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Prediction of Influenza Transmission in Mass Gathering: A Systematic Review

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Abstract

The unique characteristics of Hajj gatherings over other mass gatherings include the yearly large crowd of 3 million pilgrims who come from more than 180 countries and usually stay for several days in Mecca, Saudi Arabia. Despite the successful efforts of the authorities in Saudi Arabia in the management of this huge crowd of Hajj pilgrims, the epidemics have been an emerging concern. The presence of early warning system that can predict the occurrence of epidemics will guide the preparedness plans and strengthen the ability to contain the problem. The modeling is a powerful tool for prediction of the epidemic dissemination among Hajj pilgrims, which can guide and improve the preventive interventions. The main purpose of this review is to evaluate influenza prediction models which available in the literature. The epidemiological parameters about influenza infectivity were collected from literature. The epidemiological parameters about susceptibility and immunity of the Hajj pilgrims were obtained from health authorities. The parameters of contact rate and patterns were collected by previous surveys. The movement of the Hajj crowd in term of time and place were simulated using crowd modelling techniques. According to the distance allows the droplet transmission of influenza, a contact is defined as the surrounding person at the distance of 2 m of the patient. It were divided according to country of origin and age of pilgrims, since those factors are important in determining contact pattern of pilgrims. Based on the previous parameters, researchers can predict the transmission of influenza virus.

Keywords: Influenza, Epidemic, Modeling, Gathering, Transmission, Hajj.

Introduction

The crowd or mass gathering (MG) is defined as the gathering of 1000 or more people, while other definition requires 25000 attendee to consider it a MG [1]. The risk of transmission of respiratory infections among the MG depends on factors such as density of the crowd, period of stay, susceptibility of the crowd, infectivity of the pathogen, in addition to preparedness and containment capacities of the health facilities [2]. The unique characteristics of Hajj gatherings over other MGs include the yearly large crowd of 3 million pilgrims who come from more than 180 countries and usually stay for several days in Mecca, Saudi Arabia [3].

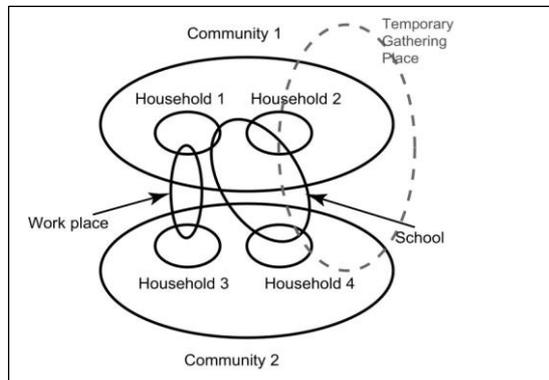
Many respiratory outbreaks have been found responsible for 14 of 21 events affected attendants of MGs [4]. Recently reported respiratory outbreaks that have been transmitted through MGs include measles outbreak involved German attendants of religious ceremony in France [5]. In addition, mumps outbreak that affected youth gathering in Australia, and an outbreak reported in a village ceremony in Spain [6, 7]. Influenza outbreaks were reported in many MGs such as Winter Olympics 2002 [8], Youth Day in 2008 [9], and at the Hajj pilgrimage 2009 [10]. The mass gathering events are the perfect settings for outbreak dissemination because of the huge number of people and close proximity. The transmission of disease depends on the characteristics of the contact networks between individuals, which can be assessed by surveys, or more recently by electronic devices [11, 12].

The mixing of the infectious and susceptible populations with the close proximity during pilgrimages can lead to rapid transmission of air-borne and droplets-borne respiratory infections. This rapid dissemination may lead in the favorable conditions to epidemics or pandemics, such as a pandemic of influenza A H1N1 in 2009 at the Hajj, which characterized by high fatality rate in the Hajj pilgrims [10]. Modeling of disease transmission simply means representing the dynamics of disease transmission in a form of mathematical equations. Generally, the recent

mathematical modeling of disease transmission can be conducted in two approaches [13]. First, by assuming homogenous mixing models (used since 1927), which is the simple model of (SIR) that was described by Kermack and McKendrick in 1927. It consists of three compartments: susceptible (S), infected (I), recovered (R), which assumes the homogenous mixing of the population [14]. Second, by using agent-based modeling (ABM) that assumes a heterogeneous mixing that became more popular during the past two decades. It incorporated heterogeneity in host contacts characteristics that significantly shape diseases dynamics at individual-level. It accounts for social contact networks, cycle of movements and demographical structure of the targeted population [15]. The main objective of crowd management is to bring people together and at the same time to keep them separated in both spatial and temporal dimensions. Agent-based models can incorporate the key features of crowd movements in addition to key parameters of epidemic dynamics [16]. The main purpose of this review is to evaluate influenza prediction models which available in the literature.

Methods

To obtain papers on the effectiveness of combination strategies, data for this review were identified by the authors through searches of the PubMed search engine for English language articles and articles translated into the English language. The authors used the following search terms to focus on modeling studies, and those which had a focus on pandemic preparedness and strategies -influenza and pandemic and (preparedness or strateg* or model*); influenza and modeling or modelling. The search included all published articles listed on PubMed from 1990 to September 2019 there were few articles on influenza pandemic planning or modeling before this period. Abstracts were reviewed where available to determine if a study met the inclusion criteria and the full manuscript was obtained for further scrutiny. Snowball searches by hand were performed on the reference lists of articles meeting the inclusion criteria to find additional studies. The inclusion criteria were



primary mathematical modeling papers that compared and reported the quantitative effectiveness of combination strategies (two or more strategies used together) versus individual strategies for human pandemic influenza. Mathematical modeling papers were those which used quantitative predictive methods to determine the likely impact of strategies, and had descriptions of these methods which could be reproduced or verified. Mathematical modeling articles that described the effectiveness of multiple singular strategies but did not analyze the quantitative effect of combination strategies were excluded. Articles that referred to general pandemic preparedness without quantitative evidence, or provided only qualitative discussion were also excluded. Reviews without primary data, articles in abstracts without full publication, and unpublished studies were excluded as their methodology and results could not be verified.

Results and discussion

The search yielded a total of 920 papers including overlaps. Of these, 72 used mathematical modeling techniques and on closer review, 60 were excluded based on the exclusion criteria listed in Methods. The remaining 12 studies were included for analysis, together with one additional study identified from the snowball searches. Recent studies have showed more accurate results of diseases modeling that uses ABM with contact network modeling [17, 18]. Other important parameters in epidemic modeling are the demographic characteristics of this crowd include age, sex, immunity, and country of origin [15, 19]. Another potential factor is the initial number of source cases

and their contact pattern and points of entrance [20]. Studies have found the increase in epidemic size associated with increase in number of initial cases [2]. Agent-based models that incorporating detailed data on individual level have been used to model dissemination of rapidly transmitted infections such influenza [21-24]. The modeling of epidemic spread in MGs should not ignore the interaction with the local community where the event is scheduled, thus studies have highlighted the use of large-scale models with network of surrounded community [2]. These large scales models can incorporate the air-travelling data with many seasonal and immunization parameters to predicted the international transmission of emergent pandemics [25-27]. They predicted the influenza pandemic of 2009 depend on simulation results. Several modeling studies found that reduction of air-traffic could delay the progression of influenza pandemic [28, 29] . These large-scale ABM have become an important tool to understand the dynamics of epidemic transmission in a city, country and the globe. The health authorities in KSA recommended use of preventive measures of respiratory infection such as use of facemasks and influenza vaccine [30]. Despite the successful efforts of the authorities in Saudi Arabia in the management of this huge crowd of Hajj and Umrah pilgrims, the epidemics have been an emerging concern. The presence of early warning system that can predict the occurrence of epidemics will guide the preparedness plans and strengthen the ability to contain the problem. The modeling is a powerful tool for prediction of the epidemics dissemination among Hajj pilgrims, which can guide and improve the preventive interventions.

The epidemic forecasting will provide early warning system for protection of pilgrims and population of Saudi Arabia from contiguous dangerous epidemics and pandemics. It can build an early warning system for an epidemic transmission among the Hajj pilgrims making health authorities proactive rather than only responsive for any epidemic threats. In the last two decades, the modeling of infectious diseases has been developed rapidly, which is mainly attributed to the great improvement of the computation capacity associated with the recent advancement in the computer industry [31]. Agent based modeling especially requires high computational capacity,

which sometimes needs Cyber-systems to run the simulation of these models [32]. Many studies have focused on the modeling of infectious diseases conducted in virtual environments based on empirical data that collected from surveys and censuses [33-36]. Del Valle et al. have conducted a simulation study supported by the data obtained from national surveys and censuses in the United States [33]. A wealth of data about contact patterns, population movement cycles, and social interactions were introduced into the simulation software called EpiSimS. This software can simulate the movement and social behavior of an individual interacting in the virtual environment. Activities for each individual were determined according to data collected by household surveys, and then locations were linked to each activity. For example, studying were assigned to the available schools and universities, shopping activity was assigned to the surrounded commercial centers and supermarkets. Similarly, recreational activities were assigned to the available restaurants bars, and cinemas.

The researchers concluded that contact patterns and social interactions had an essential role in the dissemination of infectious diseases. The infection usually occurs by the contact between infectious and susceptible populations. The recommended use of the empirical data to model the transmission of infectious diseases and it will result in predictions that are more accurate [33]. In another study conducted by Bansal et al., they compared the homogeneous mixing of the populations versus the heterogeneous mixing. In the heterogeneous mixing, they incorporated the contact patterns in the simulation process based on the concepts of social networking. They found similar results to that found by Del Valle et al. where the simulations based in the empirical data would result in predictions that are more realistic. They also found that homogenous mixing simulations are suitable only for homogenous populations, which interact in semi-random pattern [34]. In influenza H1N1 pandemic, that started in primary schools and then disseminate to the local community in 2009, the type of contact pattern showed a significant effect on the disease transmission. Cauchemez et al. found that an assortative mixing has affected the influenza transmission, where males were more likely to infect other males than females. They found that school closure, that was

applied later to control the epidemic, had no significant effect on the influenza transmission. This was attributed to the household and neighborhood spread of the infection through the playing activity of schoolchildren [35]. These findings reflected the importance of understanding the role of contact patterns in the dissemination of infectious diseases. In another simulation study that conducted by a university student called Laura. She has asked a community members (e.g., moms with kids, kids at school, parents who work outside the home, the elderly) a series of questions: "what are your groups, how big are they, how often do you go to them and for how long, and how many people do you interact with there." According to these information, she built a model of a virtual community consists of 10,000 persons. She run the simulation of influenza transmission and then tested the effect of influenza vaccination in this transmission. She found that immunization of 80% of school-aged students had the same effect in diseases transmission as the immunization of the whole community [36].

The incorporating of any epidemiological parameter during model building was found important to improve the accuracy of the modeling process. Helen et al, have conducted a mathematical analysis, which demonstrated the unfavorable effect of not incorporating incubation period or population growth on the model accuracy [37]. Wallinga et al. have demonstrated the importance of incorporating age-related parameters in the modeling of infectious respiratory diseases [38]. In addition, Mossong et al. have built a model of more than 100,000 people based on the contact data collected from European populations. The findings showed that, during the first wave of the epidemic, the children aged 5-19 years old were the most affected age group by the circulating infection [19].

During MGs activities, the contact patterns differ from that in the household, schools or workplaces. Hu et al. found that random contact of people at MGs could, at MGs, increase the contact rate but it would decrease in the high-density MGs [39]. Similarly, Chowell et al. highlighted the importance of estimating the mixing pattern of individuals during MGs and the development of initiative models that can mimic the

transmission dynamics of infectious diseases among the MGs population [2]. Although, the field of diseases modeling has developed rapidly in the last two decades, few studies have examined the modeling of diseases transmitted among attendants of MGs. This study will build an ABM model based on empirical data obtained from the Hajj pilgrims that simulates the spread of influenza epidemic.

Conclusions

Using new technology such as prediction modelling to forecast the transmission of influenza epidemics among Hajj pilgrims is very efficient. It can help in identification of the key parameters that effectively influence the size and speed of influenza epidemic. Prediction models can test the impact of the various preventive measures that could be applied to control of influenza transmission among the Hajj pilgrims. Evidence-based planning of preparedness and containment efforts, which control any epidemic threats transmitted by respiratory route, could be based on modelling results. The computer simulation is a powerful tool that can guide us to the most appropriate preventive measures. It can efficiently guide the efforts of preparedness and control of influenza epidemic.

Conflict of interests

The authors declared no conflict of interests.

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