

Contents lists available at [ScienceDirect](#)

Vaccine

journal homepage: [www.elsevier.com/locate/vaccine](http://www.elsevier.com/locate/vaccine)

## Influenza vaccination in preventing outbreaks in schools: A long-term ecological overview

Yang Pan<sup>a,b,c</sup>, Quanyi Wang<sup>a,b,c,\*</sup>, Peng Yang<sup>a,b,c,\*</sup>, Li Zhang<sup>a,b</sup>, Shuangsheng Wu<sup>a,b</sup>, Yi Zhang<sup>a,b</sup>, Ying Sun<sup>a,b</sup>, Wei Duan<sup>a,b</sup>, Chunna Ma<sup>a,b</sup>, Man Zhang<sup>a,b</sup>, Xingxing Zhang<sup>a,b</sup>, C. Raina MacIntyre<sup>d,e</sup>

<sup>a</sup> Institute for Infectious Disease and Endemic Disease Control, Beijing Center for Disease Prevention and Control (CDC), Beijing, China

<sup>b</sup> Research Centre for Preventive Medicine of Beijing, Beijing, China

<sup>c</sup> Capital Medical University School of Public Health, Beijing, China

<sup>d</sup> School of Public Health and Community Medicine, University of New South Wales, Sydney, Australia

<sup>e</sup> College of Health Solutions and College of Public Affairs and Community Solutions, Arizona State University, USA

### ARTICLE INFO

#### Article history:

Received 28 August 2017

Received in revised form 27 October 2017

Accepted 28 October 2017

Available online xxx

#### Keywords:

Influenza  
Outbreak  
Vaccine  
Schools  
Hemagglutination

### ABSTRACT

Influenza vaccination is the most effective way to reduce the incidence of influenza infections. However, the role of influenza vaccination, such as school-based influenza vaccination, in preventing the influenza outbreaks in schools remains unclear now. In this study, a total of 286 school febrile outbreaks involving 6863 cases in the Beijing area from September 1, 2006 to March 31, 2017 were analyzed. We also tested 294 circulating strains isolated in Beijing during the same period and compared with that of vaccine strains identified every influenza season. The virological match/mismatch between vaccine strains and circulating strains, and the coverage of vaccination in schools were analyzed against outbreaks during the 11 years. It showed that over 80% school febrile outbreaks were caused by influenza A/B virus, the most frequent being A(H3N2) virus (53.25%), followed by A(H1N1)pdm09 virus (25.11%) and B virus (21.64%). More importantly, low vaccine coverage (in 2006–2007 influenza season) and vaccine mismatch (in 2014–2015 and 2015–2016 influenza season) were associated with an increased number of influenza school outbreaks. High vaccination coverage with a matched vaccine can significantly reduce influenza outbreaks in schools (OR: 0.111,  $p < .001$ ). We have shown the effectiveness of school-based influenza vaccination in preventing outbreaks using trivalent inactivated influenza vaccine in schools. Thus the school-based vaccine policy should be paid more attention in China and other countries worldwide.

© 2017 Elsevier Ltd. All rights reserved.

### 1. Introduction

As one of the most common seasonal respiratory infectious disease, influenza causes a significant health burden around the world. Among all susceptible populations, school children may face the greatest risk of influenza virus infection; schools provide opportunities for close contact between children, which accelerates the spread of influenza [1,2]. School-age children play a significant role in the transmission of influenza, so that reducing infection in school-age children should directly benefit the wider community [2,3].

Influenza vaccination is the most effective way to reduce the incidence of influenza infections. World Health Organization

(WHO) recommends annual seasonal influenza vaccination for pregnant women, children aged six to 59 months, the elderly, persons with specific chronic medical conditions, and health-care workers [4]. Also, many countries recommend influenza vaccination among school-aged children as a valuable extension of existing influenza vaccination programs [5]. Based on this evidence, Beijing municipal government launched a school-based influenza vaccination campaign in September 2007, providing seasonal trivalent inactivated influenza vaccine (TIV) free-of-charge for elementary, middle school and high school students aged 6–18 years.

Some previous studies have evaluated the effectiveness of influenza vaccine in preventing influenza illness among school-age children [6,7]. However, the role of influenza vaccination in preventing influenza outbreaks in schools remains unclear, with limited previous studies. Here we report an eleven-year retrospective study, investigating the relationship between influenza vaccination and influenza outbreaks in schools in Beijing, China.

\* Corresponding authors at: Institute for Infectious Disease and Endemic Disease Control, Beijing Center for Disease Prevention and Control (CDC), Beijing, China.

E-mail addresses: [bjcdcxm@126.com](mailto:bjcdcxm@126.com) (Q. Wang), [yangpengcdc@163.com](mailto:yangpengcdc@163.com) (P. Yang).

## 2. Method

### 2.1. Study design and subjects

This study was carried out to investigate school outbreaks of influenza in elementary, middle and high schools in the Beijing area from September 1, 2006 to April 30, 2017. All elementary and middle schools in Beijing area were enrolled in this study. Surveillance for febrile illnesses of any etiology was conducted routinely by Beijing Center for Disease Prevention and Control during this period, and these surveillance data were used. Definitions used in this surveillance were as follows: (1) Febrile illnesses of any etiology: cases with measured or self-reported temperature  $\geq 37.5$  °C; (2) Febrile outbreak: 10 or more febrile illnesses within a single school classroom within 2 days. The school-based influenza vaccination program was usually conducted from 15 October to 30 November every year in Beijing area. Since typically 14 days are needed to show the protective effectiveness after vaccination [8], we examined outbreaks that occurred at least 14 days following the start of vaccination each year, and analyzed the possible association between outbreaks, vaccination rate and vaccine match. The pandemic in the 2009–2010 influenza season was not included in this analysis, due to it being a pandemic A(H1N1) pdm09 virus, and followed by widespread vaccination with monovalent PANFLU.1 vaccine that year. Ethical approval was obtained from the institutional review board and human research ethics committee of the Beijing Center for Disease Prevention and Control.

### 2.2. Information and sample collection

All febrile outbreaks in schools were reported to local CDC by school doctors and field investigation was accomplished within 2 h to 1 day. Priority was given to students who were currently sick and attending school. The epidemiological information for cases involved in school febrile outbreaks was collected through face-to-face interviews with school doctors and telephone interviews with parents using a standardized questionnaire. School information included the type of school (elementary, middle or high schools), locale, and the number of students involved in the outbreaks. At the same time, oral pharyngeal swabs were collected from up to 10 symptomatic cases from each outbreak when the outbreak was reported. The distribution records of influenza vaccine doses in schools from 2006 to 2017 were used to obtain the coverage of TIV. The virological surveillance for influenza was used to calculate the constituent ratio of each subtype/lineage every influenza season, and then determine the dominant circulating subtype/lineage in Beijing area. The numbers of schools in each year were extracted from Beijing Statistical Yearbook (<http://www.bjstats.gov.cn/tjsj/>).

### 2.3. Influenza identification

All specimens were tested for influenza virus by real-time RT-PCR according to the protocol of the Chinese National Influenza Centre (CNIC) (Standard Operating Procedure in CNIC 2007 edition ([http://ivdc.chinacdc.cn/cnic/zyzx/sysssc/201605/t20160520\\_129703.htm](http://ivdc.chinacdc.cn/cnic/zyzx/sysssc/201605/t20160520_129703.htm)) was used before 2012 and a new technical guidelines for influenza surveillance in China [9] was used after 2012). Positive specimens were typed and subtyped, then cultured in Madin-Darby canine kidney (MDCK) cells for 4–5 days to isolate the influenza virus. Hemagglutination test (HA) and Hemagglutination Inhibition test (HI) were then performed to verify the subtype or lineages of the strains. An outbreak was defined as influenza

outbreak if more than half of testing samples were positive in influenza A/B nucleic acid testing (NAT).

### 2.4. Viral gene sequencing

In order to determine the genetic distance between circulating strains and vaccine strains, 53 strains isolated in Beijing from 2009–2010 influenza to 2015–2016 influenza season were randomly selected and sequenced. These strains include 12 influenza A(H1N1) pdm09 strains (2, 2, 1, 1 and 6 strains in 2009–2010, 2010–2011, 2011–2012, 2013–2014 and 2015–2016 influenza season, respectively), 29 influenza A(H3N2) strains (3, 10, 11 and 5 strains in 2012–2013, 2013–2014, 2014–2015, and 2015–2016 influenza season, respectively) and 12 influenza B strains (5 and 7 strains in 2014–2015 and 2015–2016 influenza season, respectively). Viral RNA was extracted from those strains using QIAmp Viral Mini Kit (Qiagen, Hilden, Germany) following the manufacturer's instruction. Then reverse transcription and amplification of HA gene were carried out as described previously [10]. PCR products were sequenced by ABI Prism 3130xl automated sequencer (Applied Biosystems, Foster City, USA) and then assembled using MEGA software (ver. 6.0.4) with manual adjustment [11]. Moreover, 29 influenza A(H1N1), 50 influenza A(H1N1) pdm09, 79 influenza A(H3N2) and 83 influenza B strains isolated in northern and eastern China from 2006–2007 to 2016–2017 influenza season were randomly selected from all available records in Global Initiative on Sharing All Influenza Data (GISAID) database, as supplements in this study. The access number of all strains used in this study was listed in [Supplement material 1](#).

### 2.5. Similarity analysis for circulating strains and vaccine strains

All 294 HA gene sequences of influenza A/B virus collected in this study were aligned by MEGA, and the phylogenetic tree, including the circulating strains and vaccine strains of A(H1N1), A(H1N1) pdm09, A(H3N2), B(Victoria) and B(Yamagata), was built each year. Possible component subtype/lineage/clade-mismatch with vaccine strains was obtained from every phylogenetic tree. A season's mismatch was defined as component subtype/lineage/clade-mismatch with vaccine strains occurred in more than 50% circulating strains in Beijing area.

### 2.6. Statistical analysis

Data was analyzed using SPSS 20.0 (SataCorp, College Station, USA) and Prism 5 software (GraphPad, La Jolla, USA). Logistic regression analyses were used to identify factors predictive of school outbreaks. The high coverage of vaccination was defined as mean coverage higher than 50% in all schools. All statistical tests were 2-sided and statistical significance was defined as  $p < .05$ .

## 3. Results

From September 1, 2006 to March 31, 2017, a total of 286 school febrile outbreaks of any etiology involving 6863 cases were identified in Beijing area. Among them, most outbreaks were reported in elementary schools (151 outbreaks, 52.80%), followed by those in middle schools (135 outbreaks, 47.20%, [Table 1](#)). The median number of cases per outbreak was 17, with a range from 10 to 222.

Oral pharyngeal swab samples were collected from up to 10 symptomatic cases from each febrile outbreak. 80.77% (231 outbreaks) were caused by influenza A/B virus, including influenza A (H1N1) pdm09 (58 outbreaks, 25.11%), A(H3N2) (123 outbreaks, 53.25%), B(Victoria) (46 outbreaks, 19.91%) and B(Yamagata) (4

Download English Version:

<https://daneshyari.com/en/article/8486436>

Download Persian Version:

<https://daneshyari.com/article/8486436>

[Daneshyari.com](https://daneshyari.com)