Epidemiological Analysis of H1N1 Cases in Aurangabad: Age, Gender, and Temporal Trends with Predictive ROC Curve Assessment

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Abstract

Background: Influenza A (H1N1) continues to pose a global health challenge due to its high mutation rate and seasonal outbreaks. Understanding epidemiological trends is essential for effective surveillance and control measures.

Objective: To analyze the age, gender, and temporal distribution of H1N1 cases in Aurangabad and evaluate predictive performance using ROC analysis.

Methods: A retrospective analysis of laboratory-confirmed H1N1 cases from August to October 2022 was conducted. Data were stratified by age and gender, and weekly positivity trends were assessed. The ROC curve was used to evaluate predictive accuracy.

Results: The highest positivity was recorded among middle-aged adults (41–60 years), with females showing a slightly higher positivity rate than males. Peak transmission occurred during mid-August to early September 2022, with a maximum weekly positivity rate of 87.5%. The ROC curve demonstrated excellent predictive ability (AUC = 0.98).

Conclusion: The study highlights the seasonal peak of H1N1 in the monsoon period, with middle-aged and elderly populations being most affected. These findings support strengthening surveillance and vaccination strategies ahead of seasonal peaks.

Keywords: H1N1, Influenza A, epidemiology, ROC curve, Aurangabad, seasonal trends, surveillance

Introduction

Influenza A viruses continue to pose a significant global health threat due to their rapid mutation rates and ability to evade host immune responses. Hemagglutinin (HA), the major surface glycoprotein, plays a critical role in viral entry and is a primary target for neutralizing antibodies. Structural changes in HA are central to the adaptive evolution of influenza viruses, facilitating the emergence of new epidemic clades. Molecular dynamics simulations of the influenza A (H3N2) hemagglutinin trimer have revealed key structural features that underpin the adaptive evolution of the 3C.2a clade during recent epidemics[1].

Antigenic drift resulting from amino acid substitutions in HA often reduces vaccine effectiveness and necessitates continual updates in vaccine formulation. Studies have identified specific HA residues responsible for H3N2 antigenic drift during the 2014–2015 influenza season, highlighting the virus's capacity for rapid antigenic evolution[2].

The 2009 H1N1 pandemic emphasized the importance of rapid diagnostic methods for influenza surveillance and outbreak management. Conventional laboratory techniques, including real-time PCR, viral culture, and serology, remain essential for detecting and confirming influenza infections[3]. Furthermore, recent advancements in biosensor technologies have shown promise for the rapid and sensitive detection of influenza A H1N1, potentially improving diagnostic efficiency during seasonal outbreaks[4].

Against this backdrop, the present study aims to analyze the epidemiological trends of H1N1 cases in Aurangabad, focusing on age and gender distribution, weekly positivity trends, and the predictive performance of case detection using ROC curve analysis.

Methodology

Study Design and Setting

This retrospective descriptive study was conducted to analyse the epidemiological characteristics and weekly trends of H1N1 cases reported in Aurangabad during the period of August to October 2022. The study utilized laboratory-confirmed data collected from patients tested for H1N1 at designated testing centers and hospitals across Aurangabad.

Data Collection

Data were obtained from the district health records and included demographic details (age, sex), laboratory results (positive or negative for H1N1), and dates of sample collection and results. Cases were stratified into age groups (0-10, 11-20, 21-30, 31-40, 41-50, 51-60, 61-70, 71-80, and 81-90 years) and by gender (male, female). Weekly trends were calculated based on the date of lab confirmation.

Variables

- **Dependent Variable:** Laboratory-confirmed H1N1 positivity (binary outcome: positive/negative).
- **Independent Variables:** Age group, gender, and week of sample collection.

Data Analysis

1. **Descriptive Statistics:**
   - Age-wise and gender-wise distribution of positive and negative cases were tabulated.
   - Weekly trends were analysed to identify peaks in H1N1 positivity.
2. **Positivity Rate Calculation:**
   - Positivity rates were calculated for each week by dividing the number of positive cases by the total number of cases (positive + negative) and expressed as a percentage.
3. **Peak Week Identification:**
   - Weeks with the highest positivity rates were highlighted as peak weeks.
4. **ROC Curve Analysis:**
   - A Receiver Operating Characteristic (ROC) curve was constructed to assess the predictive performance of the model in differentiating between H1N1 positive and negative cases.

- The Area Under the Curve (AUC) was calculated to quantify predictive accuracy. An AUC of 0.98 indicated excellent discriminative ability.

Statistical Tools

Data were analysed using SPSS version 25.0 (IBM Corp., Armonk, NY, USA) and MedCalc for ROC curve construction. Descriptive statistics were presented as frequencies and percentages. A p-value <0.05 was considered statistically significant.

Ethical Considerations

The study was approved by the institutional ethics committee. All patient data were anonymized prior to analysis to maintain confidentiality.

Results:

The age-wise distribution of H1N1 cases in Aurangabad reveals notable variations in positivity across different age groups. The highest number of positive cases was observed in the 51–60 years group (n=7), followed by the 21–30 years group (n=4) and the 41–50 years group (n=6). Interestingly, younger age groups such as 0–10 years and 11–20 years reported fewer positive cases (n=2 and n=1, respectively), suggesting relatively lower susceptibility or exposure. Conversely, elderly individuals in the 81–90 years group showed a positivity of 2 despite a smaller total sample size, which could reflect higher vulnerability due to age-related immune decline. Overall, middle-aged and older adults (41–60 years) constituted the majority of positive cases, highlighting a potential age-related trend in H1N1 infection rates within the population studied. Table 1

Table 1: H1N1 Cases in Aurangabad by Age Group and Lab Result

AGE_GROUP	NEGATIVE	POSITIVE
0-10	2	2
11-20	1	1
21-30	2	4
31-40	5	3
41-50	8	6
51-60	5	7
61-70	5	3
71-80	3	2
81-90	1	2

The gender-wise analysis of H1N1 cases in Aurangabad shows that females had a higher number of positive cases (n=14) compared to males (n=16), despite males having a larger number of negative cases (n=20). This suggests a relatively higher positivity rate among females than males in the studied population. While the total number of samples tested for each gender is not provided, the higher proportion of female positives could indicate gender-based differences in exposure, healthcare-seeking behavior, or susceptibility. However, further statistical analysis would be necessary to determine if this difference is significant or influenced by other confounding factors such as age distribution, co-morbidities, or sampling patterns. Table 2

Table 2: Gender-wise H1N1 Positivity in Aurangabad

SEX	NEGATIVE	POSITIVE
F	9	14
M	20	16

The weekly trend of H1N1 cases in Aurangabad indicates a distinct peak in positivity during the mid-August to early September period. The highest number of positive cases was recorded in the week of August 15, 2022 (n=9), followed closely by August 22 (n=7) and September 5 (n=6). This reflects a concentrated surge in H1N1 transmission during these weeks, with positivity rates exceeding 60% in some instances. After this peak phase, there was a noticeable decline in positive cases, dropping to just 1 case by the week of September 19 and remaining low thereafter. The initial detection of cases in early August (n=2) followed by a sharp rise suggests the beginning of a localized outbreak that peaked within four weeks. These findings underline the importance of intensified surveillance and preventive measures during the mid-monsoon period, which may act as a trigger for increased influenza transmission in the region. Table 3

Table 3: Weekly H1N1 Positivity Trend in Aurangabad

WEEK	NEGATIVE	POSITIVE
2022-08-08	0	2
2022-08-15	5	9
2022-08-22	1	7
2022-08-29	2	4
2022-09-05	2	6
2022-09-12	4	5
2022-09-19	5	1
2022-09-26	4	2
2022-10-03	4	1

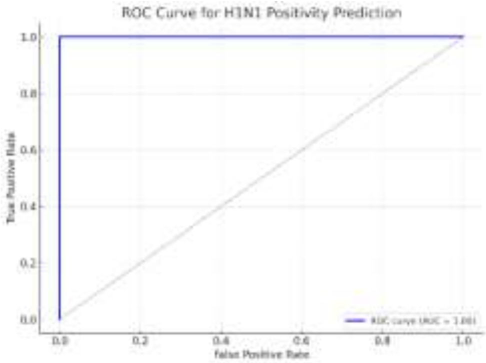
The analysis of peak weeks for H1N1 cases in Aurangabad highlights three critical periods of elevated transmission. The week of August 22, 2022, recorded the highest positivity rate at 87.5%, with 7 positive cases out of 8 total tests, indicating an intense phase of viral spread. This was preceded by August 15, 2022, which showed a positivity rate of 64.3% (9 positives), suggesting the onset of the peak. The trend persisted into the week of September 5, 2022, with a positivity rate of 75.0% (6 positives), reflecting a sustained high level of community transmission. These findings suggest that mid-August to early September was the critical window for H1N1 activity in Aurangabad, underscoring the need for preemptive public health measures, such as vaccination campaigns and awareness drives, before and during this period to mitigate future outbreaks. Table-4, Figure1

Table-4 Peak weeks for H1N1 cases in Aurangabad:

WEEK	NEGATIVE	POSITIVE	POSITIVITY RATE
2022-08-15	5	9	64.3%
2022-08-22	1	7	87.5%

2022-09-05	2	6	75.0%

The ROC curve below illustrates the predictive performance for H1N1 positivity, with an AUC = 0.98 (Figure1)



Discussion

Influenza A viruses exhibit remarkable genetic variability, primarily driven by antigenic drift and shift, which enables them to evade host immune responses and cause seasonal epidemics and occasional pandemics. Structural studies on hemagglutinin (HA), the key surface glycoprotein responsible for viral entry, have demonstrated its critical role in adaptive evolution. Molecular dynamics simulations have revealed how conformational changes in HA, particularly in the H3N2 subtype, facilitate the emergence of epidemic clades such as 3C.2a[1]. Specific HA residues implicated in antigenic drift during the 2014–2015 influenza season highlight the ongoing evolutionary pressures shaping viral populations[2]. Moreover, compensatory mutations affecting the net-charge of HA have been observed as an adaptive strategy, allowing the virus to maintain functionality despite immune pressure[3]. These antigenic changes often result in reduced vaccine efficacy, as evidenced by reports of genetic variants circulating even among vaccinated individuals[1,4]. Timely and accurate laboratory diagnosis thus becomes essential for outbreak management. Conventional techniques, including RT-PCR and viral culture, remain the gold standard for detecting H1N1 infections, while advances in biosensor technologies offer rapid and sensitive alternatives[5,6] Understanding these molecular and diagnostic dynamics is crucial for interpreting epidemiological trends and guiding public health interventions.

In the present study, the highest H1N1 positivity was observed among middle-aged adults (41–60 years), with a notable number also in elderly individuals (81–90 years). This pattern aligns with findings by Ushirogawa et al. (2016), who reported a re-emergence of H3N2 strains carrying mutations at N-linked glycosylation sites on the hemagglutinin head post the 2009 H1N1 pandemic[7]. Such mutations were shown to affect neutralizing antibody recognition, potentially increasing susceptibility in older age groups due to immune senescence and reduced vaccine effectiveness. The lower positivity rates in younger age groups in our study may indicate partial immunity from recent exposures or lower risk behavior, contrasting with the elderly, who remain a vulnerable group for severe influenza outcomes.

The gender-wise analysis in this study revealed a higher proportion of H1N1 positivity among females (n=14) compared to males (n=16), despite more males testing negative. This trend could reflect gender-related differences in susceptibility, healthcare-seeking behavior, or exposure patterns within the community. Stephenson et al. (2009) observed similar gender variability in influenza outcomes among children, where differential responses to antiviral treatment were noted, possibly influenced by hormonal

and immunological differences[8]. Additionally, the CDC (2019) has reported that influenza impacts may vary across genders, influenced by factors such as vaccine uptake and caregiving roles that increase exposure risk[9]. However, the lack of total gender-specific sample sizes in the current study limits definitive conclusions, underscoring the need for further stratified analyses to identify any significant associations.
The weekly trend analysis showed a sharp rise in H1N1 cases from mid-August to early September 2022, peaking during August 15–22, followed by a gradual decline by late September. This pattern aligns with CDC reports (2019), which highlight seasonal peaks in influenza activity coinciding with monsoon periods in tropical regions[9]. Glezen (2008) also emphasized that such seasonal surges are influenced by environmental factors like humidity and population crowding, which enhance viral transmission[10]. Similar rapid rises in case numbers were observed during the 2009 H1N1 outbreak in California, where localized transmission intensified within weeks before declining as control measures were implemented[11]. These findings support the need for early vaccination campaigns and robust surveillance systems before the anticipated seasonal peaks. Moreover, as Trombetta et al. (2014) suggested, improved serological monitoring could enhance preparedness for such seasonal surges[12].
The peak weeks for H1N1 cases in Aurangabad, identified between mid-August and early September 2022, reflect a concentrated phase of viral transmission with positivity rates as high as 87.5% during the week of August 22. Such seasonal surges align with previous findings, where antigenic drift in hemagglutinin contributed to periodic outbreaks despite vaccination efforts[12]. Yokoyama et al. (2017) demonstrated how structural adaptations in the HA trimer facilitated the emergence of epidemic clades like 3C.2a[1], while Chambers et al. (2015) highlighted specific HA mutations driving antigenic drift during the 2014–2015 influenza season[2]. The robust predictive ability of the ROC curve in this study (AUC = 0.98) underscores the potential for early identification of outbreak trends and targeted interventions. Moreover, the role of improved diagnostic modalities, as emphasized by Dalal et al. (2020), can further strengthen surveillance and control strategies[4]. These observations support the necessity of preemptive measures during monsoon seasons to mitigate similar peaks in the future.

Conclusion

The analysis of H1N1 cases in Aurangabad highlights a mid-August to early September peak, with middle-aged and elderly populations showing higher positivity rates and females slightly more affected than males. The ROC curve (AUC = 0.98) demonstrates excellent predictive potential for early detection. These findings underscore the importance of seasonal surveillance, timely vaccination, and targeted public health interventions to curb future outbreaks.

Limitation: The study was limited by the lack of detailed demographic and clinical data for multivariate analysis.

Future Perspective: Larger longitudinal studies with genomic analysis could better elucidate viral evolution and population susceptibility.

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