What relevant knowledge did we have before the COVID-19 pandemic?

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Aug 29th, 2022
Black Swan or Grey Rhino?

GPMB 2019
Annual Reports:
Flu, Coronavirus

Not ready
We cannot work together
A global pandemic exercise

Caps

Coronavirus Associated Pneumonia Syndrome

- Event 201 was a pandemic tabletop exercise.
- October 18, 2019, Friday, New York, US
- https://www.centerforhealthsecurity.org/event201/about
A novel coronavirus outbreak of global health concern

Chen Wang, Peter W Horby, Frederick G Hayden, George F Gao

In December, 2019, Wuhhan, Hubei province, China, became the centre of an outbreak of pneumonia of unknown cause, which raised intense attention not only within China but internationally. Chinese health authorities did an immediate investigation to characterise and control the disease, including isolation of people suspected to have the disease, close monitoring of contacts, epidemiological and clinical data collection from patients, and development of diagnostic and treatment procedures. By Jan 7, 2020, Chinese scientists had isolated a novel coronavirus (CoV) from patients in Wuhan. The genetic sequence of the 2019 novel coronavirus (2019-nCoV) enabled the rapid development of point-of-care real-time RT-PCR diagnostic tests specific for 2019-nCoV (based on full genome sequence data on the Global Initiative on Sharing All Influenza Data [GISIAD] platform). Cases of 2019-nCoV are no longer limited to Wuhan. Nine exported cases of 2019-nCoV infection have been reported in Thailand, Japan, Korea, the USA, Vietnam, and Singapore to date, and further dissemination through air travel is likely. As of Jan 23, 2020, confirmed cases were consecutively reported in 32 provinces, municipalities, and special administrative regions in China, including Hong Kong, Macau, and Taiwan. These cases detected outside Wuhan, together with the detection of infection in at least one household cluster—reported by Jasper Fuk-Woo Chan and colleagues in The Lancet—and the recently documented infections in health-care workers caring for patients with 2019-nCoV indicate human-to-human transmission and thus the risk of much wider spread of the disease. As of Jan 24, 2020, 835 cases reported in China (549 from Hubei province, 286 from the other 31 provinces, municipalities, or special administrative regions).

Global Concern
Published: January 24, 2020
Previous knowledge on the zoonotic viruses and spillover events

Natural Cycle of the Influenza viruses

Ecology of Ebola
Seven coronaviruses can infect human beings
Two newly discovered

- HCoV-HKU1
- HCoV-OC43
- HCoV-NL63
- SARS
- MERS
- COVID-19
Current SARS-CoV-2 is expanding the territories
Why do we have so many emerging viruses?

Climate and ecological changes

- GFS/CFSR 1-day Avg
  - 1979-2000 base
- 2m T Anomaly (°C)
  - Wednesday, Jun 23, 2021

Human behavior changes

- ClimateReanalyzer.org
- Climate Change Institute | University of Maine

https://www.washingtonpost.com/weather/
It is likely not a matter of if, but when, the next recombinant CoV will emerge and cause another outbreak in the human population.
Discovery of SARS-CoV-2

2\textsuperscript{nd} Jan. 2020
Obtaining the RT-PCR results 3 hours after receiving the samples.

3\textsuperscript{rd} Jan. 2020
Obtaining the full genome sequences of SARS-CoV-2

7\textsuperscript{th} Jan. 2020
Isolation of SARS-CoV-2
In 10th Jan. 2020, China CDC released the SARS-CoV-2 genome sequence in GISAID.
4 Stages in China
Containment
Suppression
Accurate Mitigation/Suppresion
Local transmission again
China’s Contribution to Modern Public Health

Spring Wave

Lake Tsunami
Strengthening public health at the community-level in China

An unprecedented pandemic, COVID-19 is currently hitting the world. After the initial outbreak in the city of Wuhan, Hubei province, COVID-19 is under control in China, with a few small waves caused by imported cases, all of which have been stopped in China in 2-4 weeks, with between several cases and hundreds of cases per wave. We have learned from these intervals with these small waves. It is crucial to understand why and how China has reached such success, and it might help other countries. For COVID-19, we believe that acting early at the community-level has been effective. Regional stations have been kept and renamed as local CDCs, from province to prefecture to county levels, which is different from the US CDC system. Since then, the fourth CDC system has been well built with large capacity and workforce. This system can be shown as the basis for the effective prevention and control of COVID-19. During the pandemic, community-level public health practice has supported health promotion and public understanding of science, leading to strong and intense public involvement in disease control and prevention. A good example is the effective practice of
Saturated vaccine development
Esp. in China
The vaccine: Smallpox virus eradication

In 1980, WHO announced the eradication of smallpox through vaccination
Rinderpest is Another Virus that was Eradicated by vaccination
Disease X ???
Attacks by EID Gao, Cell, 2018

From “A”IV to “Z”IKV: Attacks from Emerging and Re-emerging Pathogens

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https://doi.org/10.1016/j.cell.2018.02.025

100 years after the infamous “Spanish flu” pandemic, the 2017–2018 flu season has been severe, with numerous infections worldwide. In between, there have been continuous, relentless attacks from re-emerging viruses. To fully understand viral pathogenesis and develop effective medical countermeasures, we must strengthen current surveillance and basic research efforts.

This year marks the centenary of the “Spanish flu” pandemic, the most devastating viral pandemic in history caused by an H1N1 influenza A virus that infected over 200 million and killed between 50 and 100 million people. We know to expect a flu season every year; the question is always how severe it will be. With high numbers of influenza infections reported worldwide during this season, we are again reminded of the public health threat the ongoing influenza pandemic is to the world. The World Health Organization (WHO) reported that this is the first time in the past 15 years that states in the entire continent of Africa have reported widespread influenza activity during the same week. In China, the reported number of flu cases has increased over 2-fold compared to the flu seasons in the past several years—the second highest recorded number, just after the 2009 pandemic H1N1 (ph1N1)—and many patients have been hospitalized with severe clinical symptoms. These events have raised concerns that we are in danger of another flu pandemic. Circulating influenza strains are quite diverse this year—including the “swine flu” 2009-pH1N1, H3N2, and influenza B/Victoria and B/Yamagata—these strains are spreading across various geographical locations. The H3N2 subtype is currently dominant in the UK and the USA, but a mixed pool of pH1N1, H3N2, and influenza B/Yamagata, with a small portion of Victoria, has been reported in China. A universal influenza vaccine to combat such influenza strains is urgently needed yet still far from reach, despite the global efforts. Despite best efforts to anticipate the emergent strains, vaccines vary from year to year in terms of efficacy, with this year’s providing only modest protection.

Human infections with different subtypes of avian influenza A viruses (AIVs) have been sporadically reported since H5N1 AM was reported in Hong Kong during 1997 (Yuen et al., 1998). Infections with AIV typically result in high case fatality rates (CFRs) ranging from 30% to 100%, and at least 14 influenza A virus subtypes—including the three seasonal flu viruses, H1N1, H2N2, and H3N2—have been sporadically reported to date (Figure 1). Of note, influenza A virus has a segmented genome with 8 genomic segments encoding at least 15–16 proteins, two of which are hemagglutinin (HA) and neuraminidase (NA). There are currently 16 (Hx) HA genes and 9 (Nx) NA genes (2 means two more HA or NA from last derived influenza-like viruses, for which only genomic sequences are available, but no virus has yet been isolated. Wu et al., 2015). The combination of HA and NA would theoretically yield 144 subtypes of viral viruses. Due to the migratory birds’ travel and live poultry trade, which includes the transport of poultry and operation of live poultry markets (LPMs) throughout China and Southeast Asia (Wu et al., 2015), we should expect more human infections with AIVs in the future. AIVs may supply genomic segments for reassortment with circulating seasonal influenza viruses to generate a novel pathogen with high CFR and pandemic potential. As we can’t yet eradicate seasonal flu, efforts to change the traditional live poultry trade—for example, the traditional LPMs—in order to restrict the flow of domestic poultry migration may help decrease the probability of the emergence of novel AIV subtypes, and hence the potential pandemic viruses.

Flu isn’t alone. Coronavirus is another family of emerging pathogens with public health concern. A devastating but quickly controlled outbreak of severe acute respiratory syndrome coronavirus (SARS-CoV) during 2003 transformed China’s approach to outbreak control. A successful surveillance system has since been put in place. While primarily government led, there is extensive collaboration with various institutes in the academic, industry, and healthcare fields to produce a wide-ranging, comprehensive network that issues warnings of an impending outbreak at the earliest opportunity. As exemplified by the Chinese Academy of Sciences Center for Influenza Research and Early Warning (CASICR) network, in addition to the Chinese National Influenza Center/WHO Collaborating Center for Reference and Research on Influenza under China COID, such systems can draw basic, applied, and translational research on infectious diseases control and prevention (Wu et al., 2017). A related coronavirus, the Middle East respiratory syndrome coronavirus (MERS-CoV), emerged in the Middle East during 2012 and has evocatively caused sporadic infections with imported cases from returning travelers, some of which go on to infect others. One such instance was the importation of a MERS-CoV case into China from South Korea during 2015 (Ji et al., 2015), in which the traveler was promptly
THANK YOU!