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Chinese Pneumonia Outbreak 2023: Is It Reasonable to Be Concerned If the Illness is a Novel Strain of Disease X?

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Dear Editor,

The World Health Organization (WHO) defined “Disease X” in February 2018 as a novel illness caused by an undiscovered pathogen with epidemic or pandemic potential.¹ It was hypothesized then that the first “Disease X” was the SARS-CoV-2 found in bats that produced a contagious disease that could be spread from person to person. The hypothesis was founded upon the identification of SARSr-CoV-WIV1, a live SARS-related coronavirus, which was obtained from bat fecal samples and cultured in Vero E6 cells. The overall genome sequence of this strain was almost identical to that of SARSr-CoV-Rs3367, which was isolated from Chinese horseshoe bats, and SARSr-CoV-RsSHC014. Both SARSr-CoV-RsSHC014 and SARSr-CoV-Rs3367 and SARSr-CoV-RsSHC014 utilized the angiotensin converting enzyme II (ACE2) host cell receptor for cellular entry of human, civet, and Chinese horseshoe bats.^{2,3} The Wuhan Municipal Health Commission issued a report on December 2019, detailing the identification and hospitalization of 27 cases of anomalous pneumonia associated with the wholesale Huanan Seafood Market in Wuhan. As of that moment, the inquiry had not yielded any substantial evidence of human-to-human transmission, and there were no infected medical personnel.^{3,4}

At present, there is global apprehension regarding the pneumonia epidemic that emerged in China in November 2023.⁵ Children in northern China were the target of concentrations of undiagnosed pneumonia, as reported by various news outlets. Additionally, the number of affected individuals has grown. In the midst of this circumstance, over 200 cases of pneumonia among children have been reported in South Korea. These are all caused by *Mycoplasma* as report says⁶; therefore, either this pandemic is distinct from the ones in China, or the cases in China are also attributable to *Mycoplasma*. It is unknown whether these occurrences are distinct from the overall increase in respiratory infections that Chinese authorities have previously documented.

As a result, WHO used the International Health Records (IHR) to investigate these patient cluster reports and collect more epidemiologic, clinical, and diagnostic data. Can it be deemed such, however, given that the WHO has decreed that pneumonia of unknown origin should be classified as the new Disease X?

The entire world is worried about what to do next. Understanding the present load on healthcare systems and

the current trajectory of influenza, SARS-CoV-2, RSV, and *mycoplasma pneumoniae* is crucial. Right now it is the ideal moment to explore the major reasons for disease development. The mortality rate in individual cases needs careful examination. While the source is still unknown for the time being, it is imperative that molecular epidemiology data be investigated immediately to prevent a global outbreak. An effective investigation of the development of the illness can involve the identification and genetic analysis of the causative microbes. Another critical factor is determining how the illness is spread from one person to another, such as by the air, water, or a person’s saliva while they are speaking, or eating any specific food from a certain source. High priority should also be given to tracing the patients’ last known whereabouts and/or activities in an effort to discover the source of the illness. Once the location has been pinpointed, free access to those areas might be denied until the underlying causes have been identified. Last but not least, it is vital to raise people’s awareness and worry about diseases without causing undue fear. Primarily, the same precautions that were taken during the COVID-19 outbreak can be implemented again: people should wear masks, wash their hands often or use hand sanitizer, avoid crowded areas, and make sure that healthcare facilities are ready for any unexpected outbreaks, especially in low- and middle-income countries that lack the financial resources to deal with emergencies adequately.

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Author Contributions

SMRD conceptualized, wrote the article, and supervised the project. MSI revised the draft. All the authors agreed to submit the manuscript in its current form.

Data Availability

Data sharing is not applicable to this article as no datasets were generated or analyzed during the current study.

Ethic Statement

Not applicable.



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