

Emergence of swine flu in Andhra Pradesh: Facts and future

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Abstract Swine flu is a common term representing the respiratory viral infections caused by influenza A virus strain H1N1. This disease was noticed for the first time in Mexico during early 2009, spread worldwide very soon and took nearly 4000 lives. It is observed that this infection is due to an evolved virulent version of previously existing H1N1. The first report of this infection was noticed in a traveler from USA to India at the Hyderabad international airport. Later, because of its highly contagious and fast-spreading nature through air, many people reported to have the infection throughout the country. In Andhra Pradesh, there were 735 officially confirmed cases of which 44 died. These cases were not only from Hyderabad which is the state capital having frequent travelers from abroad but are also reported from different parts of the state. The incidence and mortality rate is less in Andhra Pradesh compared to some of the other Indian states. This raises a question whether the type of the strain is different or genetic features of the population is playing the role in reducing the severity of the disease. In this review we have discussed about the occurrence, spread and mortality of the current H1N1 pandemic. We have also discussed about the current status of research on H1N1 and efforts in the state of Andhra Pradesh.

Keywords Swine flu · H1N1 · Andhra Pradesh · Influenza

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Introduction

Influenza viruses are a group of viruses causing mainly respiratory tract infections which belongs to the family Orthomyxoviridae. There are three genera of influenza viruses namely, influenza A viruses of which the natural hosts are birds and occasionally causes devastating diseases in humans; influenza B which exclusively infects humans and influenza C which infects humans, dogs and pigs. The genome of these viruses is a single-stranded negative sense RNA which is divided into 8 segments coding for 11 different functional proteins which includes polymerase complex proteins such as PA, PB1, PB1-F2, PB2 and NP; surface glycoproteins such as hemagglutinin (HA) and neuraminidase (NA); matrix proteins M1 and M2; and non-structural proteins NS1 and NS2. Although the principal hosts of these influenza viruses are birds, influenza virus A causes infections to humans, swine and birds. H1N1 was first reported in 1918 which caused enormous mortality [1]. Viruses having segmented genome, possesses high tendency of undergoing re-assortment when a cell happen to be infected by more than a single virus and hence leads to evolution of a new influenza A virus in a particular host [2]. In addition, some RNA viruses undergo frequent mutations during their replication since the RNA dependent RNA polymerase possess less proof reading activity. These situations demand the development of a new vaccine for each strain especially in cases like common flu which shows frequent seasonal variations. Swine is susceptible for avian, swine and human influenza A viruses and contributes as a vessel for mixing all the strains enabling the re-assortment of genes [3]. Evolution of H1N1 in 1918, H2N2 in 1957 and H3N2 in 1968 are the quotable examples of such re-assortment process where HA and NA sequences are majorly involved, however sometimes sequences from PB1 are also involved [4].

The current influenza A virus strain H1N1 infection is being commonly termed as swine flu and is considered a

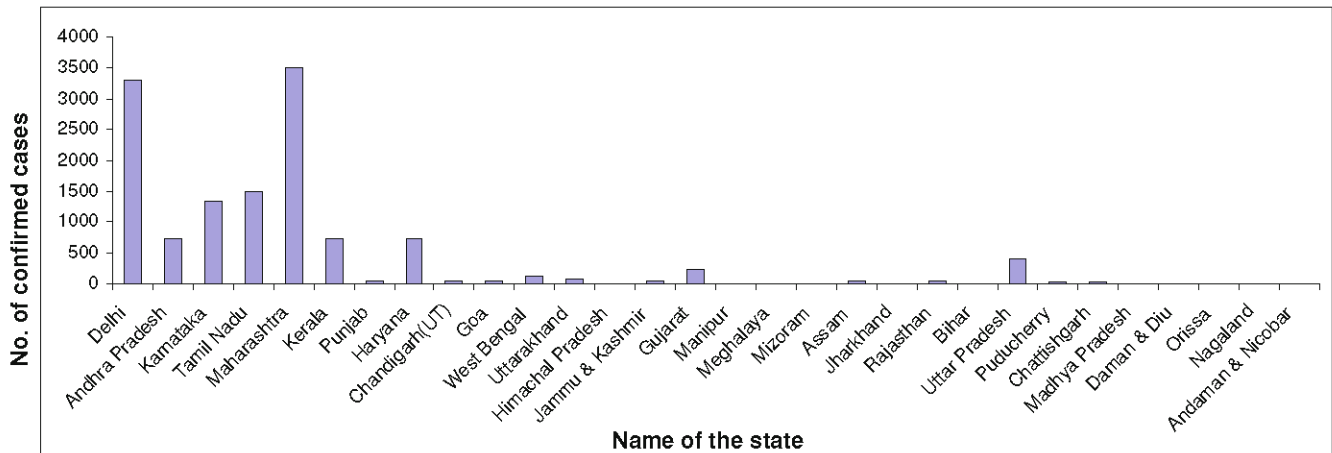


Fig. 1 Bar diagram displaying lab-confirmed cases of 2009 H1N1 pandemic in India

novel infection. This H1N1 which is responsible for the recent pandemic was first noticed and characterized in Mexico and USA during the early period of 2009 which was thereafter reported in many countries. This disease is contagious which can spread from human to human through coughing or sneezing of infected people. The symptoms resemble the seasonal human flu and include fever, cough, sore throat, runny nose, body aches, head ache, chills and fatigue. Severe illness which includes pneumonia, failure of breathing are the remarkable symptoms of the current pandemic swine flu. The reports indicated that the 1918 H1N1 pandemic caused the death of 20–50 million people worldwide and current H1N1 pandemic is feared of resulting into the similar effect [5]. The World Health

Organization (WHO) announced the level 6 precaution, the highest precaution level, for the 2009 influenza pandemic [6]. It was discovered that the new H1N1 strain evolved as a result of strong purifying selection, widely different from the strains that are reported during recent past few years, but surprisingly it is closely related to the ancient strain reported in 1918 [7]. The current H1N1 pandemic is novel, highly virulent and evolved through double reassortment involving parts of virus genomes from swine, avian and human influenza A viruses. There is no vaccine available at present for this new strain and it may take considerable time for development. Presently there are certain drugs in practice such as Tamiflu, Oseltamivir (a modified version of Tamiflu), Natflu and Starflu. But it is

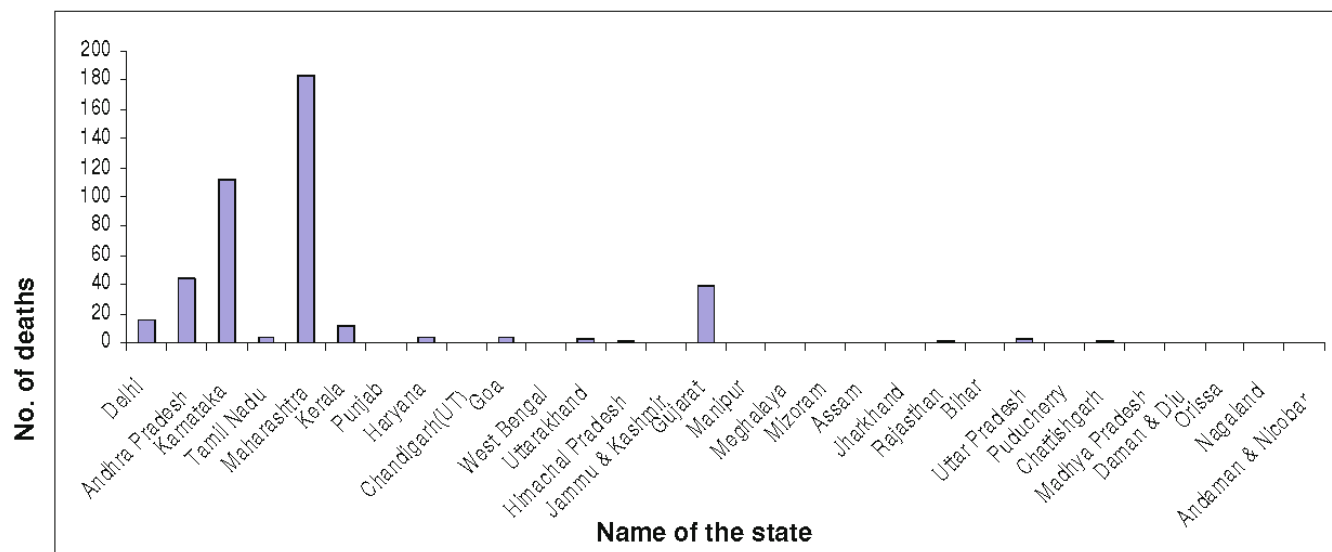


Fig. 2 Bar diagram displaying the deaths of lab-confirmed cases of 2009 H1N1 pandemic in India

known that symptoms associated with swine flu are very similar to the common flu and hence it is not advisable to use the above drugs without prescription to avoid drug-oriented health complications.

India and Andhra Pradesh

In India, the first swine flu case was noticed at the Hyderabad international air port on 13 May 2009 when a person arrived from the US [8]. The transmission of the disease progressed at very high rate and more number of cases were reported across all the states of the country with the first death case recorded in Pune, Maharashtra [9]. As per the official records of India (as on 21 October 2009) there were 13,030 H1N1 positive cases where approximately 427 people died [10, 11]. The state Maharashtra reported large number of disease confirmed cases (3515), in which the numbers of death cases (183) were also high. On the other hand, in Andhra Pradesh 735 cases were confirmed among which 44 people died [10]. Both the incidence and mortality rate were less compared to some of the states (Figs. 1 and 2). Although the first swine flu case was recorded in Andhra Pradesh, the rate of incidence and mortality were less compared to that in Maharashtra and Karnataka. The mortality rate is very low in some states like Delhi, Tamil Nadu, Uttar Pradesh and Haryana in comparison to the incidence. This indicates that either the type of the strain or the immunological response of the diseased people in this area is playing crucial role in reducing the severity of the disease.

Since the first H1N1 positive case was identified at Hyderabad, it is believed that the H1N1 strain in Andhra Pradesh is similar to the strain reported in USA. But there is not much evidence to exclude the presence of H1N1 infection before that as it was the beginning of the pandemic worldwide and there was no specific diagnostic tool available in the state at that moment. It may be possible that clinicians considered swine flu as a regular common flu due to the similarity in their symptoms. It was reported that the influenza virus strains are much more closely related to the European strains rather than American strains or else these lineages reported to be originated and present only in Asia [12]. Hence the possibility of emergence of novel H1N1 variants in the state may not be ruled out. This is evident from the fact that the H1N1 positive reports and even deaths have occurred in different parts of the state for which there were no travelers from abroad. This was evidenced by the reports indicating that the disease presence and the resulting deaths from other parts of the state like Vishakapatnam, Tirupati, Chittoor and their surrounding areas. This information is available only with local media and is not being recorded as scientific information which would help

for proper analysis. The problem for diagnosing the new diseases in Andhra Pradesh is due to limited infrastructure for scientific evaluation. State capital Hyderabad is actively associated with production of generic drugs such as Oseltamivir for controlling the current pandemic influenza. Although the drugs are available for H1N1 treatment but prescription is recommended only after the confirmation of the disease, since the consumption of these drugs leads to health complications and drug resistance.

Defining the H1N1 strains is mainly based on the nucleotide sequence of the virus genome especially the sequences of surface proteins hemagglutinin and neuraminidase and some times the polymerase protein PB1. Several hundreds of sequences of 2009 pandemic H1N1 are being deposited from worldwide in the NCBI Gene Bank database [13]. But there is no single report from Andhra Pradesh. Hence it is very difficult to confirm the causative agent of current pandemic whether it is similar to the reported ones from elsewhere or different. There is an urgent need for the establishment of the infrastructure at state level for characterization of the viral isolates in this region, which will form an input for developing a vaccine or a specific drug. This issue has been discussed in the discussion meetings on avian influenza hosted by University of Hyderabad in November 2008.

Some of the questions need to be addressed are like, the H1N1 strain is similar to one reported elsewhere in the world, any resistant variants in circulation towards existing drugs, why the incidence and mortality rate is less in Andhra Pradesh in comparison to some of the Indian states? Is type of the strain or genetic features of the host is playing role in reducing the devastating nature of the virus?

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