Detection of Influenza Virus and its Subtypes by real time RT-qPCR in a tertiary care centre, Maharashtra.

Dr. Rupali S. Mantri, Dr. Nitin A Ambhore, Mr. Jeetendra Thakur, Dr. Premjith Lal UA, Miss. Sunayana Narwade

Corresponding Author: Dr. Premjith Lal UA, Senior Resident, Department of Microbiology, Government Medical College, Akola, shan3135@gmail.com, +91-7594943135, +91-9541661439

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ABSTRACT

Background: Influenza is a highly communicable viral infection capable of causing widespread epidemics and pandemics. Influenza A and B viruses are the major causative agents of human respiratory infections. Continuous surveillance of influenza virus activity and its circulating subtypes is essential to enable policymakers to make effective and appropriate decisions regarding its control. Therefore, A hospital-based observational study was conducted at the ICMR-Viral Research and Diagnostic Laboratory (VRDL), Government Medical College, Akola to determine the pattern of influenza virus activity in relation to various meteorological and clinical parameters.

Methods: Nasopharyngeal swabs from 317 patients presenting with influenza-like illness, collected between September 2022 and August 2024, were included in the study. All samples were tested for Influenza A, Influenza A (H1N1) pdm09, Influenza A (H3N2), Influenza B, Influenza B/Yamagata, and Influenza B/Victoria.

Results: A total of 317 samples were received for testing. The influenza positivity rate among symptomatic patients was 17.03% (54/317). Of the positive samples, 48 (15.14%) were influenza A and 6 (1.89%) were influenza B. Influenza A–positive samples were further subtyped as pdmH1N1 in 29 (60.41%), seasonal H3N2 in 16 (33.33%), and unsubtypable influenza A in 3 (6.22%). Among the influenza B–positive samples, 4 (66.66%) belonged to the Victoria lineage, while no samples of the Yamagata lineage were detected.

Conclusions: The study describes the distribution of different Influenza viruses and their subtypes in Akola, along with their seasonal trends. This investigation provides hospital-based epidemiological data that contributes to a more precise and accurate understanding of Influenza A (H1N1). Regular surveillance is essential for the early detection of cases, timely clinical management, reduction of mortality, and implementation of measures to prevent the spread of this important infectious disease.

Keywords: Influenza virus, Influenza A, H1N1 pdm09, Subtyping, Tertiary care hospital, Central India, Influenza B, Akola, Real-time RT-PCR.

1. Introduction

Influenza is highly communicable viral infection that can lead to widespread epidemics and pandemics.[1] Influenza virus infections can range from mild respiratory symptoms to life-threatening severe acute respiratory illness (SARI), causing significant public health burden worldwide.[2] It contribute to substantial morbidity and mortality globally.[3]

Influenza viruses are an enveloped single negative stranded RNA virus which belong to the family Orthomyxoviridae and it have been classified into types A, B, C and D based on antigenic differences in their nucleoprotein (NP) and matrix (M) protein.[4,5]Major four pandemics was associated with Influenza A virus and Swine influenza was the most lethal flu killed around 20 million people.[6] Influenza B is highly contagious and cause minor localised outbreaks. Two genetically and antigenically distinct lineages of influenza B virus, namely, B/Victoria/2/87-like (B/Victoria lineage) and B/Yamagata/16/88-like (B/Yamagata lineage), has be identified in the late 1980s.[7]

The influenza virus exhibits antigenic variation through processes known as antigenic drift and antigenic shift, particularly involving the hemagglutinin (HA) and neuraminidase (NA) proteins. These changes allow the virus to evade host immune responses. Antigenic drifts in the HA subtype are linked to seasonal epidemics. The precise mechanism behind these drifts is not fully understood, but shifts are thought to be facilitated by the virus's segmented genome and its ability to infect a diverse range of animal reservoirs. On the other hand, antigenic shifts in HA subtypes are associated with pandemics.[8]

The World Health Organization (WHO) declared a global pandemic alert for swine flu on June 11, 2009, marking the first such alert in over 70 years. The ongoing outbreaks of swine flu H1N1 remain a significant challenge in developing countries like India, where early diagnosis and treatment can be challenging due to socioeconomic limitations.[9]

Limited data exists on the circulating influenza virus subtypes in our region. Additionally, there was a significant rise in undiagnosed SARI cases at our tertiary care hospital during 2022. Therefore, this study was conducted to detect Influenza virus and its subtypes in our region. It will help us to understand about the disease magnitude locally about the strains. This information is critical for regional public health readiness and influenza prevention and management efforts.

2. Material & Methods

This hospital based observational study was conducted in ICMR-Viral Research and Diagnostic Laboratory (VRDL), Government Medical College, Akola from September 2022 to August 2024. This study was approved by the Institutional ethical committee vide letter no. Sr. No. 78/2024. Nasopharyngeal swabs were collected from the patients presenting with the influenza like illness (ILI) included in the study as per the standard definition.[10]

Samples were collected in viral transport medium (VTM) and transported to the VRDL while maintaining the cold chain.

The sample size was calculated using the Kish and Leslie formulation (Kish 1965).

$n = Z^2 P (1 – P)/d^2$

Where, n = sample size, Z = critical value that corresponds to 95% confidence interval,

P= prevalence rate of influenza virus which is estimated as 29.3% (0.29)[11]

d= degree of accuracy that is desired usually set at 0.05.

q= 1-p, q= 1-0.29 =0.71

$n= (1.96)^2 \times 0.29 \times 0.71/ (0.05)^2 =317$

using the above formula a sample size of 317 Influenza like illness was calculated.

a. Viral Nucleic Acid Extraction

Viral nucleic acid extraction from the sample was done by using "MagRNA-II Viral RNA Extraction Kit" manufactured by GENES2ME PRIVATE LIMITED as per manufacturer's instructions.

b. Multiplex Real Time-RT-qPCR for Detection of Influenza and SARS CoV-2

Real Time-RT-qPCR for Detection of Influenza A and B was done using ICMR-NIV Multiplex combo kit for detection of Influenza and SARS CoV-2 as per manufacturer's instruction. All the tests were multiplexed and 7 µL of template RNA added to each reaction. The results were generated as cycle threshold (Ct) values and interpreted according to the ICMR guidelines provided with the kit. Samples were considered positive if the Ct value was ≤36, and negative if there was no Ct value or the Ct was ≥36.[12]

c. Multiplex Real-Time RT-PCR for Influenza Subtype Detection

Influenza Positive samples were further subtyped using multiplex real-time RT-PCR to identify Influenza A (H1N1) pdm09 and Influenza A (H3N2). Similarly, Influenza B Positive samples were subtyped into B/Yamagata and B/Victoria lineages using reagents provided by ICMR-NIV, Pune. Samples with RNase *P* Ct values at or below 35 cycles confirmed the presence of sufficient human RNA, indicating good specimen quality. RNase *P* positivity served as an internal control to assess sample integrity. A sample was interpreted as positive for Influenza A (H1N1) pdm09 and Influenza A (H3N2) when the Ct value is ≤35. If a sample tested positive for Influenza A, but neither H1N1pdm09 nor H3N2 subtype targets were detected within 35 cycles, it was classified as Influenza A unsubtypable. A sample was considered positive for Influenza B Yamagata or Victoria if both the Influenza B and the respective Yamagata or Victoria subtype amplification curves crossed the threshold within 35 cycles.

The RT-PCR thermal cycling protocol for both reactions consisted of three stages: reverse transcription at 50°C for 5 minutes (1 cycle), followed by polymerase activation at 95°C for 20 seconds (1 cycle), and then 40 amplification cycles involving denaturation at 95°C for 5 seconds and annealing/extension at 55°C for 30 seconds, during which data acquisition was performed.

d. Statistical analysis

Descriptive analysis was used wherever necessary. The positive rate of influenza was compared with regard to age, gender by using chi-square test and p-value. All categorical variables were summarized as percentages. For statistical analysis of data, SPSS (Statistical Package for Social Sciences version 20.1, Armonk, New York) software was used.

3. Results

In our study period, a total of 317 samples of ILI belonging to the category C as per definition were received for testing. Out of the total samples tested, 54 (17.03%) were positive for Influenza A and B subtypes, of which 48 (15.14%) cases of Influenza A and 6 (1.89%) cases of Influenza B, while 263 (82.96%) samples tested negative for both influenza subtypes. 4 samples out of 317 were found to be positive for Covid-19.

The Influenza A positive samples were further characterized as Influenza A (H1N1) pdm09 in 29 cases (60.41%), Influenza A (H3N2) in 16 cases (33.33%), and Influenza A unsubtypable in 3 cases (6.22%). The Influenza B positive samples were subtyped as Influenza B (Victoria) in 4 cases (66.66%), while no cases were identified as Influenza B (Yamagata) **[See Fig.01].**

Demographic characteristic of these 55 patients showed that 50% (n=27) were females and 50% (n=27) were male patients. Influenza A (H1N1/pdm09) was the most common subtype, consisting of 16 males (55.17%) and 13 females (44.82%). Influenza A (H3N2) was detected in 16 cases, with 7 males (43.75%) and 9 females (56.25%). Influenza A unsubtypable was reported in 3 cases, with 1 male (33.33%) and 2 females (66.66%). Influenza B (Victoria) was identified in 4 cases, equally distributed among males and females (50% each). Influenza B (unsubtypable) was detected in 2 cases, also equally distributed between males and females **[See Table 01].**

Out of the 54 confirmed positive cases, majority 38 (70.37%) were reported from urban areas and 16 (29.62%) were from rural areas. Two deaths were reported with case fatality rate is 3.70%.

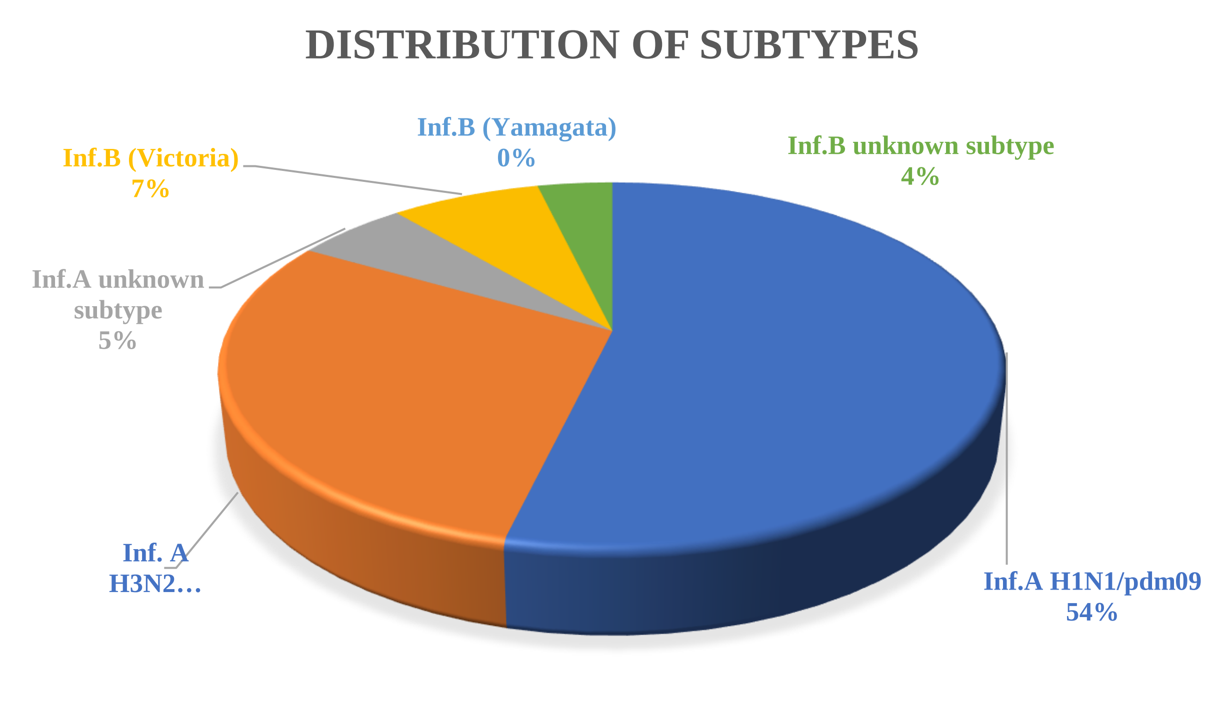

Fig.01. Distribution of Subtypes of Influenza Virus

Gender wise distribution of Influenza Subtypes.			
Influenza type/subtype	**Total positive cases n=54 (%)**	**Male n=27 (%)**	**Female n=27 (%)**
Inf. A (H1N1/pdm09)	**29 (53.70%)**	**16 (55.17%)**	**13 (44.82%)**
Inf. A (H3N2)	**16 (29.62%)**	**7 (43.75%)**	**9 (56.25%)**
Inf. A (unsubtypable)	**3 (5.55%)**	**1 (33.33%)**	**2 (66.66%)**
Inf. B (Victoria)	**4 (7.40%)**	**2 (50%)**	**2 (50%)**
Inf. B(Yamagata)	**0**	**0**	**0**
Inf. B (unsubtypable)	**2 (3.70%)**	**1 (50%)**	**1 (50%)**

Table.01. Gender wise Distribution of Influenza Subtypes

The majority of cases were reported in the 20–29 years age group (20.5%), followed by individuals aged 30–39 years (17.98%) and 40–49 years (14.19%). The lowest proportion of cases was observed in the <20 years age group (5.67%). The mean age of the study population was 38.6 years, with a standard deviation of 13.8 years. The highest number of positive cases was identified in the ≥60 years age group (40.74%), followed by the 50–59 years (16.66%) and 30–39 years (14.81%) age groups. The <20 years age group had the lowest proportion of positive cases (5.55%). The largest deviations are in the 60+ and 20–29 age groups. The p-value from the previous Chi-square test (~0.054) makes this marginally significant **[See Table 02].**

Statistical analysis of Influenza Cases-Age wise.			
Age(years)	**No. of cases n=317 (%)**	**No. of positives n=54 (%)**	**No. of negatives n=263 (%)**
<20	18 (5.67%)	3 (5.55%)	15 (4.73%)
20-29	65 (20.50%)	6 (11.11%)	59 (18.61%)
30-39	57 (17.98%)	8 (14.81%)	49 (15.45%)
40-49	45 (14.19%)	6 (11.11%)	39 (12.30%)
50-59	38 (11.98%)	9 (16.66%)	29 (9.14%)
60 and above	94 (29.65%)	22 (40.74%)	72 (22.17%)

Table.02. Age- wise analysis of Influenza Cases.

Most common clinical symptoms associated with influenza cases was high grade fever (96.29%), cough (83.33%), Breathlessness (81.48%), Sore throat (50%), Rhinitis (44.44%), Dyspnoea (38.88%) other symptoms have been listed in **Table 03**.

Clinical presentation of the cases.	
Clinical presentation	**No of positives n=54 (%)**
Fever	52 (96.29%)
Cough	45 (83.33%)
Rhinitis	24 (44.44%)
Sore throat	27 (50%)
Dyspnoea	21 (38.88%)
Myalgia	11 (20.37%)
Diarrhoea	4 (7.40%)
Headache	6 (11.11%)
Loss of smell	2 (3.70%)
Breathlessness	44 (81.48%)
Chest Pain	4 (7.40%)

Table.03 Clinical presentation of the cases (n=54)

Among the confirmed cases, diabetes was the most commonly observed comorbidity (44.44%), followed by hypertension (35.18%), coronary heart disease (9.5%), bronchial asthma (7.40%), and chronic kidney disease (3.70%) **[See Table 04].**

Comorbid conditions.		
Condition	**Total no of cases n=317 (%)**	**Positive Inf. A/B cases n=54 (%)**
Diabetes mellitus	115 (36.27%)	24 (44.44%)

Hypertension	**69 (21.76%)**	**19 (35.18%)**
Coronary artery disease	**34 (14.82%)**	**5 (9.25%)**
Bronchial asthma/ COPD	**38 (11.98%)**	**4 (7.40%)**
Chronic kidney disease	**12 (3.78%)**	**2 (3.70%)**

Table.04 Comorbid conditions of the Influenza cases.

A total of 317 influenza-suspected cases were reported from September 2022 to February 2024, out of which 54 confirmed cases. The highest number of total cases (67) and positive cases (30) were reported in October 2023, with H1N1 being the predominant strain. Seasonal peaks of positivity were observed in early 2023 (Jan–Mar) and again in late 2023 (Sep–Nov) **[See Fig.02].**

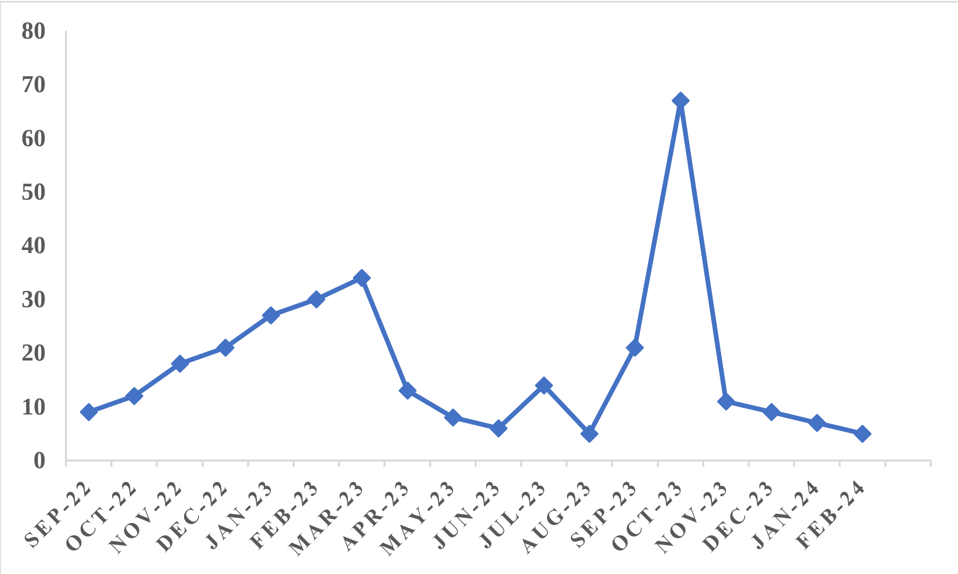

Fig.02. Month-wise distribution of Influenza cases.

Out of four samples which were COVID-19 positive, 03 were Females and 01 male falling in the age group 20-29 years.

4. <u>Discussion</u>

World Health Organization has pointed out that pandemic viruses, such as seasonal influenza from 2009 may persist, with potential local outbreaks in the post-pandemic period. In India, number of laboratory's confirmed influenza cases were reported between 2010 and 2025.[13,14] Real time RT-qPCR is the most reliable diagnostic tests for influenza viruses with great sensitivity and specificity compare with rapid antigen diagnostic test and immunofluorescence assay.[4,15] In 2023, several states across India reported multiple outbreaks caused by different subtypes of Influenza-A viruses, resulting in significant morbidity and mortality.[16]

A total of 317 ILI samples collected between September 2022 and August 2024 at the ICMR-VRDL Laboratory, GMC Akola, were included in this study. Among these, 17.03% (34 samples) tested positive for influenza, indicating the continued circulation of the virus during this period. Comparable positivity rates were reported by Dangi T. et al.[17] from Lucknow (15.8%) and Chadha M.S. et al.[18] (14.0%). In contrast, higher prevalence rates were observed in studies by Sona S. et al.[11] from Assam (42.2%) and Deva A. et al.[2] from Karnataka (25.58%). Such variations across regions may be attributed to factors including differences in temperature, humidity, surveillance categories, vaccination coverage, population density, and human mobility.[2,19]

In the present study, 15.14% of cases tested positive for Influenza A. This positivity rate is comparable to that reported by Chadha et al.[18] (14%) from different regions of India during 2009–2013, and by Baruah M. et al.[20] (18.85%) from Assam. Among the positive cases, H1N1 pdm09 was the predominant subtype, accounting for 60.41% (29/48), followed by H3N2 at 33% (16/48), and unsubtyped strains at 6.22% (3/48). These findings are correlates with the results of Dangi T. et al.[17] who reported 67.2% positivity for H1N1 pdm09 and 32.8% for H3N2. Out of the 6 samples that tested positive for Influenza B, 66.66% (4/6) belonged to the B/Victoria lineage and no Influenza B/Yamagata were identified. Our result is corroborating with the study by Nakauchi M. et al.[21] in which they reported 70% for Influenza B/Victoria and 30% for Influenza B/Yamagata. These findings indicate that rRT-PCR assays show high sensitivity and specificity for each target gene, making them highly valuable for detecting and differentiating influenza virus lineages.

No significant sex-based difference was observed, with males and females each accounting for 50% of the cases. This finding aligns with the study by Shendre et al.[22] (Central India, 2015–2019), which reported nearly equal distribution between sexes except in 2019, as well as with Mudhigeti et al.[23] who also observed a similar pattern. In contrast, Shrikhande S. et al.8 reported a male predominance (65.67% vs. 34.32%), attributing it to women's limited access to healthcare and the greater outdoor activities and travel undertaken by men for business purposes.

In our study, individuals aged 60 years and above were more commonly affected, which is concerning compared to findings from other studies in this region, such as those by Shendre et al.[22] and Humne AY et al.[24] The higher involvement of the elderly may be attributed to increased social interactions. Diabetes mellitus was the most common co-existing medical condition in our study, followed by hypertension, coronary artery disease, bronchial asthma/COPD, and chronic kidney disease. Previous literature has identified chronic respiratory conditions, chronic liver disease, chronic renal disease, diabetes, and pregnancy as risk factors for influenza infection. [14,25,26] However, in the present study, these factors were not associated with increased mortality or the need for mechanical ventilation. Of the 54 confirmed positive cases, the majority were from urban areas. There were 2 reported deaths, corresponding to a mortality rate of 3.70%, which is comparable to the findings of Samara T et al.[27] (5%) and Mehta AA et al.[28] (6.8%). The most common presenting symptom was fever, followed by breathlessness, cough, sore throat, and rhinitis—similar to observations from other Indian studies. [7,22]

In our study, the highest number of positive cases was reported in October 2023 (30 cases) and during the early months of 2023 (January–March). These findings are consistent with the study conducted by Shendre et al.[22] which also reported the highest positivity in October 2015 in the same region. We observed two distinct peaks: one in early 2023 (January–March) and another in late 2023 (August–November), which is comparable to the findings of Shendre et al.[22] Similar observations of biannual peaks were also reported by Mudhigeti N. et al.[23] during an outbreak in Andhra Pradesh.

In summary our study shows the circulation patterns of influenza in our region and underscores the need for India's influenza vaccination policy to account for state-specific variations. In particular, cities with a late monsoon season could benefit from adopting a winter vaccination strategy using the most recent WHO-recommended formulation. These findings provide valuable evidence to guide policymakers in selecting the most appropriate vaccine formulation and timing for different regions of the country.

References

1. Papagiannis D, Perlepe G, Tendolouri T, Karakitsiou P, Damagka G, Kalaitzi A, et al. Proportion of Respiratory Syncytial Virus, SARS-CoV-2, Influenza A/B, and Adenovirus Cases via Rapid Tests in the Community during Winter 2023—A Cross Sectional Study. Diseases. 2023 Sep 1;11(3).

2. Deva A, Madhavi B, Kumar Nagaiah S, PM B. Prevalence and Characteristics of Influenza Cases From 2017 to 2019 at a Tertiary Care Teaching Hospital in Karnataka. Cureus. 2024 Jan 30;
3. Mudhigeti N, Racherla R, Mahalakshmi P, Pamireddy M, Nallapireddy U, Kante M, et al. A study of influenza 2017-2018 outbreak in Andhra Pradesh, India. Indian J Med Microbiol. 2018 Oct 1;36(4):526–31.
4. Suwannakarn K, Payungporn S, Chieochansin T, Samransamruajkit R, Amonsin A, Songserm T, et al. Typing (A/B) and subtyping (H1/H3/H5) of influenza A viruses by multiplex real-time RT-PCR assays. J Virol Methods. 2008 Sep;152(1–2):25–31.
5. Javanian M, Barary M, Ghebrehewet S, Koppolu V, Vasigala VKR, Ebrahimpour S. A brief review of influenza virus infection. Vol. 93, Journal of Medical Virology. John Wiley and Sons Inc; 2021. p. 4638–46.
6. Girard MP, Tam JS, Assossou OM, Kieny MP. The 2009 A (H1N1) influenza virus pandemic: A review. Vol. 28, Vaccine. 2010. p. 4895–902.
7. Nakauchi M, Takayama I, Takahashi H, Oba K, Kubo H, Kaida A, et al. Real-time RT-PCR assays for discriminating influenza B virus Yamagata and Victoria lineages. J Virol Methods. 2014 Sep 1;205:110–5.
8. Shrikhande S, Bhoyar SK, Tenpe SH, Deogade NG. Epidemiology of pandemic H1N1 strains in a tertiary hospital of Maharashtra. Indian J Public Health. 2012;56(3):242–4.
9. World Health Organization. Human infection with pandemic A (H1N1) 2009 influenza virus: clinical observations in hospitalized patients, Americas, July 2009—update. Weekly Epidemiological Record= Relevé épidémiologique hebdomadaire. 2009;84(30):305-8.
10. Ministry of Health and Family Welfare. Seasonal influenza. 2019. Available from: https://ncdc.mohfw.gov.in/wp-content/uploads/2024/02/72513234671561442053-1.pdf.
11. Sona S, Sharma A, Chamuah K, Henbi LN, Rajbongshi G. Influenza virus and its subtypes circulating during 2018–2019: A hospital-based study from Assam. Indian J Med Microbiol. 2022 Oct;40(4):525–30.
12. Aggarwal N, Potdar V, Vijay N, Mukhopadhyay L, Borkakoty B, Manjusree S, et al. SARS-CoV-2 and Influenza Virus Co-Infection Cases Identified through ILI/SARI Sentinel Surveillance: A Pan-India Report. Viruses. 2022 Mar 1;14(3).
13. Murhekar M, Mehendale S. The 2015 influenza A (H1N1) pdm09 outbreak in India. Vol. 143, Indian Journal of Medical Research. Indian Council of Medical Research; 2016. p. 821–3.
14. Vijayalakshmi J, Sreekanth Reddy B, Surekha A, Renuka Devi A. Surveillance of swine flu influenza H1N1 by chip based real time PCR technology from the clinical specimens in a tertiary care hospital. Journal of Clinical and Diagnostic Research. 2018 Dec 1;12(12):DC01–4.
15. Schulze M, Nitsche A, Schweiger B, Biere B. Diagnostic approach for the differentiation of the pandemic influenza A(H1N1)v virus from recent human influenza viruses by real-time PCR. PLoS One. 2010;5(4).
16. Baruah M, Dutta H, Kalita DJ. A surge of H3N2 influenza cases in patients presenting with flu-like symptoms: an experience from a tertiary care hospital. Indian J Appl Res. 2023;13(12):15–17. doi:10.36106/ijar.
17. Dangi T, Jain B, Singh AK, Mohan M, Dwivedi M, Singh JV, Kumar R, Singh KP, Chaddha MS, Mishra AC, Jain A. Influenza virus genotypes circulating in and around Lucknow, Uttar Pradesh, India, during post pandemic period, August 2010-September 2012. Indian Journal of Medical Research. 2014 Mar 1;139(3):418-26.
18. Chadha MS, Potdar VA, Saha S, Koul PA, Broor S, Dar L, et al. Dynamics of influenza seasonality at sub-regional levels in India and implications for vaccination timing. PLoS One. 2015 May 4;10(5).
19. Sharma P, Gupta S, Singh Di, Verma S, Kanga A. Influenza A(H1N1)pdm09 cases in sub-Himalayan region, 2014-2015 India. Indian J Pathol Microbiol. 2016 Jan 1;59(1):63–5.
20. Baruah M, Dutta H, Kalita DJ. A surge of H3N2 influenza cases in patients presenting with flu-like symptoms: an experience from a tertiary care hospital. Indian J Appl Res. 2023;13(12):15–17. doi:10.36106/ijar.
21. Nakauchi M, Takayama I, Takahashi H, Oba K, Kubo H, Kaida A, et al. Real-time RT-PCR assays for discriminating influenza B virus Yamagata and Victoria lineages. J Virol Methods. 2014 Sep 1;205:110–5.

22. Shendre P, Raut S, Khadse R. A five-year study of Influenza A (H1N1) pandemic 09 from Central India. IP International Journal of Medical Microbiology and Tropical Diseases. 2020 Apr 28;6(1):33–8.
23. Mudhigeti N, Racherla R, Mahalakshmi P, Pamireddy M, Nallapireddy U, Kante M, et al. A study of influenza 2017-2018 outbreak in Andhra Pradesh, India. Indian J Med Microbiol. 2018 Oct 1;36(4):526–31.
24. Humne AY, Thakre SB, Ughade SM, Rathod PG, Thakre SS, Chavan AB. An epidemiological investigation of influenza like illness (ILI) to confirm the A H1N1 among patients admitted to secondary and tertiary care hospital of Nagpur, central India. International Journal of Scientific and Research Publications. 2013;3(8):383-8.
25. Nandhini G, Sujatha S. Epidemiology of influenza viruses from 2009 to 2013–A sentinel surveillance report from Union territory of Puducherry, India. Asian Pacific journal of tropical medicine. 2015 Sep 1;8(9):718-23.
26. Patel KK, Patel AK, Mehta PM, Amin RP, Patel KP, Chuhan PC, Naik E, Patel KR. Clinical outcome of novel H1N1 (swine flu)-infected patients during 2009 pandemic at tertiary referral hospital in Western India. Journal of global infectious diseases. 2013 Jul 1;5(3):93-7.
27. Samra T, Pawar M, Yadav A. One year of experience with H1N1 Infection: clinical observations from a tertiary care hospital in Northern India. Indian Journal of Community Medicine. 2011 Jul 1;36(3):241-3.
28. Mehta AA, Kumar V, Nair SG, Joseph FK, Kumar G, Singh SK. Clinical profile of patients admitted with swine-origin influenza A (H1N1) virus infection: an experience from a tertiary care hospital. Journal of clinical and diagnostic research: JCDR. 2013 Oct 5;7(10):2227.

Authors:

First Author: Dr. Rupali S. Mantri, Associate Professor and Head, Department of Microbiology, Government Medical College, Akola, r.mantri@rediffmail.com, 9822500958, 7020090184

Second Author: Dr. Nitin A Arnbhore, Professor and Head, Department of Microbiology, Government Medical College, Parbhani, nitinaambhore@gmail.com.

Third Author: Mr. Jeetendra Thakur, Research Scientist B, VRDL, Department of Microbiology, Government Medical College, Akola.

Fourth Author: Corresponding Author: Dr. Premjith Lal UA, Senior Resident, Department of Microbiology, Government Medical College, Akola, shan3135@gmail.com, 7594943135.

Fifth Author: Miss. Sunayana Narwade, Assistant Research Scientist, VRDL, Department of Microbiology, Government Medical College, Akola.

Corresponding Author: Dr. Premjith Lal UA, Senior Resident, Department of Microbiology, Government Medical College, Ako la, shan3135@gmail.com, +91-7594943135, +91-9541661439