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El virus de la gripe H1N1 y su impacto en comunidades vulnerables

El virus de la grip H1N1 i el seu impacte en comunitats vulnerables

The H1N1 flu virus and its impact on vulnerable communities

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Resumen:

Este artículo trata sobre la virología de H1N1, sus orígenes y transmisión. También aborda el impacto del virus en las comunidades vulnerables, especialmente en los países del tercer mundo. El artículo propone formas para mejorar la situación en estos países y subraya la necesidad de un enfoque global y coordinado de la preparación y respuesta ante las pandemias, centrado en la protección de las comunidades vulnerables.

Palabras clave: H1N1, pandemia, Asia del Sur, vacunación, investigación.

Resum:

Aquest article tracta sobre la virologia de H1N1, els seus orígens i transmissió. També aborda l'impacte del H1N1 en les comunitats vulnerables, especialment als països del tercer món. L'article proposa mesures per millorar la situació en aquests països i subratlla la necessitat d'un enfocament global i coordinat de la preparació i resposta davant les pandèmies centrat en la protecció de les comunitats vulnerables.

Paraules clau: H1N1, pandèmia, Àsia del Sud, vacunació, recerca.

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Summary:

This article discusses the virology of H1N1, its origins, and transmission. It also addresses the impact of H1N1 on vulnerable communities, particularly in third world countries. The article proposes ways to improve the situation in these countries and underlines the need for a comprehensive and coordinated approach to pandemic preparedness and response, with a focus on protecting vulnerable communities.

Keywords: H1N1, pandemic, South Asia, vaccination, research.

The H1N1 flu virus

H1N1 flu is a respiratory disease that can affect humans and animals. It first emerged in 1918 and again in 2009, quickly spreading around the world and causing two pandemics that affected millions of people. Although H1N1 is usually a mild illness, it can cause serious complications and even death, especially among vulnerable populations such as the elderly, children, and people with underlying health conditions.

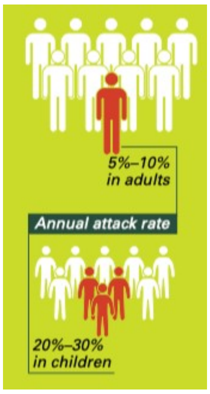

Fig1. Frequently Asked Questions on Zoonotic Influenza. India: World Health Organization; 2017. License: CC BY-NC-SA 3.0 IGO.

Zoonosis: Taking the first steps

Historical data shows that all cases of pandemic influenza originated in animals. All subtypes of influenza A virus have zoonotic potential. The reassortment of the virus in pigs creates optimal conditions for influenza pandemics such as the influenza A(H1N1) pandemic that occurred in 2009-2010. A zoonotic influenza virus must cross three sets of barriers before it can become a human pandemic virus: animal-to-human transmission barriers; virus-cell interaction barriers; and barriers to person-to-person transmission. This highlights the importance of effective surveillance and control measures to prevent the spread of zoonotic viruses.

Pigs: “a mixing bowl”

One of the unique characteristics of the H1N1 virus is that it contains genetic material from avian and swine influenza viruses, as well as human influenza viruses. This means that it has the potential to infect a wide range of species, including humans, pigs, birds, and other animals. The virus can also undergo frequent mutations, which can lead to the appearance of new, more virulent strains or resistant to current treatments.

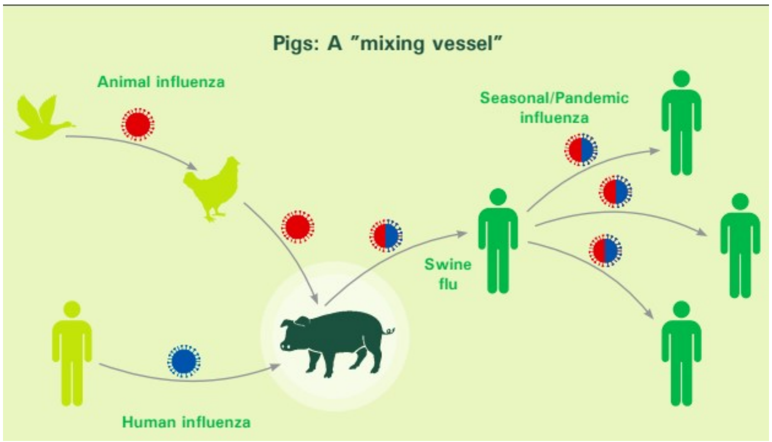

Fig2. Frequently Asked Questions on Zoonotic Influenza. India: World Health Organization; 2017. License: CC BY-NC-SA 3.0 IGO.

Taking a closer look

The H1N1 virus is part of the Orthomyxoviridae family, which also includes influenza A, B, and C viruses. Like other influenza viruses, H1N1 is an enveloped virus with a segmented RNA genome. The genome encodes several proteins, including hemagglutinin (HA) and neuraminidase (NA), which are found on the surface of the virus and are important for infecting host cells.

Is H1N1 still a thing?

As of the Influenza Update Nº 439 published by the World Health Organization (with the participation of 124 countries), of the positive for influenza viruses that were tested by the WHO's Global Influenza Surveillance and Response System laboratories, an outstanding 68.7% were typed as influenza A and of the sub-typed influenza A viruses, the majority (57.9%) were influenza A(H1N1)pdm09.

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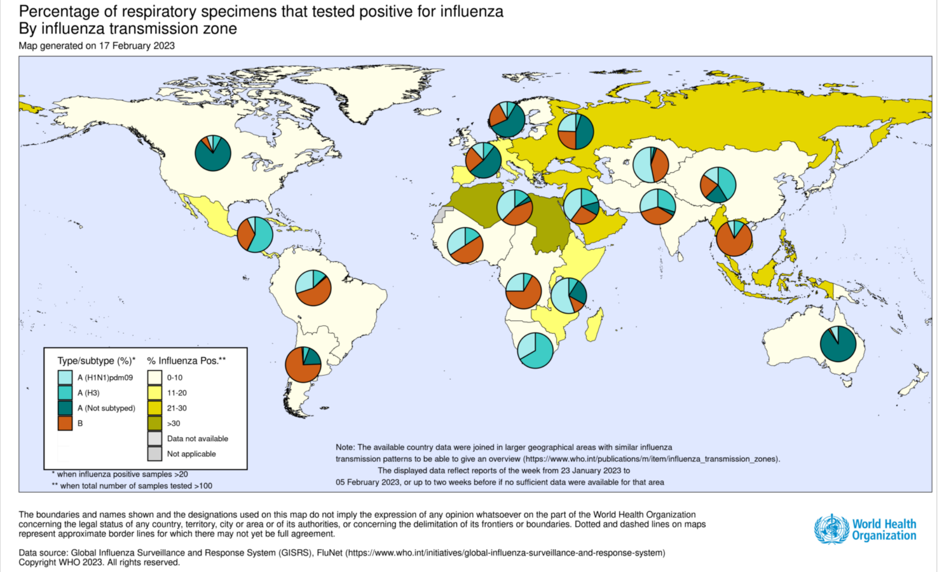
Percentage of respiratory specimens that tested positive for influenza
By influenza transmission zone
Map generated on 17 February 2023

* when influenza positive samples >20
** when total number of samples tested >100

Note: The available country data were joined in larger geographical areas with similar influenza transmission patterns to be able to give an overview (https://www.who.int/publications/m/item/influenza_transmission_zones). The displayed data reflect reports of the week from 23 January 2023 to 05 February 2023, or up to two weeks before if no sufficient data were available for that area

The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data source: Global Influenza Surveillance and Response System (GISRS), FluNet (https://www.who.int/initiatives/global-influenza-surveillance-and-response-system)
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Fig3. Influenza Update Nº 439. World Health Organization; 2023.

Epidemics Following the 2009 Pandemic: A pattern emerges.

It is known that 8 significant outbreaks of A(H1N1)pdm09 have been registered since 2009, 6 of which have occurred in South Asia (Pakistan, Iran, Maldives, Myanmar and two in India), which is interesting when contrasting this information with the number of cases reported by these member states to the WHO, since they seem to be even less than those reported in southwestern Europe (a region with a much higher GDP per capita and a much lower total population) during the same period.

This most likely has its explanation in a lack of resources to carry out the corresponding diagnoses, but one thing is clear and that is that influenza A(H1N1) is more persistent in Southern Asia (with cases appearing to be more distributed throughout the year) than it is in Southern Europe.

How to help?

Despite now being considered “just” a seasonal virus, H1N1 has been particularly persistent on vulnerable populations in developing countries such as those in South Asia. Limited access to healthcare, poor sanitation, and inadequate nutrition all contribute to the spread of the virus and its associated complications. Additionally, many people in these countries lack access to vaccines and other preventive measures, putting them at greater risk of infection.

To address this problem, it is essential to take a multifaceted approach that addresses both the biological and social determinants of H1N1 transmission. This includes increasing access to healthcare and vaccinations, improving sanitation and hygiene practices, and addressing underlying health disparities that contribute to vulnerability to infection.

Another key approach to addressing H1N1 is through continued research into the virus and its evolution. This includes studying the genetic and molecular mechanisms of the virus, as well as developing new treatments and vaccines that are effective against a variety of strains. As with other infectious diseases, a comprehensive approach is necessary to address the ongoing threat of H1N1 and ensure that vulnerable populations have access to the resources they need to prevent and treat this disease.

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