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A CENTURY OF INFLUENZA IN TAIWAN: EPIDEMIOLOGICAL PATTERNS AND THE EVOLUTION OF GENOMIC SURVEILLANCE

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Abstract

Influenza remains a major global public health concern, and Taiwan has experienced repeated pandemic waves, seasonal epidemics, and zoonotic threats over the past century. This review aims to summarize the historical development of influenza in Taiwan and its implications for surveillance and preparedness. A systematic literature review was conducted using scientific publications, government reports, historical archives, and genomic surveillance data accessed through indexed academic platforms. All sources were synthesized to describe pandemic history, seasonal patterns, avian influenza risks, and advancements in laboratory-based monitoring. The findings show that Taiwan was significantly affected by major pandemics, including the 1918 H1N1, 1957 H2N2, 1968 H3N2, and 2009 H1N1 outbreaks, each contributing to improvements in health system readiness. Seasonal influenza in Taiwan displays a dual-peak pattern driven by local transmission and international virus introductions, with shifting dominance among H1N1, H3N2, and influenza B. Zoonotic threats from H5N1 and H7N9 continue to demand strict poultry surveillance and One Health coordination. Since 2000, Taiwan's nationwide laboratory network has strengthened rapid detection, genome sequencing, mutation analysis, and global migration modeling, supporting more effective responses to emerging strains. In conclusion, Taiwan's robust surveillance capacity and genomic monitoring have enhanced preparedness for influenza threats. Nevertheless, rapid viral evolution, global mobility, and persistent zoonotic risks highlight the need for continuous genomic surveillance, improved international collaboration, and optimized vaccine strategies.

Keywords: Evolution surveillance; Genome; Influenza pandemic

INTRODUCTION

Influenza is one of the most easily transmissible respiratory infectious diseases and continues to pose a significant public health threat worldwide (1). The influenza virus can infect individuals across all age groups, causing symptoms ranging from mild to severe, and in some cases leading to serious complications or even death (2). Since the 20th century, the world has experienced several major influenza pandemics caused by genetic changes in the virus, including the 1918 H1N1 pandemic known as the "Spanish Flu," the 1957 H2N2 pandemic, the 1968 H3N2 pandemic, and the 2009 H1N1 pandemic that emerged in a new form. Each of these pandemics has left substantial impacts on public health, society, and the global economy (3).

Taiwan, as an island nation in East Asia, has extensive experience in confronting these global pandemics (4). Although geographically separated from mainland Asia, the spread of influenza viruses has continued to occur, resulting in large numbers of cases and deaths (5). During the 1918 pandemic, for example,

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Taiwan recorded more than 25,000 deaths, largely attributed to poor health standards and limited medical facilities at the time (6). In the following decades, subsequent pandemic waves—such as the 1957 H2N2 and the 1968 H3N2 pandemics—also affected Taiwan, each contributing to increased disease burden and mortality (7).

In addition to seasonal influenza viruses, Taiwan faces threats from avian influenza viruses such as H5N1 and H7N9 originating from poultry (8). Although most reported cases have been imported, the risk of zoonotic transmission remains a persistent concern due to Taiwan's high level of poultry trade activity. For this reason, strict monitoring of viruses with pandemic potential has become a national priority (8).

To strengthen preparedness against influenza threats, Taiwan has developed a nationwide laboratory surveillance system since the year 2000 (9). This system enables healthcare professionals and researchers to monitor virus transmission patterns, identify genetic mutations, isolate viral strains, and predict global influenza movement (10). Taiwan's experience during the 2003 SARS outbreak further enhanced its readiness to respond to the 2009 influenza pandemic. The well-coordinated laboratory network provided major advantages in rapid detection, case reporting, and the development of control strategies (11).

This article presents a comprehensive review of the history of influenza in Taiwan over the past century, covering various pandemics, avian influenza threats, seasonal epidemic dynamics, and technological advancements supporting virus surveillance. Understanding Taiwan's influenza epidemiology offers important insights into the role of genomic surveillance and public health preparedness in addressing future influenza threats.

RESEARCH METHODS

This study employed a literature review approach by collecting, reading, and analyzing various scientific sources that discuss influenza in Taiwan. The sources included international scholarly articles reviewing the history of influenza pandemics and their transmission dynamics; official reports from the Taiwan Centers for Disease Control (CDC) on seasonal influenza cases, avian influenza outbreaks, and laboratory surveillance data; research findings related to viral genetic analysis and evolution; phylodynamic

records of influenza; historical documents such as 1918 pandemic reports from Japanese archives; and genomic data of influenza viruses compiled by Taiwan's laboratory network since 2000. All of this information was then organized, compared, and synthesized to illustrate the development of influenza in Taiwan, covering the history of disease circulation, the types of viruses present, epidemic seasonality patterns, zoonotic threats such as H5N1 and H7N9, and advancements in surveillance and genomic monitoring technologies. Through this method, the study did not collect primary data but instead utilized synthesized data and findings from previous studies to produce a comprehensive overview of the influenza situation in Taiwan.

The literature search in this study was carried out comprehensively using academic databases, primarily Google Scholar, which provides access to a wide range of scientific publications. Although the search was focused on Google Scholar, the platform indexes numerous reputable international journals, including those listed in Scopus, PubMed, and Web of Science. so that the quality and diversity of sources remain preserved. The search was conducted using Boolean strings designed to enhance the relevance of articles related to influenza in Taiwan, the history of global pandemics, seasonal epidemic dynamics, threats from avian viruses such as H5N1 and H7N9, as well as developments in laboratory surveillance technology and genomic analysis. This approach ensures that the articles obtained are strongly related to the research focus and can provide a comprehensive overview of the topic being studied.

RESULTS AND DISCUSSION

Results

The systematic literature review indicates that the development of influenza in Taiwan is an epidemiological phenomenon shaped by the interaction between global pandemic history, seasonal viral dynamics, zoonotic threats, and advancements in surveillance and genomic analysis technologies implemented over the past two decades. Numerous scientific publications describe how Taiwan experienced a significant impact from the 1918 H1N1 pandemic, which caused tens of thousands of deaths due to limited healthcare facilities, insufficient understanding of viral transmission mechanisms, and slow medical response at

the time. Subsequently, the 1957 H2N2 and 1968 H3N2 pandemics displayed similar patterns of rapid spread, resulting in increased morbidity and mortality and compelling Taiwan's health system to strengthen essential healthcare capacity. The re-emergence of the H1N1 virus in 1977 is widely discussed in the literature, as genetic analyses revealed that the virus was nearly identical to strains circulating in the 1950s, leading to speculation about a laboratory escape or accidental release related to vaccine research (12). The peak of the 2009 H1N1 pandemic placed considerable pressure on Taiwan's healthcare facilities; however, the response was deemed rapid and well-coordinated because the country had built a stronger surveillance infrastructure following the 2003 SARS outbreak, including digital reporting systems, enhanced laboratory capacity, and school-based quarantine measures (13).

Beyond global pandemics, avian influenza threats are a major topic discussed across almost all analyzed articles. The H5N1 and H7N9 viruses, although mostly imported, have caused severe disease in humans in Taiwan, with higher clinical severity than seasonal influenza (14). The Taiwanese government subsequently tightened poultry monitoring policies, banned the slaughter of live poultry in traditional markets, expanded biosurveillance capacity, and strengthened networks linking veterinary and human health laboratories. Nonetheless, the literature emphasizes that zoonotic risks remain high given Taiwan's rapidly expanding poultry industry and ongoing poultry trade with other Asian regions (15).

For seasonal influenza, Taiwan demonstrates a unique pattern compared to other subtropical countries, with two epidemic peaks: genomic and epidemiological studies show that the winter peak is driven by local virus circulation and declining population immunity, whereas the summer peak often results from the introduction of new viruses from abroad through international mobility. Dominance among influenza viruses shifts annually among H3N2, H1N1, and influenza B, influenced by antigenic changes, global travel patterns, and population immunity levels (16). One of the most significant outbreaks occurred in 2015–2016, when H1N1 caused more than 160 deaths, mostly among patients with chronic comorbidities (17).

The literature also highlights that Taiwan possesses one of the most comprehensive laboratory influenza surveillance systems in Asia. Since 2000, the national influenza laboratory network has conducted viral detection through RT-PCR, virus isolation, mutation mapping, genome sequencing, and phylodynamic analyses to trace viral migration routes (18). Research shows that Taiwan frequently receives influenza viruses from other countries—particularly South Korea, Japan, China, and the United States—explaining the emergence of summer epidemics and rapid strain turnover. Genomic analysis plays a crucial role in selecting vaccine strains, yet challenges persist because H3N2 mutates more rapidly, resulting in reduced vaccine effectiveness in certain years (19).

Overall, this systematic review indicates that Taiwan's success in managing influenza is strongly supported by long-term investments in robust surveillance systems, public health preparedness, and real-time genomic data analysis capabilities. However, the rapid evolution of the virus, global mobility, emerging zoonotic risks, and dependence on international collaboration remain substantial challenges. Therefore, the literature consistently underscores the need for strengthened cross-country collaboration, integrated animal–human surveillance, and enhanced genomic analysis to ensure Taiwan remains prepared for the potential emergence of future influenza pandemics.

CONCLUSION AND RECOMMENDATION

This review concluded that influenza in Taiwan is influenced by historical pandemic events, unique seasonal patterns, ongoing zoonotic risks, and robust laboratory-based surveillance supported by genomic monitoring. Although Taiwan has demonstrated excellent preparedness, continued viral evolution and global mobility still pose significant challenges. Therefore, it is recommended that Taiwan strengthen genomic surveillance, enhance One Health collaboration, enhance international data sharing, optimize vaccine strategies, and strengthen public health preparedness to ensure more effective prevention and rapid response to future influenza outbreaks.

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