


Review Article for Seasonal Influenza A (H3N2) Virus

Maryam Kareem Ali¹, Jaafar Sataar Shia^{2*}¹Department of Microbiology, College of Medicine, University of Baghdad, Iraq²College of Pharmacy, Al-Farabi University, Baghdad, IraqDOI: <https://doi.org/10.36348/sjmps.2026.v12i04.009>

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*Corresponding author: Jaafar Sataar Shia

College of Pharmacy, Al-Farabi University, Baghdad, Iraq

Abstract

People can contract influenza, an infectious respiratory illness. Fever, sore throat, runny nose, cough, headache, aches in the muscles, and fatigue are among the symptoms. In severe cases, pneumonia frequently results in death. There are worldwide influenza pandemic outbreaks, despite the fact that these illnesses are marked by sporadic seasonal epidemics and irregular and unpredictable occurrences, a zoonotic viral strain. Severe influenza seasons are linked to the H3N2 subtype. Three of the previous five extremely severe influenza seasons were dominated by H3N2 viruses. Influenza viruses are evolving so quickly, even with known techniques, the best ways to avoid and cure influenza is viewed as a tremendous task. Only thorough research on the currently dominating H3N2 influenza viruses will lead to improvements in vaccination efficacy and pandemic risk assessment. The different characteristics of the H3N2 viruses and their ability to cause seasonal outbreaks and pandemics are covered in great length in this article.

Keywords: Influenza Virus, H3N2, seasonal.

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INTRODUCTION

Influenza virus can infect people anywhere in the globe. Both the Northern and Southern hemispheres frequently experience wintertime seasonal influenza outbreaks, which are estimated to cause 500,000 fatalities per year. [1] An infectious disease that has increased in frequency over the past 20 years and predicted to do so in the near future is referred to as an emerging infectious disease (EID). [2] There are three components to the influenza virus: the core protein, the matrix, and the envelope. The envelope contains glycoproteins called hemagglutinin (HA) and neuraminidase (NA), which are essential for the invasion and release of viruses. As a result, hemagglutinin (HA) and neuraminidase (NA) are now pivotal targets for the development of therapeutic drugs and influenza vaccines. [3] Influenza A or B viruses are the main cause of this infectious virus. Additionally, it may impact the nervous system, skeletal muscles, and cardiovascular, it mostly impacts the bronchi, nose, throat, and, in rare circumstances, the lungs. [2] Influenza epidemics have sickened a large number of people. Human interaction with a bird reassortant virus of the H3N2 subtype occurred in 1968, over a million people died as a result of the worldwide pandemic. [4]

A new strain of H1N1 sparked an influenza pandemic in 2009 that infected millions of people in more than 214 nations. [5] H1N1, H2N2, and H3N2 viruses, between 1982 and 1990, human and swine sera were far more common in India [6]. The 1st report of influenza disease in pigs created in 2009. When pig samples from a farm in Uttar Pradesh were discovered to have the A(H1N1) pdm09 virus. Remarkably, the acquired sequences of the virus were similar to those found in Korea & North America. This may have resulted from trade or long-distance transmission [7]. The Indian Council of Medical Research (ICMR) concluded on March 4, 2023, that Influenza Subtype H3N2 was the source of the illness.

The first nine weeks of 2023 saw an upsurge in H3N2 infections, according to ICMR data. This virus has been the most common since December 15 (92% hospitalized SARI, 86% cough, 27% dyspnea, and 16% wheeze. symptoms, 6% seizures, and 16% pneumonia [8]. Since 1968, The WHO recommends 28 vaccine strain alterations because H3N2 influenza viruses show significant genetic and antigenic development, leading to many seasonal outbreaks. Over the past 50 years, these viruses' receptor binding characteristics have also evolved; their sensitivity for oligosaccharide has diminished. [9] According to recent studies, most contemporary viruses have developed capacity to

agglutinate red blood cells through interactions between SA and neuraminidase. [10] As a result, numerous researchers have developed novel techniques and altered current assays to characterize contemporary H3N2 influenza viruses. A number of Human influenza infections can today be diagnosed using a variety of techniques, such as virus separation in tissue culture, immunofluorescence assays, genetic element amplified tests, immune-chromatography based rapid diagnostic techniques. The shortcomings of several conventional detection techniques are being addressed by the development of newer diagnostic techniques. [11].

Types of Influenza Viruses:

Currently, A, B, and C are the three kinds of influenza viruses. The 8 segmented, negative-sense RNA genomes of influenza and other enveloped viruses belong to the Orthomyxoviridae family. [12] IV (B and C) viruses only infect humans, influenza A viruses (I AV) effect horses, pigs, birds, & other animals. [1-3] IAV is categorized using surface HA and neuraminidase NA [1 4–15]. There are currently 11 known NA subtypes (N1–11) and 18 identified HA subtypes (H1–18) that are circulating in humans, including H1N1, H3N2, H3N3, and H5N1. [13]

H3N2

H3N2 was the cause of 1 of the 3 main influenza pandemics in the past century. A/Hong Kong/1/1968 [HK/68], a unique strain of the H3N2 virus, first appeared in Hong Kong in 1968. This led to a worldwide outbreak that killed over a million people. [17] There was no evidence of H3N2 viruses circulating in humans prior to this outbreak A novel H3N2 viral strain that may infect and spread among humans was most likely created by recombining circulating human H2N2 viruses with avian H3N2 viruses. [18] The avian H3N2 HA and PB1 fragments were combined with the NA from the 1957 H2N2 pandemic strain to generate a novel H3N2 viral strain, according to further investigation of this virus. [16]

Humans were still infected with H2N2 and H2N3 viruses until 1971, when H2N2 viruses started to diminish.[18] 1-2 mutations in the (RBS) cause the (H R) proteins on the surface of pandemic influenza viruses to differ from those of their bird equivalents. This causes the viral receptor specificity to change from Ideally binding to α 2,3 linked SAs Ideally binding to α 2,6 SAs. The virus's shift from birds to people and the start of the pandemic were linked to 5 AA Modifications in the HA of Hong Kong 1968 H3N2 isolates. It was originally observed in the United States in September 1968. It was estimated that one million people worldwide and about 100,000 Americans had perished. Ages 65 and above accounted for the majority of additional deaths. Seasonal influenza is caused by the H3N2 virus. a virus that continues to spread globally. [19,20]

Important studies carried out in the 1980s revealed that 131 A.A. locations at five antigenic sites (A–E) in the globular head of H3 near the RBS were the main targets for specific antibodies. This implies that antigenic shift is most likely caused by alterations in these locations. [21, 22]. Clade 3c.2a H3N2 IAVs initially surfaced during the 2014–2015 influenza season. [24] This virus differed by 10–12 amino acids from the previous vaccine strain, A/Texas/50/2012 (Tx/12) (Clade 3c.1). The modifications F159Y and K160T at antigenic site B, along with an existing N at site 158, suggested the potential acquisition of a glycosylation site, which is anticipated to hide viral epitopes and restrict antibody access to the antigenic site. [25]

These modifications to antigenic site B greatly reduce the binding of human, sheep, and ferret Ab produced by the Tx/12 vaccine strain. Another A (H3N2) clade, 3c.3a, co- flowed in humans during the same influenza season. In 2015–2016, the WHO recommended adding an (Sz/13) (clade 3c.3a) virus to the northern hemisphere influenza vaccination since both clade 3c.2a and 3It was found that c.3a viruses differed antigenically from Tx/12.However, c.3a viruses differ due to clade 3c.2a and 3's antigenic site B Glycosylation at position 159 on 3c.2a viruses, and by early 2015, c.3a viruses had begun to vanish from human circulation. [24] It's possible that the extra glycosylation site gave 3c.2a viruses a favourable evolutionary advantage over 3c.3a viruses, making them more effective in spreading from person to person. Because of this, the WHO once again suggested changing the vaccine strain for the northern hemisphere for the 2016–2017 season, adding A/Hong Kong/4801/2014 (HK/14), a clade 3c.2a representative. Currently, there are two sub-clades of clade 3c.2a viruses: 3c.2a1 and 3c.3a2, both of which differ from clade 3 due to the N121K mutation.c.2a.

The characteristic amino acid change N171K at antigenic site D is seen in viruses from 3c.2a1. Antigenic site A alterations further differentiate these viruses. N-linked glycosylation sites are lost as a result of D122N and Standard T135K.Clade 3c.2aTwo viruses are part of a newly created group that has not yet been officially recognised as a clade by the WHO. Viruses from this lineage are identified by the S144K mutation, which is found in an antigenic area that borders the RBS. Two groups of c.2a2 viruses are further distinguished. I58V and S219Y are found in Cluster I, but N122D and S262N are noticed in Cluster II. N122D results in a reduction of a potential N-linked glycosylation site. During the 2016–2017 flu season, influenza monitoring & vaccination research on effectiveness conducted in Greece, London, Canada, & Japan were connected to the newly discovered clade 3.c.2a viruses to the recent A (H3N2) outbreaks. [26]

Detection techniques of virus

Traditional techniques, elisa techniques, quick and sophisticated methods, and biosensing methods are the four categories of influenza virus detection techniques. Conventional procedures include viral culture (Fig. 2). Serological procedures include complement fixation, hemagglutination, immunodiffusion testing, virus neutralization, immunofluorescence assays, and quick antigen testing. It has been discovered that nasopharyngeal swabs offer more rapid influenza detection than nasal and throat swabs (CDC 2018). In addition to serological methods, quick and effective methods based on elemental molecular biology are investigated. The fast influenza approach, RT-PCR, multiplex PCR, Amplification based on nucleic acid sequence (NASBA), RNA-specific detection methods that are not PCR-based, and traditional PCR are all included. Large magneto-resistance biosensors, optical biosensors, We provide a thorough analysis of every technique for identifying H3N2, with an emphasis on biosensing techniques. We have covered a variety of H1N1 detection techniques. [27-28]

H3N2 treatment

Whether it's H3N2 or another strain, a straightforward case of seasonal flu is treated with symptom control while the patient heals. Getting adequate sleep is one of the options. Drinking enough water treating symptoms like fever, headaches, and aches and pains with over-the-counter painkillers in certain situations, doctors may recommend an antiviral drug such oseltamivir (Tamiflu). Further clinical study is necessary, however there is evidence that several antiviral medications, especially neuraminidase inhibitors (oseltamivir and zanamivir), can reduce the length of viral replication and increase survival rates. There have been reports of oseltamivir resistance. When used within 48 hours of the onset of flu symptoms, antiviral medicine can help reduce the length of the disease and avoid complications. [29]. Serious flu complications are more likely to occur in some people than in others. Pneumonia or a worsening of an already-existing illness, such asthma, are examples of these consequences. If you fit any of the following descriptions and think you might have the flu, see a doctor: Adults 65 years of age, Youngsters younger than five; pregnant women; and anyone with chronic illnesses (diabetes, heart disease, or asthma). individuals whose IM-S found compromised drugs (steroids, chemotherapy) or infections (HIV, leukaemia). [30]

Protection and Management:

Take the following safety measures to prevent contracting seasonal flu viruses:

- Vaccinate yourself against the flu each year. If at all possible, try to get it by the last day of October .
- You should wash your hands often, especially after using the restroom, before you eat, and

before you contact your mouth, nose, or face. • Steer clear of busy areas where the flu can spread quickly. Examples include business buildings, schools, and public transit.

- Steer clear of sick people. [31-32].

Influenza vaccines

true catalyst for the development of the vaccine was Edward Jenner's outstanding work against smallpox in 1796. Regardless of the concerted efforts of the World Health Organization, the smallpox virus was eradicated from the world on May 8, 1980, after almost two centuries of development of an effective vaccination and international campaigns to give the vaccine. [33].

CONCLUSION

Wellbeing of human society is now seriously threatened by seasonal and pandemic breakouts in the contemporary circumstances. In more detail, viruses are said to have several times faster rates of mutation, and Their rate of development is comparable to that of humans. In order to develop better and more effective vaccinations and to curate treatment regimens, it is imperative that the structural and functional aspects of these viral agents be studied. There are currently a number of viral vaccines against influenza on the market, but only research focused on this group of viruses can further improve the preventive efficacy of vaccines. My research's objectives to offer a number of ideas into the influenza virus's capabilities, highlighting the necessity of creating a successful protection against pathogenic viruses.

REFERENCES

1. Kuszewski K, Brydak L. The epidemiology and history of influenza. *Biomedicine & pharmacotherapy*. 2000 May 1;54(4):188-95.
2. Shrestha S, Foxman B, Berus J, van Panhuis W, Steiner C, Viboud C, et al. The role of influenza in the epidemiology of pneumonia. *Sci Rep*. 2015; 5:15314. doi: 10.1038/srep15314.
3. Huang Z-Z, Yu L, Huang P, Liang LJ, Guo Q. Charged amino acid variability related to N-glycosylation and epitopes in A/H3N2 influenza: Hemagglutinin and neuraminidase. *PloS one*. 2017;12(7):e0178231. doi: 10.1371/journal.pone.0178231.
4. Novel Swine-Origin Influenza AVIT. Dawood FS, Jain S, Finelli L, Shaw MW, Lindstrom S, et al. Emergence of a novel swine-origin influenza A (H1N1) virus in humans. *N Engl J Med*. 2009; 360:2605– 15. doi: 10.1056/NEJMoa0903810.
5. Influenza WP. Report of the WHO pandemic influenza A (H1N1) vaccine deployment initiative. 2012.
6. Chatterjee, S.; Mukherjee, K.K.; Mondal, M.C.; Chakravarti, S.K.; Chakraborty, M.S. A serological survey of influenza a antibody in human and pig sera in Calcutta. *Folia. Microbiol. (Praha)* 1995, 40,

7. Nagarajan, K.; Saikumar, G.; Arya, R.S.; Gupta, A.; Somvanshi, R.; Pattnaik, B. Influenza A H1N1 virus in Indian pigs & its genetic relatedness with pandemic human influenza A 2009 H1N1. *Indianj. Med. Res.* 2010, 132, 160–167.
8. H3N2 outbreak: Know this strain that caused two pandemics and is now an outbreak in India. Influenza A viruses are the only influenza viruses known to cause flu pandemics. DownToEarth Published: Tuesday 07 March 2023.
9. Lin Y, Wharton SA, Whittaker L, Dai M, Ermetal B, Lo J, Pontoriero A, Baumeister E, Daniels RS, McCauley JW. The characteristics and antigenic properties of recently emerged subclade 3C. 3a and 3C. 2a human influenza A (H3N2) viruses passaged in MDCK cells. *Influenza Other Respir Viruses.* 2017;11(3):263–74. doi: 10.1111/irv.12447.
10. Zhu X, McBride R, Nycholat CM, Yu W, Paulson JC, Wilson IA. Influenza virus neuraminidases with reduced enzymatic activity that avidly bind sialic acid receptors. *J Virology.* 2012;86(24):13371–83. doi: 10.1128/JVI.01426-12. PMID:23015718.
11. Koski RR, Klepser ME. A systematic review of rapid diagnostic tests for influenza: considerations for the community pharmacist. *Journal of the American Pharmacists Association.* 2017 Jan 1; 57 (1):13–9.
12. Mosnier A, Caini S, Daviaud I, Nauleau E, Bui TT, Debost E, et al. Clinical Characteristics Are Similar across Type A and B Influenza Virus Infections. *PLoS One.* 2015;10: e0136186. doi: 10.1371/journal.pone.0136186.
13. Vemula SV, Zhao J, Liu J, Wang X, Biswas S, Hewlett I. Current approaches for diagnosis of influenza virus infections in humans. *Viruses.* 2016;8(4):96. doi: 10.3390/v8040096. PMID:27077877.
14. Huang Z-Z, Yu L, Huang P, Liang LJ, Guo Q. Charged amino acid variability related to N-glycosylation and epitopes in A/H3N2 influenza: Hemagglutinin and neuraminidase. *PloS one.* 2017;12(7):e0178231. doi: 10.1371/journal.pone.0178231. PMID:28708860.
15. Peng W, de Vries RP, Grant OC, Thompson AJ, McBride R, Tsogtbaatar B, Lee PS, Razi N, Wilson IA, Woods RJ, et al., Recent H3N2 viruses have evolved specificity for extended, branched human-type receptors, conferring potential for increased avidity. *Cell Host & Microbe.* 2017;21(1):23–34. doi: 10.1016/j.chom.2016.11.004.
16. Yang J, Liu S, Du L, Jiang S. A new role of neuraminidase (NA) in the influenza virus life cycle: implication for developing NA inhibitors with novel mechanism of action. *Rev Med Virology.* 2016;26(4):242–50. doi: 10.1002/rmv.1879.
17. Alymova IV, York IA, Air GM, Cipollo JF, Gulati S, Baranovich T, Kumar A, Zeng H, Ganseboom S, McCullers JA. Glycosylation changes in the globular head of H3N2 influenza hemagglutinin modulate receptor binding without affecting virus virulence. *Scientific Rep.* 2016; 6:36216.
18. Westgeest KB, Russell CA, Lin X, Spronken MI, Bestebroer TM, Bahl J, van Beek R, Skepner E, Halpin RA, de Jong JC, et al., Genomewide analysis of reassortment and evolution of human influenza A (H3N2) viruses circulating between 1968 and 2011. *J Virology.* 2014;88(5):2844–57.
19. Van Poucke S, Doedt J, Baumann J, Qiu Y, Matrosovich T, Klenk HD, Van Reeth K, Matrosovich M. Role of Substitutions in the Hemagglutinin in the Emergence of the 1968 Pandemic Influenza Virus. *J Virology.* 2015;89(23):12211–6. doi: 10.1128/JVI.01292-15. PMID:26378170.
20. Ushirogawa H, Naito T, Tokunaga H, Tanaka T, Nakano T, Terada K, Ohuchi M, Saito M. Re-emergence of H3N2 strains carrying potential neutralizing mutations at the N-linked glycosylation site at the hemagglutinin head, post the 2009 H1N1 pandemic. *BMC Infectious Dis.* 2016;16(1):380. doi: 10.1186/s12879-016-1738-1.
21. Koel BF, Burke DF, Bestebroer TM, van der Vliet S, Zondag GC, Vervaeet G, Skepner E, Lewis NS, Spronken MI, Russell CA, et al., Substitutions near the receptor binding site determine major antigenic change during influenza virus evolution. *Science.* 2013;342(6161):976–9. doi: 10.1126/science.1244730. PMID:24264991.
22. Yang H, Carney PJ, Chang JC, Guo Z, Villanueva JM, Stevens J. Structure and receptor binding preferences of recombinant human A (H3N2) virus hemagglutinins. *Virology.* 2015; 477:18–31. doi: 10.1016/j.virol.2014.12.024. PMID:25617824.345–348.
23. Yokoyama M, Fujisaki S, Shirakura M, Watanabe S, Odagiri T, Ito K, Sato H. Molecular dynamics simulation of the influenza A (H3N2) hemagglutinin trimer reveals the structural basis for adaptive evolution of the recent epidemic clade 3C. 2a. *Frontiers in Microbiology.* 2017; 8:548. doi: 10.3389/fmicb.2017.00584.
24. Chambers BS, Parkhouse K, Ross TM, Alby K, Hensley SE. Identification of hemagglutinin residues responsible for H3N2 antigenic drift during the 2014–2015 influenza season. *Cell Rep.* 2015;12(1):1–6. doi: 10.1016/j.celrep.2015.06.005.
25. Melidou A, Gioula G, Exindari M, Ioannou E, Gkolfinopoulou K, Georgakopoulou T, Tsiodras S, Papa A. Influenza A (H3N2) genetic variants in vaccinated patients in northern Greece. *J Clinical Virology.* 2017; 94:29–32. doi: 10.1016/j.jcv.2017.07.003.
26. Chauhan N, Narang J, Pundir S, Singh S, Pundir CS. Laboratory diagnosis of swine flu: a review. *Artificial cells, nanomedicine, and biotechnology.* 2013 Jun 1;41(3):189-95.
27. Dalal A, Mohan H, Prasad M, Pundir CS. Detection methods for influenza A H1N1 virus with special

- reference to biosensors: a review. *Bioscience reports*. 2020 Feb;40(2): BSR20193852.
28. Stephenson I, Democratis J, Lackenby A, McNally T, Smith J, Pareek M, et al. Neuraminidase inhibitor resistance after oseltamivir treatment of acute influenza A and B in children. *Clin Infect Dis*. 2009; 48:389–96.
 29. Centers for Disease Control and Prevention, National Center for Immunization and Respiratory Diseases (NCIRD). January 3, 2019.
 30. Glezen WP. Clinical practice. Prevention and treatment of seasonal influenza. *N Engl J Med*. 2008; 359:2579–85.
 31. Chen KF, Gaydos C, Rothman RE. Update on emerging infections: news from the Centers for Disease Control and Prevention Hospitalized patients with novel influenza A (H1N1) virus infection--California, April-May 2009. *Ann Emerg Med*. 2009; 54:732–6.
 32. Trombetta CM, Perini D, Mather S, Temperton N, Montomoli E. Overview of serological techniques for influenza vaccine evaluation: past, present and future. *Vaccines*. 2014;2(4):707–34.