Section: Microbiology

Original Research Article

RISK FACTORS, DEMOGRAPHIC PROFILE OF PATIENTS OF INFLUENZA A, H1N1 ATTENDING THE TERTIARY CARE CENTRE OF KASHMIR, NORTH INDIA

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ABSTRACT

Background: The present study aimed to study Risk factors, Demographic profile of patients of Influenza A, H1N1 attending the tertiary care centre of Kashmir, North India.

Materials and Methods: The present study was carried out at Government Medical College and associated Hospitals Srinagar, Department of Microbiology. Patients with symptoms of Influenza like illness (ILI) attending outpatient department of SMHS and chest diseases hospital as well as hospitalized cases in the month of February 2019, were recruited. 128 Patients of all age groups were included in the study. Clinical specimens of nasopharyngeal and throat swabs (nasal swab/TS) were collected.

Results: Out of total 46 influenza positive cases, majority 39% patients belonged to 41-60 years age group followed by 21-40 years (26%), 61-80years (19.5%), 0-20years (10%) and least fraction of patients 4.3% belonged to 81-100 years. 58.6% patients were males while 31.3% patients were females. Hypertension was the chief predisposing factor 10.1% for influenza followed by diabetes mellitus 7.8%. From the 46 influenza patients, 23.9% patients were vaccinated and 76% were non vaccinated. 78.2% patients were reported in IPD and 21.7% cases were reported in OPD. 17 cases of CAP were reported in IPD and 3 cases reported in OPD. 56.5% patients had severe acute respiratory infections and 43.4% patients had influenza like illness.

Conclusion: Despite the fact that the H1N1 pandemic has concluded, epidemics serve as a perpetual reminder of the underlying threat. The sole method of minimizing the disease progression and associated mortality appears to be vaccination, early recognition of the disease, and prompt initiation of treatment.

Keywords: Co-morbidity, H1N1, Pandemic, Swine flu, Tertiary Care Center.

INTRODUCTION

Influenza virus, a single stranded negative sense RNA virus of the family Orthomyxoviridae, is a major cause of acute respiratory illness. Influenza viruses infect 10%–20% of world population and cause 250,000–500,000 deaths annually.[1] Among the three types of influenza viruses (A, B and C), influenza B and C are restricted to human host only while influenza A virus infects a variety of avian and mammalian hosts and carries zoonotic significance. In March 2009, an outbreak of novel H1N1 influenza A virus infection was detected in Mexico, with a rapid spread across many countries, resulting in pandemic.[2] This infection was associated with increased morbidity and mortality among children and younger adults compared with the usual seasonal influenza virus strains.[3,4]

Influenza A virus possesses eight segmented genomes encoding 11 proteins. Based on variation

of surface glycoproteins, haemagglutinin (HA) and neuraminidase (NA), influenza A viruses are categorised into 18 HA (H1–H18) and 11 NA (N1–N11) subtypes. Influenza viruses have their ability to undergo rapid and consistent genetic and antigenic evolution due to point mutations in genome, especially HA and NA genes and reassortment of gene segments from intra and interspecies influenza viruses.[5] Consequently, there is emergence of novel variants with increased virulence and pathogenicity that escape the immune system of their hosts resulting in annual outbreaks, epidemics and occasional pandemics. The novel swine origin influenza virus A (H1N1) was responsible for the recent outbreaks and epidemics in various parts of the world which emerged as reassortment between swine influenza viruses of two distinct lineages and Eurasian avian like swine(triple reassortment).[1]

MATERIALS AND METHODS

Study site

The present study was carried out at Government Medical College and associated hospitals Srinagar, Department of Microbiology. Patients with symptoms of Influenza like illness (ILI) attending outpatient department of SMHS and chest diseases hospital as well as hospitalised cases in the month of February 2019, were recruited. The timing of study was selected based on the peak circulation of influenza in Srinagar. A case of ILI was defined as a person with sudden onset of fever >38°C and cough or sore throat in the absence of other diagnosis.

Patients and samples

Patients of all age groups were included in the study. Total 128 clinical specimens of nasopharyngeal and throat swabs (nasal swab/TS) were collected in viral transport medium from the enrolled patients and transported to the laboratory in cold condition (+4°C). Clinical history was recorded in a structured case investigation form, and a written informed consent was obtained from all the patients or guardians before collection of samples.

Sample processing and RNA extraction

The collected clinical specimens of nasopharyngeal and throat swabs were vortex mixed followed by centrifugation at 1000 g for 10 min. The supernatant of the specimens were aliquoted into two Eppendorf tubes each tube containing 1ml of sample and frozen at −80°C. Viral RNA was extracted from 1ml of the specimens using (Invitrogen RNA extraction kit) according to manufacturer's instruction with proper biosafety measures.

Molecular detection of Influenza viruses

The extracted RNA was subjected to real time reverse transcription polymerase chain reaction (RT-PCR) for detection of influenza virus (Type A), influenza A(H1N1) subtype utilising Taqman chemistry with three sets of primers and probes (Inf A, SWH1 and RNase P).The reactions were performed using Super Script III Platinum One step quantitative RT-PCR system with Rox (Invitrogen, USA) following manufacturer's instructions. The RT-PCR was carried out at 50°C for 15 min, 95°C for 2 min, followed by 40 cycles of amplification at 95°C for 15 s and 60°C for 30 s.5.

RESULTS

Out of total 46 influenza positive cases, majority 39% patients belonged to 41-60 years age group followed by 21-40 years (26%), 61-80years (19.5%), 0-20years (10%) and least fraction of patients 4.3% belonged to 81-100 years. 58.6% patients were males while 31.3% patients were females. [Table 1]

In our study, Hypertension was the chief predisposing factor 10.1% for influenza followed by diabetes mellitus 7.8%, hypertension and diabetes 7.0%, coronary heart disease and rheumatoid arthritis 4.6%, osteoporosis 3.1% and least common factors were Hypothyroid 2.3%, Peripheral vascular disease 1.56%, Diabetes and CHD, SLE 0.78%. [Table 2]

Out of total 128 patients, 46 patients were influenza positive. From these 46 influenza patients, 23.9% patients were vaccinated and 76% were non vaccinated. [Table 3]

Out of total 46 influenza positive cases, 78.2% patients were reported in IPD and 21.7% cases were reported in OPD. 17 cases of CAP were reported in IPD and 3 cases reported in OPD. [Table 4]

Out of total positive cases, 56.5% patients had severe acute respiratory infections and 43.4% patients had influenza like illness. [Table 5]

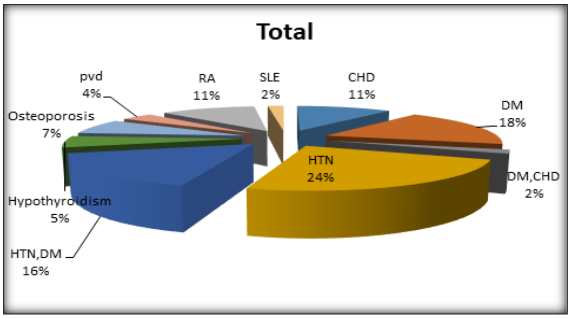

Figure 1: Distribution of predisposing factors in Influenza

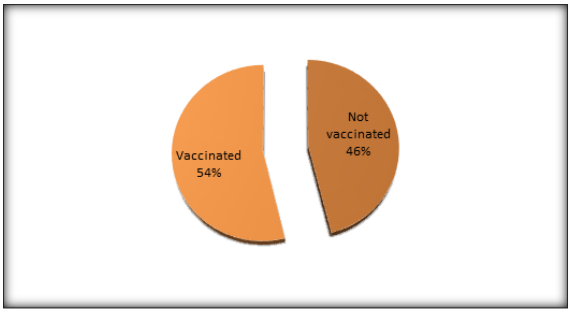

Figure 2: Vaccination status percentage wise in total population

Table 1: Age distribution in positive patients

		Number (n=46)	Percentage n=%
Age groups	0-20 years	5	10
	21-40 years	12	26
	41-60 years	18	39
	61-80 years	9	19.5
	81-100 years	2	4.3
Gender	Male	27	58.6
	female	19	41.3

Table 2: Distribution of predisposing factors in Influenza

Factors	Number (n=128)	Percent (%)
Hypertension	13	10.1
Diabetes mellitus	10	7.8
Hypertension and Diabetes	9	7.0
Coronary heart disease	6	4.6
Rheumatoid arthritis	6	4.6
Hypothyroid	3	2.3
Peripheral vascular disease	2	1.56
Diabetes and CHD	1	0.78
Osteoporosis	4	3.1
SLE	1	0.78

Table 3: Vaccination status in positive patients (n=46)

Total no of patients	128
Influenza positive cases	46
Vaccinated (n=46)	11(23.9)%
Non vaccinated (n=46)	35(76.0)%

Table 4: IPD and OPD patients among positive cases and distribution of CAP cases

Total cases (n=46)	IPD	OPD
	36(78.2%)	10(21.7%)
CAP	17	3

Table 5: Distribution of ILI and SARI in positive cases

Total positive cases n=(46)	
ILI	20(43.4%)
SARI	26(56.5%)

DISCUSSION

In February 2019, we documented a recrudescent epidemic of A/H1N1 in the temperate region of Kashmir during the winter. Frequent hospitalizations and a few fatalities were linked to this resurgent A/H1N1. A/H1N1 has also been reported to circulate in other regions of India during the winter of 2019. The data from the past three years from this temperate region of India exhibits discrete surges of influenza during the winter season, which are similar to those observed in temperate regions of the northern hemisphere, from December to March. The timing of influenza circulation in the United States and most European countries of the Northern Hemisphere is comparable to that of the winter peak in Srinagar. In the winter of 2019, Influenza A/H1N1 reemerged in Kashmir, resulting in severe illness that necessitated hospitalizations and fatalities.

In our study Out of total 128 patients, 46 patients (35.9%) were influenza positive. The positive cases reported in the study of Malhotra et al were 34.11%. These results were comparable to our study. The percent of positive cases in the present study were higher than the studies of Choudhary A et al,[6] 22%, chowell G et al,[7] 23.3% and singh M et al,[8] 21.1%. Due to peak winter season at time of study, more positive cases were observed.

Out of total 46 influenza positive cases, majority 39% patients belonged to 41-60 years age group followed by 21-40 years (26%), 61-80years (19.5%), 0-20years (10%) and least fraction of patients 4.3% belonged to 81-100 years. Pandita AK et al,[9] observed 41.1% patients belonged to age group 41-60 years. The results were consistent with the results of our study. Sidhu et al. have also reported a maximum positivity rate of 37.5% for the H1N1 influenza virus in the 40–55 age group.3 pandita Middle age people were most commonly affected population in the present study.

58.6% patients were males while 31.3% patients were females. Male predominance was reported in the various studies conducted by Malhotra B et al,[10] 51%, Pandita AK et al,[9] 60.9% and Prakash G et al,[11] 56.6%. This could be attributed to the fact that males have a greater amount of contact and exposure to the infection than females in most regions of India, as a result of the higher number of males labouring outside.

This study also confirms the well-established fact that a variety of co-morbidities can substantially exacerbate the disease trajectory. In our study,

Hypertension was the chief predisposing factor 10.1% for influenza followed by diabetes mellitus 7.8%, hypertension and diabetes 7.0%, coronary heart disease and rheumatoid arthritis 4.6%, osteoporosis 3.1% and least common factors were Hypothyroid 2.3%, Peripheral vascular disease 1.56%, Diabetes and CHD, SLE 0.78%. Dwibedi B et al,[12] reported hypertension in 4.4% patients while Pandita AK et al,[9] found hypertension in 29% patients. Prasad S et al,[13] reported equal number hypertension and diabetes cases in their study. Chudasama RK et al,[14] also commented on the fact that diabetes and hypertension were the most prevalent risk factors in India, while bronchial asthma and COPD were the most prevalent risk factors in the United States. Patients with co-morbidities are at an elevated risk of experiencing a suboptimal clinical outcome. Variations in outcomes have been documented across numerous investigations.

It was hypothesised that the H1N1 component, a sub-type of the virus protein hemagglutinin, in both swine flu and human flu, was derived from a common ancestor H1 that circulated in humans and evolved continuously during the 1918 and 1957 influenza pandemics. Subsequently, H1 was rendered inactive and was succeeded by other subtypes of hemagglutinin, including H3. In 1977, H1 reemerged in humans and has remained a prevalent subtype of human flu ever since. Despite the fact that H1 has undergone substantial evolution in humans from 1977 to the present, the H1N1 has undergone minimal evolution in swine. The 1918 and 1930 versions of H1 have been strikingly similar to the swine flu H1. Therefore, it is presumed that the immune systems of the majority of individuals born before 1957 who were exposed to human H1 influenza produce antibodies to the old H1 strain. Old H1 has not been observed in humans in many years, and as a result, younger individuals do not possess antibodies that would render them immune to the old H1 virus, which is highly similar to the 2009 H1 swine flu.[15] In our study, From the 46 influenza positive patients, 23.9% patients were vaccinated and 76% were non vaccinated. 78.2% patients were reported in IPD and 21.7% cases were reported in OPD. 17 cases of CAP were reported in IPD and 3 cases reported in OPD. We cannot anticipate that the influenza vaccine will prevent all cases of influenza, as the immune response is contingent upon age, underlying diseases, and immunosuppression.

In the present study, out of total positive cases, 56.5% patients had severe acute respiratory infections and 43.4% patients had influenza like illness. Young and healthy individuals were affected by severe respiratory failure, the most frequently reported cause of mortality associated with the H1N1 pandemic, according to a study conducted by Jagannatha Rao SR et al.[15]

A recent article by Murhekar M et al,[16] on the influenza A (H1N1) pdm09 outbreak in India suggested that the virus's virulence is not significantly impacted by any genetic changes. Our results from the current study also indicate that the clinical profile has remained consistent throughout the pandemic. Vaccination and health education are promising strategies for averting future epidemics. Vaccination should not be limited to patients in the high-risk group, despite the fact that they are certain candidates. It is also recommended that healthcare personnel and individuals who come into direct contact with infected individuals receive vaccinations.

CONCLUSION

Despite the fact that the H1N1 pandemic has concluded, epidemics serve as a perpetual reminder of the underlying threat. The sole method of minimizing the disease progression and associated mortality appears to be vaccination, early recognition of the disease, and prompt initiation of treatment. Patients with risk factors necessitate additional monitoring due to the unpredictable nature of their clinical course.

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