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Original Research Article

Clinico-Epidemiological Profile and Study of Influenza and Their Subtypes Among Suspected Influenza Patients in a Tertiary Care Teaching Hospital of Vadodara

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ABSTRACT

Background: Influenza viruses cause significant respiratory illness, with seasonal epidemics and occasional pandemics influenced by antigenic variation. Monitoring local prevalence and subtype distribution is vital for guiding public health responses.

Material and methods: A descriptive cross-sectional study was conducted from March to December 2024. A total of 601 throat or nasopharyngeal swabs from suspected influenza cases were collected and tested using the PathoDetect™ multiplex real-time RT-PCR kit, which detects influenza A, B, and subtypes A(H1N1) and A(H3N2). Quality control included internal and external validation.

Results: Overall positivity was 20.46%. The highest number of cases occurred in individuals >60 years, while the highest positivity rate was in children <10 years. Fever (78.86%) was the most common symptom; COPD (29.26%) was the leading comorbidity. Influenza A was predominant (92.97%), with H1N1 (53.90%) as the leading subtype, followed by H3N2 (8.59%). Two seasonal Peaks of H1N1 were observed in March–April and August–October. Five co-infections were detected: two with H1N1 and H3N2, and three involving Influenza B co-infected with H1N1, H3N2, and Untypable Influenza A.

Conclusion: H1N1 is the dominant circulating strain. Findings highlight the need for continuous surveillance, timely diagnosis, and targeted vaccination. Broader community-based studies are recommended for comprehensive influenza control.

Key Words: Influenza, H1N1, H3N2, Untypable Influenza

INTRODUCTION

The influenza virus is a significant human pathogen that causes acute respiratory tract infections. These can range from mild flu-like symptoms to severe acute respiratory illness (SARI). The influenza virus spreads easily from person to person, leading to rapid transmission and the potential for widespread epidemics and even pandemics.[1]

Antigenic variations in influenza viruses, caused by genetic reassortment, contribute to their distinct ability to spread rapidly and lead to a wide range of clinical presentations. As a result, influenza viruses significantly impact the general population in terms of disease burden, morbidity, and mortality.[2]

Pandemic influenza A (H1N1) 2009 is a new strain of influenza A virus that evolved through genetic reassortment. This virus was first reported in Mexico in April 2009 and quickly spread to various countries around the world.[3]

The World Health Organization (WHO) announced the global pandemic in June 2009 which was declared post-pandemic phase in August 2010. As per the WHO, the pandemic influenza A (H1N1) virus is now considered as seasonal influenza virus. There have been reports of high morbidity, with 27236 cases, and a mortality rate of 981 deaths in India.[4]

The World Health Organization (WHO) declared the H1N1 pandemic in June 2009 and transitioned to the post-pandemic phase in August 2010. According to the WHO, the pandemic influenza A (H1N1) virus is now classified as a seasonal influenza virus.[5]

The H1N1 influenza virus, which led to a pandemic in 2009, has continued to cause periodic epidemics around the world, including in India. This ongoing issue poses significant public health challenges globally. Timely diagnosis of these outbreaks in various regions is crucial for implementing effective preventive and control measures within communities.[6-8]

The present study aimed to determine the prevalence, subtypes, and epidemiology of influenza. The goal was to generate knowledge about the magnitude of the disease and the locally prevalent subtypes of the influenza virus. This information is crucial for public health awareness and preparedness in managing and preventing influenza cases at the regional level.

MATERIAL AND METHODS

Study design and duration:

This descriptive cross-sectional study was conducted over a period of 10 months, from March 2024 to December 2024, at the Viral Research and Diagnostic Laboratory in the Department of Microbiology at the Medical College Baroda and S.S.G. Hospital in Vadodara.

Study Population

Inclusion criteria All clinically suspected cases of influenza categorized as category C, according to the Ministry of Health and Family Welfare (MoHFW) guidelines, were included in the study.[9]

Epidemiological data Demographic and clinical details about all suspected cases were collected from the swine flu isolation wards and hospital.

Collection of samples: Throat or nasopharyngeal swab samples of suspected cases with Influenza-like illness were collected in Viral Transport Medium and sent to laboratories maintaining cold-chain.

Testing for the influenza virus was conducted using the PathoDetect™ (Mylab) Human Influenza Detection Kit. This kit employs a multiplex real-time reverse transcriptase polymerase chain reaction (RT-PCR) assay, which is designed for the simultaneous qualitative detection and differentiation of influenza A, influenza B, and subtypes of influenza A. It achieves this by using primers and probes specific to influenza A (M gene), influenza B (NS2 gene), and influenza A subtypes A(H3N2) and A(H1N1)pdm09 (HA gene).

The quality control and assurance of the testing procedure were conducted through both internal controls provided in the kit and external controls utilizing pooled positive and negative samples.

Statistical Analysis

The collected data was organized and analyzed using a Microsoft Excel spreadsheet. Further calculations were performed using relevant statistical methods, including frequency tables and their corresponding percentages.

RESULTS

During the study period from March to December 2024, a total of 601 samples were collected from patients suspected of having Category C influenza-like illness. Among these samples, 123 (20.46%) tested positive for influenza. Of the influenza-positive cases, 76 (61.79%) were male patients, while 47 (38.21%) were female patients.

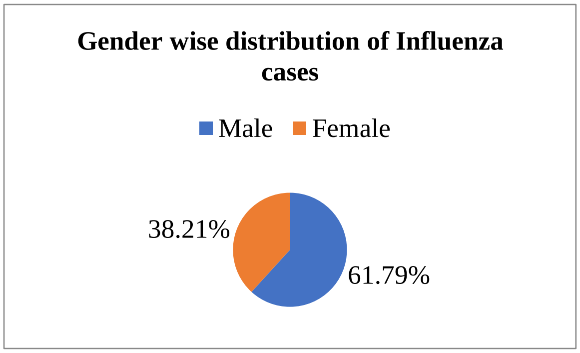


Figure-1: Gender wise distribution of Influenza positive cases among suspected patients

Table-1: Age wise distribution among patients having suspected influenza infection

		Influenza A			**Influenza B**	**Total**	**Positivity**
Age (Year)	**Total**	**H1N1**	**H3N2**	**Untypable Influenza A**			
<10	43	06	00	04	02	12	27.90%
11-20	48	02	00	04	01	07	14.58%
21-30	97	11	03	02	03	19	19.59%
31-40	69	10	00	05	01	16	23.18%
41-50	72	08	01	04	00	13	18.05%
51-60	111	11	03	09	00	23	20.72%
>60	161	21	04	11	02	38	23.60%
Total	601	**69**	**11**	**39**	**09**	**128**	**21.29%**

The most commonly affected age group suffering from influenza infections was individuals over 60 years old, accounting for 38 cases (30.89%). This was followed by the 51–60 year age group, which had 23 cases (18.70%), and the 21–30 year age group, with 19 cases (15.44%). The least affected group was those aged 11–20 years, with only 7 positive cases (5.69%).

Overall, the highest positivity rate was observed in the age group under 10 years old, at 27.90%. This was followed by the over 60 age group at 23.60% and the 31–40 year age group at 23.18%. The lowest positivity rate was found in the 11–20 year age group, which had only 14.58%.

A total of 128 influenza viruses were detected from 123 patients who tested positive for influenza. Among these, 119 (92.97%) were classified as Influenza A and 9 (7.03%) as Influenza B. Of the 119 Influenza A cases, 69 (57.98%) were identified as the H1N1 subtype, 11 (9.24%) as the H3N2 subtype, and 39 (32.78%) were untypable Influenza A viruses.

The overall positivity rates for H1N1 and H3N2 among the 128 detected influenza viruses were 53.90% and 8.59%, respectively.

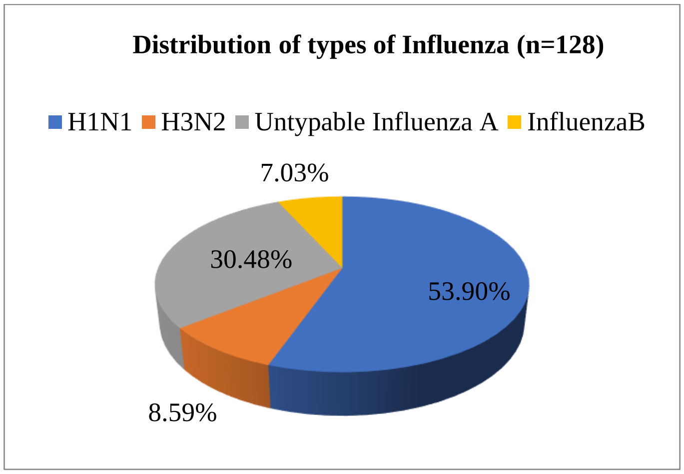


Figure-2: Distribution of types of Influenza among Influenza positive patients

Additionally, 5 patients were found to have co-infections. Among these, 2 patients had co-infections with both H1N1 and H3N2, while the other 3 patients had Influenza B along with co-infections of H1N1, H3N2, and untypable Influenza A, respectively.

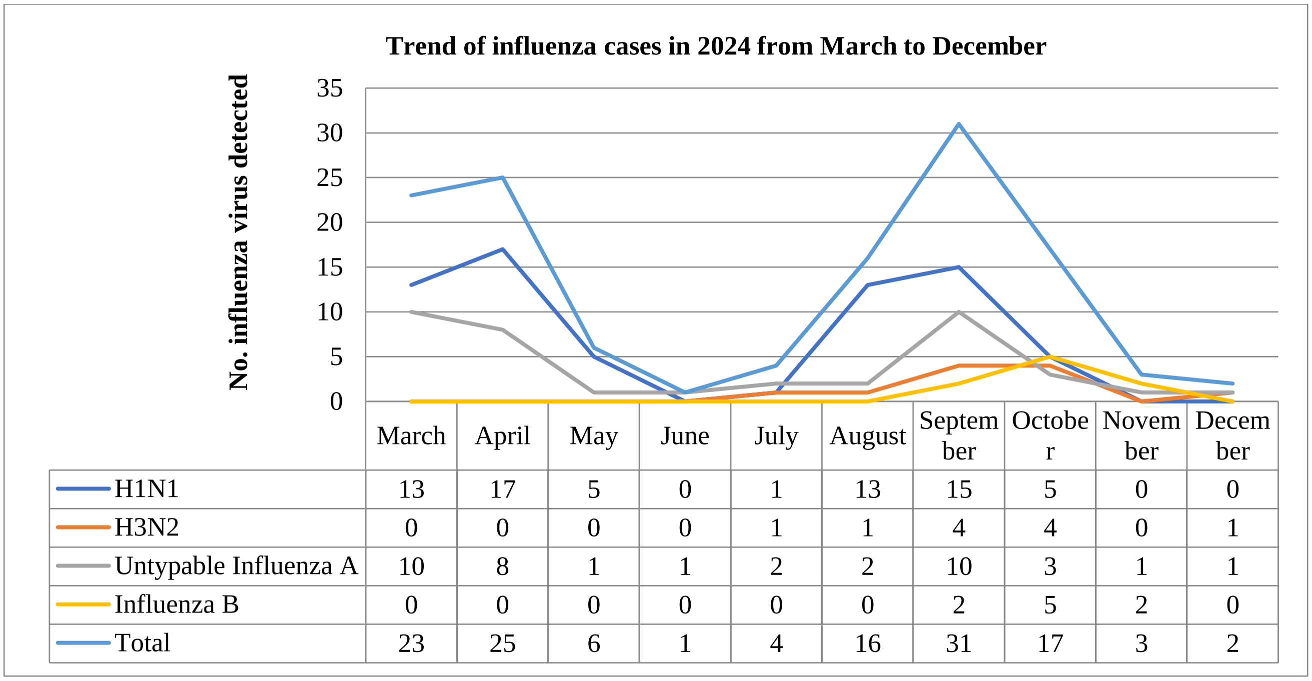
Fever was most common symptom in our study which were present in 97(78.86%) of the cases. Followed by cough 77(62.60%) and breathlessness 66(53.66%).

COPD was the most common comorbidity, observed in 36 (29.26%) patients, followed by neurological conditions and hypertension, which were observed in 7 (5.69%) and 6 (4.88%) patients, respectively.

The least common comorbidities were pregnancy and diabetes-mellitus , as depicted in the Table 2.

Table-2. Distribution according to clinical symptoms and comorbidities(n=123)

Symptoms	No. of Patients	Comorbidities	No. of Patients
Fever	97 (78.86%)	COPD	36 (29.26%)
Productive cough	77 (62.60%)	Neurological disorder	07 (5.69%)
Breathlessness	66 (53.65%)	Hypertension	02 (1.62%)
Sorethroat	61 (49.59%)	Chronic cardiovascular disorder	06 (4.88%)
Cyanosis	1 (0.81%)	Immunocompromised	03 (2.44%)
Hemoptysis	2 (1.62%)	Diabetes mellitus	02 (1.62%)
		Pregnancy	01 (0.81%)



	March	April	May	June	July	August	September	October	November	December
H1N1	13	17	5	0	1	13	15	5	0	0
H3N2	0	0	0	0	1	1	4	4	0	1
Untypable Influenza A	10	8	1	1	2	2	10	3	1	1
Influenza B	0	0	0	0	0	0	2	5	2	0
Total	23	25	6	1	4	16	31	17	3	2

Figure-3: Month wise distribution of influenza positive patients during March to December-2024

Overall, influenza cases exhibited two peaks: one from March to April and another from August to October. The highest peak occurred in September. During the March to April peak, the H1N1 subtype was dominant, while H3N2 and influenza B were not detected. The H1N1 peak reappeared from August to September, with H3N2 and influenza B also being detected during the August to October period as depicted in figure 3.

DISCUSSION

Influenza testing is crucial because the virus can lead to frequent epidemics and periodic pandemics. In 2009, India reported 27,236 confirmed cases and 981 deaths due to the influenza A H1N1 pdm09 strain[6]. WHO has established national influenza laboratories worldwide to study the epidemiology and causes of influenza infections.[10]

Our study found an influenza prevalence of 20.46%, with 123 out of 601 cases identified in our region. This finding is consistent with reports from Chadha et al., who observed an overall prevalence of 14% in a multicentric study conducted in India. Additionally, Dangi et al. reported a prevalence of 15.8% in Uttar Pradesh.[11,12] Biswas et al. reported higher rates in West Bengal, with a prevalence of 29.3%.[13] Differences in regional temperature, humidity, surveillance categories, vaccination coverage, and variations in population density and mobility may have contributed to differing rates across various parts of India.[14]

In our study, the highest number of cases was observed in individuals over the age of 60. This may be attributed to a weakened immune system and an increased risk of complications from preexisting conditions, which can lead to rapid deterioration. However, Mudhigeti et al. reported in 2018 that the most affected age group was between 6 and 18 years, accounting for 44.8% of cases.[15] Our study found the highest influenza positivity in the age group of less than 10 years. Cohen et al. (2014) also reported that influenza positivity was highest in the age group of less than 5 years (49.5%).[16] It may be due to their naïve immune system. In our study, 59.38% (n=76) of the cases were males, and 36.71% (n=47) were females. Other studies have shown a preponderance of female patients.[17]

In our study, the most common symptom was fever, observed in 78.86% (n=97) of patients. A similar finding was reported by Deva et al. at 81.81%.[17] In other studies, fever was present in nearly all cases.[18,19] In our study, other predominant clinical features were a productive cough, breathlessness, and sore throat, as depicted in the Table 2.

The most common comorbid conditions associated with influenza infection include Chronic Obstructive Pulmonary Disease (COPD), which affects 29.26% of patients. This increased susceptibility to infection may be attributed to compromised lung function and impaired immune response in the lungs. Other significant comorbidities include neurological disorders, hypertension, chronic cardiovascular conditions, diabetes, renal dysfunction, and pregnancy, as shown in the accompanying Table 2.

In our study, Influenza A was found to be more prevalent than Influenza B, with rates of 92.97% and 7.03%, respectively. Among the subtypes of Influenza A, H1N1 was the most common, accounting for nearly 53.90% of the overall positivity. Additionally, H3N2 subtypes (n=11) were detected, showing an overall positivity of 8.59%. These findings are consistent with those reported by Mudhigeti et al. in their study.[15] In our study, 39 cases of Influenza A virus were detected, which did not include H1N1 and H3N2, and were therefore classified as untypable Influenza A, showing an overall positivity rate of 30.46%. A similar result was reported in Hsu JC et al., where untypable Influenza A positivity was found to be 28.4%.[20]

In our study, two peaks of H1N1were seen during March-April and August-October. Similar findings were seen in Dwibedi B et al.,where two peaks of epidemic of Influenza A(H1N1)pdm09 were observed. First peak started in winter season during February–March and second peak was observed in post monsoon season i.e. August–September where second was dominant.[21]

In our study, we observed that five patients had co-infections. Among them, two patients were co-infected with H1N1 and H3N2, which aligns with the findings reported by Sarder et al.[22] The other three patients had influenza B infections, each co-infected with H1N1, H3N2, and a strain of untypeable influenza A, respectively.

STRENGTH OF STUDY

1. Comprehensive Scope: The study covers a broad time frame and analyzes detailed demographic, clinical and virological data from a significant sample size.

2. Subtype Differentiation: It effectively differentiates between Influenza A subtypes (H1N1, H3N2) and B, particularly highlighting the dominance of H1N1 providing valuable subtype-specific prevalence data.

3. Epidemiological Insight: Seasonal peaks and age wise distributions are clearly mapped, offering vital public health insights.

4. Clinical Relevance: It identifies key symptoms and co-morbidities, enhancing understanding of influenza’s clinical burden.

5. Public Health Utility: By identifying patterns of co-infections, it offers a strong foundation for public health preparedness for continuous surveillance and vaccination strategy refinement at a regional level

LIMITATION OF STUDY

Our study focuses exclusively on hospital settings, and it is crucial to note that we do not address the outcomes of patients in terms of treatment and prognosis. A comprehensive understanding of these factors is essential for advancing patient care and outcomes.

CONCLUSIONS

The study illuminates the local landscape of influenza viruses, revealing intricate details about their epidemiological, virological, and clinical characteristics across various age groups and genders. With a striking prevalence rate of 20.46%, our region is witnessing a substantial wave of influenza infections. Among the viruses, the H1N1 strain emerged as the predominant player, while the H3N2 and influenza B strains made their presence felt in 8.59% and 7.03% of cases, respectively. The phenomenon of coinfection among these strains adds another layer of complexity to our understanding of this viral threat.

Regular surveillance stands as a crucial sentinel, enabling early diagnosis and swift treatment with oseltamivir, a key player in combatting the flu and reducing mortality. Furthermore, there is an imperative need to fortify year-round influenza monitoring efforts, equipping us to proactively confront potential outbreaks and epidemics shaped by the nuances of local prevalence. This strategic preparation should also guide the formulation of targeted influenza vaccination policies, ensuring our community is well-protected against future challenges.

This investigation is rooted in a hospital setting, focusing on the intricate dynamics of the influenza virus. However, to truly capture the full spectrum of its epidemiology and the profound effects it has on community health, it is crucial to conduct a community-based study. Such an approach will provide a more comprehensive view, illuminating how this virus weaves through the fabric of society and influences the well-being of individuals beyond the clinical walls.

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