

**Study of Influenza Virus Infection at Tertiary Care Center, Ahmedabad****Anokhi Goswami<sup>1</sup>, Mital Vinzuda<sup>2</sup>, Toral Trivedi<sup>3</sup>, Anil Rajput<sup>4\*</sup>, Sanjay Rathod<sup>5</sup>,  
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Received: 01-01-2024 Revised: 27-01-2024 / Accepted: 08-02-2024

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Conflict of interest: Nil

**Abstract**

**Background:** Influenza viruses belong to Orthomyxoviridae family of viruses. Orthomyxoviridae family viruses are negative-sense ssRNA viruses. Four genera are described; Influenza A, B, C & D. Among this, Influenza type A infects humans and is responsible for all flu pandemics. In 2009, an Influenza pandemic caused by a novel strain of H1N1 resulted in millions of infections in more than 214 countries. Since their introduction in 1968, H3N2 Influenza viruses have undergone extensive genetic and antigenic evolution leading to numerous seasonal epidemics. In the present study, patients categorized as category C under national Influenza guidelines and admitted to hospital were screened for Influenza viruses. The aim of current study was to determine the occurrence of Influenza virus infection, to determine circulating subtype of Influenza virus, to determine whether the age & gender affects susceptibility to Influenza viruses

**Method:** In present study, rRT-PCR method was used. As per standard guidelines, received samples were processed in the Molecular laboratory of Microbiology Department. Viral RNA was extracted from the sample using automated extraction method (GeneMag Quick Viral DNA/RNA Purification Kit). rRT-PCR reaction mixture was prepared using Tru PCR kit. The instrument used was CFX96/C1000 Touch Thermal Cycler System (BIO RAD).

**Result:** Out of 728 samples received in the laboratory for influenza virus testing, 89 samples were positive for Influenza virus. 88 samples were positive for Influenza A virus and 1 for Influenza B virus from total 89 positive samples. The most dominant subtype of Influenza A virus was H3N2 53 (60.22%) followed by H1N1 20 (22.72%) and other subtype 15 (17%). Gender wise distribution of subtype does not show any significant difference. Among 728 samples received, 347 and 381 samples from male & female patients respectively.

Detection of influenza virus was found more in age group of 18 – 60 years as compared to other age group. Month wise distribution of H3N2 subtype shows that there was sudden increasing trend of this strain from August 2022 to February 2023.

**Conclusion:** In present study, an influenza A (H3N2) outbreak was confirmed with a co-circulation of A (H1N1) pdm09. Positivity rate of H3N2 is slightly higher among male patients and among age group of 18-60 years. Influenza cases were maximum during winter.

**Keywords:** Influenza, H3N2, Real time RTPCR.

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**Introduction**

Influenza viruses belong to Orthomyxoviridae family of viruses. Orthomyxoviridae family viruses are negative-sense ssRNA viruses. Four genera are described; Influenza A, B, C & D. Among this, Influenza type A infects humans and is responsible for all flu pandemics. [1]

In 1968 an avian reassortant virus of the H3N2 subtype (Hongkong Flu) was introduced into the human population that caused a global pandemic associated with more than one million deaths

worldwide. [2] In 2009, an Influenza pandemic caused by a novel strain of H1N1 resulted in millions of infections in more than 214 countries. Since their introduction in 1968, H3N2 Influenza viruses have undergone extensive genetic and antigenic evolution leading to numerous seasonal epidemics.

Emergence of novel H1N1 subtype of Influenza A virus, thought to contain genes from human, swine & avian strains. This novel strain rapidly spread

across the world and caused pandemic. In 2010, WHO declared pandemic to have crossed its peak and warned that it will continue as seasonal Influenza outbreaks in winter seasons. [1]

In the present study, patients categorized as category C under national Influenza guidelines and admitted to hospital were screened for Influenza viruses. Real-time reverse transcriptase PCR (rRT-PCR) was used for detection of Influenza viral RNA. The result was interpreted as either Influenza A or B/H1N1/2009pdm/H3N2 strain positive or negative.

**Aims & Objectives**

- To determine the occurrence of Influenza virus infection.
- To determine circulating subtype of Influenza virus.
- To determine whether the age & gender affects susceptibility to Influenza viruses.

**Material and Method:**

The study is carried out in the Microbiology department, Narendra Modi Medical College, Sheth L.G. General Hospital, Maninagar,

Ahmadabad from August 2022 to February 2023 with considering 728 samples. During study period patients categorized as category C under national Influenza guidelines and admitted in hospital were screened for Influenza viruses. [3]The sample collected was nasopharyngeal swab and/or throat swab in viral transport media (VTM). Out of various methods available for detection of Influenza virus, in present study, rRT-PCR method was used. As per standard guidelines, received samples were processed in the Molecular laboratory of Microbiology Department. Viral RNA was extracted from the sample using automated extraction method (GeneMag Quick Viral DNA/RNA Purification Kit). rRT-PCR reaction mixture was prepared using Tru PCR kit. The instrument used was CFX96/C1000 Touch Thermal Cycler System (BIO RAD). The result was interpreted as Influenza A or B/H1N1/2009pdm/H3N2 strain positive or negative.

**Results:**

Out of 728 samples received in the laboratory for influenza virus testing, 89 samples were positive for Influenza virus.

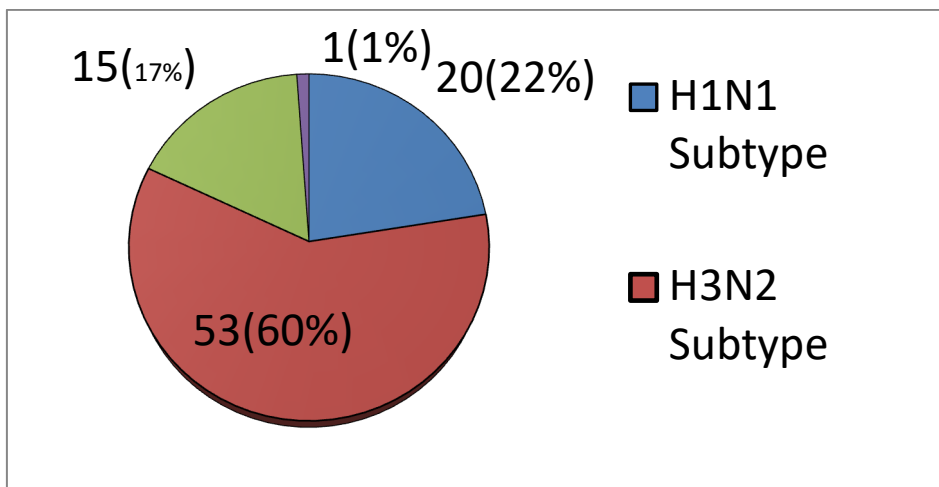


Figure 1:

88 samples were positive for Influenza A virus and 1 for Influenza B virus from total 89 positive samples. The most dominant subtype of Influenza A virus was H3N2 53 (60.22%) followed by H1N1 20 (22.72%) and other subtype 15 (17%). Gender wise distribution of subtype does not show any significant difference. Among 728 samples received 347 and 381 samples from male & female patients respectively.

Table 1: Gender wise distribution

Gender	Samples tested	Samples positive with rate	Samples positive for H3N2	Samples positive for H1N1	Samples positive for other serotypes (Inf A)	Samples positive for other serotypes (Inf B)
Male	347	42(12.10%)	28	9	4	1
Female	381	47(12.33%)	25	11	11	0
Total	728	89(12.22%)	53	20	15	1

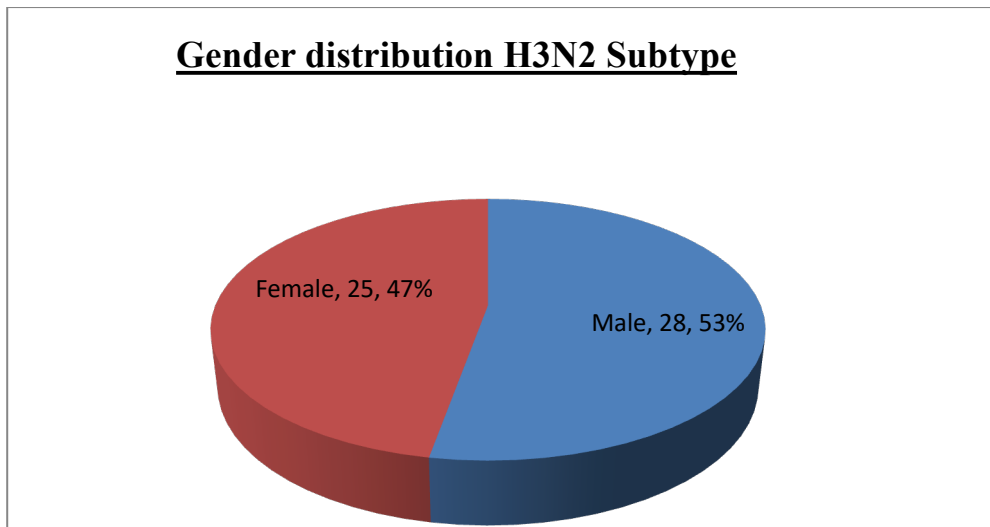


Figure 2: Gender distribution H3N2 Subtype

Detection of influenza virus was found more in age group of 18 – 60 years as compared to other age group. (See Table – 2 & Figure – 3).

Table 2: Age wise samples and positives

Age group	Samples tested	Samples positive	Samples positive for H3N2	Samples positive for H1N1	Samples positive for other serotypes (Inf A)	Samples positive for other serotypes (Inf B)
0-17	211	18(8.5%)	10	3	5	0
18-30	138	28(20.28%)	18	4	4	1
31-60	212	27(12.73%)	18	6	4	0
>60	167	16(9.5%)	7	7	2	0
Total	728	89(12.22%)	53	20	15	1

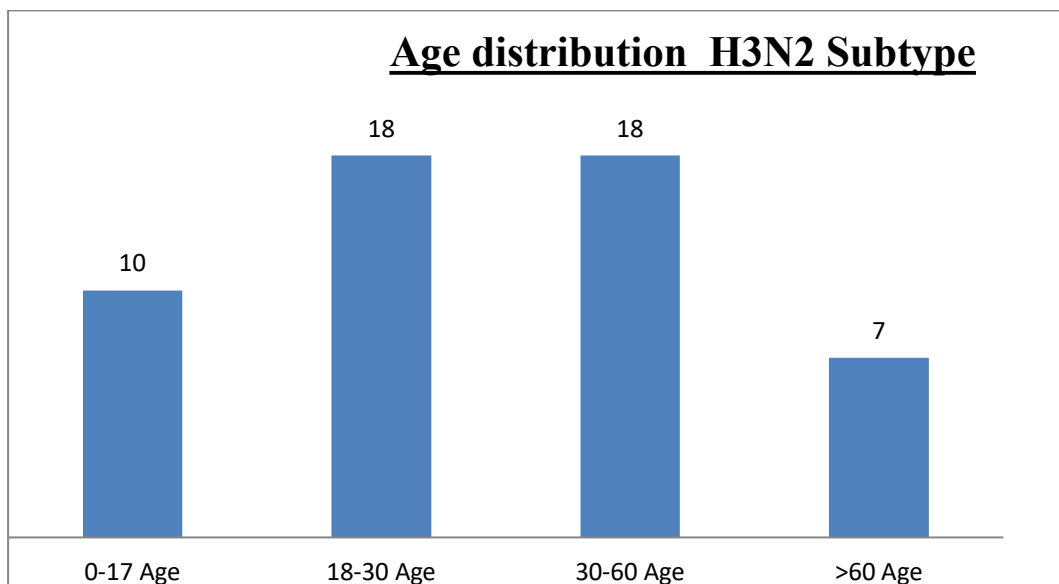


Figure 3: Age distribution H3N2 Subtype

Month wise distribution of H3N2 subtype shows that there was sudden increasing trend of this strain from August 2022 to February 2023.

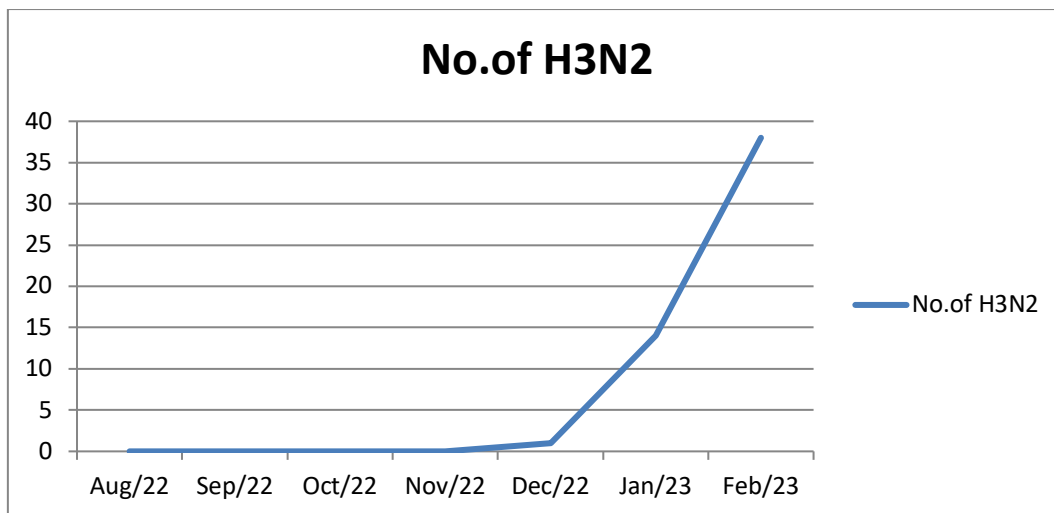


Figure 4: No. of H3N2

### Discussion

Influenza testing is important in every aspect because it may cause frequent epidemics and periodic pandemics. Various studies have given different opinions regarding the influenza infection spread. Some study shown no defined season for influenza spread while others reported the rainy season. In present study, the maximum peaks of influenza cases were observed during winter season.

Further, on looking into the relative proportion of age distribution and influenza positivity, present study observed that the most of the influenza positive cases were found in the age group of 18-60 years.

In case of influenza H3N2 and Influenza B positivity were insignificantly different in all age groups. Reason for the high infection rate in age group of 18-60 years could be due to active and working population. Positivity rate of H3N2 among male patients is slightly higher. Assessment of influenza virus infection in rural tertiary care hospital in North India, Narendra Kumar et al shows similar results. [4]

The early diagnosis of influenza virus is very important in developing countries including India because of very low vaccine compliance (below 30%), lack of knowledge and concern about the efficacy of vaccine. Hence, regular surveillance and early diagnosis will prevent the spread of Influenza virus. This also emphasizes importance of high compliance for vaccination.

### Conclusion

In present study, an influenza A (H3N2) outbreak was confirmed with a co-circulation of A (H1N1) pdm09. Positivity rate of H3N2 is slightly higher among male patients and among age group of 18-60 years. Influenza cases were maximum during

winter. In outbreak investigation, confirmation of diagnosis is the essential step. Studying the incidence, seasonality and identification of virus strain is crucial for the prevention of Influenza Virus. Timely notification to public health authorities and prompt implementation of control measures by health authorities helped to reduce the spread of infection. PCR technique is useful to detect present circulating respiratory viruses & it is useful for epidemiological aspects that alert about outbreak of particular virus strain & taking precaution like isolation/quarantine.

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