific focusing on china statistics as main sources of outbreak . Operational definition of variables regarding case confirmation, case recovery, case admission, and case contacts has been adopted as per WHO definitions. Unofficial statistical reports excluded as a source of data.

Results: The current study showed that the number of cases of N corona-virus 2019 infection, started with (41) cases at the beginning of January 2020 increased up to 855 cases in 23rd January 2020 and 7700 case of infection in 29th of January 2020 which keep raising up reached up to 78823 in 23rd of February as for mortalities , the current research revealed that number of death was only (1) case in 4th of Feb 2020 increased up to 25 death in 23rd of February 2020 and keep raising reached up to 170 deaths in January 29th 2020 and 2462 death case in 23rd of Feb 2020 as reflected by). In regards of geographical spread of the n corona –virus 2019 infection outbreak, the study showed that in January 4th 2020 only one country was affected which was china, on 8th of January 2020 two countries were affected as Thailand discovered cases, on 13th of January 3 countries were affected by adding Singapore to the list, on Feb 5th 27 country reported incidence of N Corona –virus 2019 infection and reached up to 35 country by 23rd of February

Conclusions: The natural history and course of the current outbreak revealed high explosive nature linked to significant aggressiveness in terms of complications and mortalities, within only two months period speeded out to 35 countries worldwide and reached you 80000 incidence within only two months. The study forecasted that the peak of the outbreak is not yet attended and more dramatic events still has high potentials.

Corresponding author: Hamid Yahya Hussain, Dubai Health authority, UAE. E-mail: hussainh569@Hotmail-com

Received: February 26, 2020 ; **Accepted:** April 25, 2020 ; **Published:** May 10, 2020.

Keywords: (N-Corona Virus 2019, Mortality, Morbidity, explosiveness, aggressiveness)

Introduction

Emerging and reemerging pathogens are recognized as global public health challenges [1]. Coronaviruses are a kind of RNA enveloped viruses that are broadly distributed among mammals, birds and humans, and causing acute and severe respiratory infection, hepatic, neurologic and enteric diseases [2,3]. Six coronavirus species are known to cause human disease [4]. Four viruses — 229E, OC43, NL63, and HKU1 — are prevalent and typically cause common cold symptoms in immunocompetent individuals [4]. The two other strains — severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) — are zoonotic in origin and have been linked to sometimes-fatal illness [5-8]. In late December 2019, several local health facilities reported clusters of patients with pneumonia of unknown cause that were epidemiologically linked to a seafood and wet animal wholesale market in Wuhan, Hubei Province, China. On December 31, 2019, the Chinese Center for Disease Control and Prevention (China CDC) dispatched a rapid response team to accompany Hubei provincial and Wuhan city health authorities and to conduct an epidemiologic and etiologic investigation. We report the results of this investigation, identifying the source of the pneumonia clusters, and describe a novel coronavirus detected in patients with pneumonia whose specimens were tested by the China CDC at an early stage of the outbreak. We also describe clinical features of the pneumonia in two of these patients. In December 2019, a series of pneumonia cases of unknown cause emerged in Wuhan, Hubei, China, with clinical presentations greatly resembling viral pneumonia [9]. Deep sequencing analysis from lower respiratory tract samples indicated a novel coronavirus, which was named 2019 novel coronavirus (2019-nCoV). Thus far, more than 800 confirmed cases, including in health-care workers, have been identified in Wuhan, and several exported cases have been confirmed in other provinces in China, and in Thailand, Japan, South Korea, and the USA [10-13].

Objectives

To study the short-term morbidities and mortalities and international spread time trends of the N Corona Virus 2019 outbreak, to study, to study the explosiveness and aggressiveness of the outbreak and the gaps in response.

Methodology

Outbreak events follow up and observation study over two months has been carried out through daily statistical reports issuing by world health organizations as well as different national authorities regarding (mortalities and morbidities incidents) all over the world with specific focusing on china statistics as main sources of outbreak. Operational definition of variables regarding case confirmation, case recovery, case admission, and case contacts has been adopted as per WHO definitions. Unofficial statistical reports excluded as a source of data.

Results

The current study showed that the number of cases of N corona-virus 2019 infection, started with (41) cases at the beginning of January 2020 increased up to 855 cases in 23rd January 2020 and 7700 case of infection in 29th of January 2020 which keep raising up reached up to 78823 in 23rd of February as shown in the figure (1) as for mortalities , the current research revealed that number of death was only (1) case in 4th of Feb 2020 increased up to 25 death in 23rd of February 2020 and keep raising reached up to 170 deaths in January 29th 2020 and 2462 death case in 23rd of Feb 2020 as reflected by figure number (2). In regards of geographical spread of the n corona -virus 2019 infection outbreak, the study showed that in January 4th 2020 only one country was affected which was china, on 8th of January 2020 two countries were affected as Thailand discovered cases, on 13th of January 3 countries were affected by adding Singapore to the list, on Feb 5th 27 country reported incidence of N Corona -virus 2019 infection and reached up to 35 country by 23rd of February as reflected by figure (3)

Figure 1: Time trend of corona infection morbidity over two months period.

Figure 2: Time trend mortality of N- Corona Virus 2019 infection over two months period.

Figure 3: Time trend international spread of N Corona Virus 2019 infection over 2 months' time.

Discussions

The current study revealed dramatic explosive outbreak of N Corona virus 2019 infection in terms of number of

confirmed cases, number of deaths and number of countries affected with the outbreak within 50 days, the explosion of the epidemic with high morbidity and mortality incidences reflected another nature of the diseases which is the aggressiveness of the virus. Both the explosiveness and the aggressiveness nature of the epidemic alarming global as well as national health care systems in regards of responsiveness capacity, containment strategies and applying effective transmission chain break down strategies, the nature of the current epidemic reflected the fragile status of global capacity of health system response along with lack of preparedness and an ability of prediction and forecasting. Furthermore the current epidemic is taking new trend, moving from localized area to worldwide zones which make containment much harder and needs more efforts at the level of global mobility, which may push toward more economical loss. The other significant observation in the current pandemic is, that we did not reach yet to the peak of the explosion, and there will be further potentials of the epidemic that can be expressed in coming days and months until it reach to the peak and decline down.

The symptoms of this novel pneumonia were also non-specific. With patient have other comorbidities had more severe systemic symptoms of generalized weakness and dry cough. As expected, they might have decreased total white blood cell, lymphocyte, or platelet counts, with also extended activated thromboplastin time and increased C-reactive protein level. The multifocal ground-glass changes on lung CT scan were typical of viral pneumonia. Their lung involvement was also more diffuse and extensive than those of the younger patients, whose blood test results were largely normal. Patient, who had a history of chronic sinusitis, might have a bacterial superinfection because he had a productive cough instead of a dry cough. He also had a high white blood cell count, although the bacterial test was negative [14-20].

An outbreak of novel coronavirus is ongoing at Wuhan in the winter of 2019–20. Similar to the 2003 SARS outbreak in Guangzhou, Wuhan is also a rapidly flourishing capital city of the Hubei province and the traffic hub of central China. Moreover, both outbreaks were initially connected to wet markets where game animals and meat were sold. In the case of SARS, person-to-person transmission was efficient and super-spreading events had led to major outbreaks in hotels and hospitals. Learning from the SARS outbreak, which

started as animal-to-human transmission during the first phase of the epidemic, all game meat trades should be optimally regulated to terminate this portal of transmission. But as shown in this study, it is still crucial to isolate patients and trace and quarantine contacts as early as possible because asymptomatic infection appears possible (as shown in one of our patients), educate the public on both food and personal hygiene, and alert health-care workers on compliance to infection control to prevent super-spreading events. Unlike the 2003 SARS outbreak, the improved surveillance network and laboratory capability of China was able to recognize this outbreak within a few weeks and announced the virus genome sequences that would allow the development of rapid diagnostic tests and efficient epidemiological control. Our study showed that person-to-person transmission in family homes or hospital, and intercity spread of this novel coronavirus are possible and therefore vigilant control measures are warranted at this early stage of the epidemic [20-26].

Conclusions

The natural history and course of the current outbreak revealed high explosive nature linked to significant aggressiveness in terms of complications and mortalities, within only two months period speeded out to 35 countries worldwide and reached you 80000 incidence within two months only. The study forecasted that the peak of the outbreak is not yet attended and more dramatic events still has high potentials of further enormous damages worldwide.

Recommendations

Rigorous international as well as national public health measures and clinical measures at population, contacts, cases, needs to be strictly secured, breaking down transmission chain at all its events shall be the most effective strategy can be applied ever.

References

1. DD Richman, RJ Whitley (2016) FG Hayden Clinical virology, (4th edn.), ASM Press, Washington.
2. TG Ksiazek, D Erdman, CS Goldsmith, et al. (2003) A novel coronavirus associated with severe acute respiratory syndrome Engl J Med 348: 1953-1966.
3. T Kuiken, RAM Fouchier, M Schutten, et al. (2003) Newly discovered coronavirus as the primary cause of severe acute respiratory syndrome. Lancet 362: 263-270.
4. C Drosten, S Günther, W Preiser, et al. (2003) Identification of a novel coronavirus in patients with severe acute respiratory syndrome Engl J Med 348: 1967-1976.
5. RJ de Groot, SC Baker, RS Baric, et al. (2013) Middle East respiratory syndrome coronavirus (MERS-CoV): announcement of the Coronavirus Study Group. J Virol 87: 7790-7792.
6. AM Zaki, S van Boheemen, TM Bestebroer, ADME Osterhaus (2012) RAM Fouchier Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. N Engl J Med 367: 1814-1820.
7. WHO Summary of probable SARS cases with onset of illness from 1 November 2002 to 31 July 2003, https://www.who.int/csr/sars/country/table2004_04_21/en/.
8. WHO Middle East respiratory syndrome coronavirus (MERS-CoV) <http://www.who.int/emergencies/mers-cov/en/>.
9. WHO Novel coronavirus – China, <http://www.who.int/csr/don/12-january-2020-novel-coronavirus-china/en/>.
10. WHO Novel coronavirus – Thailand (ex-China), <http://www.who.int/csr/don/14-january-2020-novel-coronavirus-thailand/en/>.
11. WHO Novel coronavirus – Japan (ex-China), <http://www.who.int/csr/don/17-january-2020-novel-coronavirus-japan-ex-china/en/>.
12. WHO Novel coronavirus – Republic of Korea (ex-China), <http://www.who.int/csr/don/21-january-2020-novel-coronavirus-republic-of-korea-ex-china/en/>.
13. CDC First travel-related case of 2019 novel coronavirus detected in United States, <https://www.cdc.gov/media/releases/2020/p0121-novel-coronavirus-travel-case.html>.
14. W Tan, X Zhao, X Ma, et al. (2020) A novel coronavirus genome identified in a cluster of pneumonia cases — Wuhan, China 2019–2020, <http://weekly.chinacdc.cn/en/article/id/a3907201-f64f-4154-a19e-4253b453d10c>.
15. Centre for Health Protection of the Hong Kong Special Administrative Region Government CHP closely monitors cluster of pneumonia cases on Mainland, <https://www.info.gov.hk/gia/general/201912/31/P2019123100667.htm>
16. Centre for Health Protection of the Hong Kong Special Administrative Region Government CHP provides further information on cluster of pneumonia cases in Wuhan, <https://www.info.gov.hk/gia/general/202001/12/P2020011200710.htm> (Jan 12, 2020), Accessed 21st Jan 2020, Google Scholar
17. D Juan Wuhan wet market closes amid pneumonia outbreak, ChinaDaily (Jan 1, 2020), <https://>

- www.chinadaily.com.cn/a/202001/01/WS5e0c6a49a310cf3e35581e30.html,
18. J Cohen Chinese researchers reveal draft genome of virus implicated in Wuhan pneumonia outbreak, American Association for the Advancement of Science, Washington, DC (Jan 11, 2020)<https://www.sciencemag.org/news/2020/01/chinese-researchers-reveal-draft-genome-virus-implicated-wuhan-pneumonia-outbreak>.
 19. KK To, KH Chan, IW Li, et al. (2010) Viral load in patients infected with pandemic H1N1 2009 influenza A virus Med Virol 82: 1-7.
 20. KKW To, CCY Yip, CYW Lai, et al. (2019) Saliva as a diagnostic specimen for testing respiratory virus by a point-of-care molecular assay: a diagnostic validity study, Clin Microbial Infect 25: 372-378.
 21. KH Chan, KKW To, PTW Li, et al. (2017) Evaluation of NxTAG Respiratory pathogen panel and comparison with xTAG respiratory viral panel fast v2 and film array respiratory panel for detecting respiratory pathogens in nasopharyngeal aspirates and swine/avian-origin influenza A subtypes in culture isolates. Adv Virol, 2017: 1324276.
 22. JS Perris, ST Lai, LL Poon, et al. (2003) Coronavirus as a possible cause of severe acute respiratory syndrome. Lancet 361: 1319-1325.
 23. JF Chan, AJ Zhang, CC Chan, et al. (2016) Zika virus infection in dexamethasone-immunosuppressed mice demonstrating disseminated infection with multi-organ involvement including orchitis effectively treated by recombinant type I interferons Ebio Medicine 14:112-122.
 24. KKW To, WM Chan, KSM Li, et al. (2017) High prevalence of four novel astrovirus genotype species identified from rodents in China Gen Virol 98: 1004-1015.
 25. PC Woo, SK Lau, JL Teng, et al. (2014) Metagenomic analysis of viromes of dromedary camel fecal samples

Copyright: ©2020 Hamid Yahya Hussain. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.