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Influenza Vaccine Effectiveness Against Medically Attended Outpatients Illness, United States, 2023–2024 Season

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Abstract

Background. The 2023–2024 US influenza season was characterized by a predominance of A(H1N1)pdm09 virus circulation with cocirculation of A(H3N2) and B/Victoria viruses. We estimated vaccine effectiveness (VE) in the United States against mild-to-moderate medically attended influenza illness in the 2023–2024 season.

Methods. We enrolled outpatients aged ≥ 8 months with acute respiratory illness in 7 states. Respiratory specimens were tested for influenza type/subtype by reverse-transcriptase polymerase chain reaction. Influenza VE was estimated with a test-negative design comparing odds of testing positive for influenza among vaccinated versus unvaccinated participants. We estimated VE by virus subtype/lineage and A(H1N1)pdm09 genetic subclades.

Results. Among 6629 enrolled patients, 1780 (27%) tested positive for influenza, including 806 with A(H1N1)pdm09, 567 with B/Victoria, and 328 with A(H3N2). VE against any influenza illness was 44% (95% confidence interval, 36%–51%); 29% (15%–41%) against influenza A(H1N1)pdm09, 74% (65%–81%) against B/Victoria, and 30% (8%–47%) against A(H3N2). Statistically significant protection against any influenza was found for all age groups except adults aged 50–64 years. Lack of protection in this age group was specific to influenza A–associated illness. We observed differences in VE by birth cohort and A(H1N1)pdm09 virus genetic subclade.

Conclusions. Vaccination reduced outpatient medically attended influenza overall by 44% and provided protection overall against circulating influenza A and B viruses. Serologic studies would help inform differences observed by age groups.

Keywords

influenza; vaccine effectiveness; vaccination; test-negative design; case control

Influenza vaccination is a proven safe and effective strategy for mitigating the burden of influenza-associated disease. In the United States, influenza vaccination continues to be recommended annually for all persons aged ≥ 6 months who do not have contraindications [1, 2]. US adults aged ≥ 65 years are preferentially recommended to receive a higher dose or adjuvanted vaccine. During the 2022–2023 US influenza season, vaccination was estimated to have prevented 5.9 million illnesses, 2.9 million medical visits, 64 000 hospitalizations, and 3600 deaths associated with influenza [3]. Despite the known benefits of influenza vaccination, coverage rates are far below the Healthy People 2030 target of achieving 70% coverage for all age groups [4, 5]. In the 2023–2024 influenza season, an estimated 45% of adults and 55% of children were vaccinated against influenza [6].

The 2023–2024 influenza season in the United States was characterized by a predominance of A(H1N1)pdm09 virus circulation with cocirculation of A(H3N2) and B/Victoria viruses

[7]. Three-quarters of sequenced A(H1N1)pdm09 viruses belonged to hemagglutinin clade 6B.1A.5a subclade 2a.1 (which includes the 2023–2024 vaccine reference strain), with the remaining quarter belonging to clade 6B.1A.5a subclade 2a. Cocirculation of 2 genetic subclades of the predominant A(H1N1)pdm09 virus provided the opportunity to investigate clade-specific protection. Midseason data through January 2023 from 4 US vaccine effectiveness (VE) platforms showed significant protection against outpatient and inpatient influenza illness [8]. Here we report updated VE for the 2023–2024 season against mild-to-moderate outpatient medically attended influenza overall by influenza A subtype, influenza B lineage, and age group.

METHODS

Study Population

The US Flu VE Network has been described elsewhere [9, 10]. In brief, the public health surveillance network enrolls participants aged ≥ 8 months with an acute respiratory illness ≤ 7 days in duration including new or worsening cough at sites in Arizona, Michigan, Missouri, Ohio, Pennsylvania, Texas, and Washington. Duke University, North Carolina, served as the Network's data coordinating institution. Enrollment began at each site based on local evidence of increasing influenza activity. Trained staff interviewed participants or their parent/guardian to obtain demographic and clinical information and inquired about receipt of current season influenza vaccination. Underlying chronic health conditions were defined as electronic health record (EHR) documentation within the previous year of medical encounters with *International Classification of Diseases, Tenth Revision* codes for high-risk conditions according to the Advisory Committee on Immunization Practices [1]. Enrollment dates ranged from 1 October 2023 to 30 April 2024 (Supplementary Table 1). The study protocol was reviewed by the US Centers for Disease Control and Prevention (CDC), determined to be public health surveillance, and conducted consistent with applicable federal law and CDC policy (45 CFR 46.102[1][2]).

Influenza Vaccination

Northern Hemisphere 2023–2024 quadrivalent influenza vaccines included 2 influenza A antigens and 2 influenza B antigens. Egg-based vaccines were recommended to include A/Victoria/4897/2022-like (H1N1pdm09-like genetic subclade 2a.1)m and cell culture–based (ccIIV4) or recombinant-based (RIV) vaccines were recommended to include A/Wisconsin.67/2022-like (H1N1pdm09-like genetic subclade 2a.1). Each of the 3 vaccine types were recommended to also include A/Darwin/9/2021-like (A/H3N2-like genetic clade 3C.2a1b.2a.2), B/Austria/1359417/2021-like (B/Victoria-like genetic clade V1A.3a.2), and B/Phuket/3073/2013-like (B/Yamagata genetic clade Y3) [11]. Participant influenza vaccination status was determined by combining data from EHRs, state immunization information systems, and plausible self-report. A plausible self-reported influenza vaccination was a dose reported by the participant (or parent/guardian of participant aged 9–17 years) that was received >14 days before illness onset and included a vaccination provider location. All participants were classified as vaccinated if they had received ≥ 1 dose of any licensed influenza vaccine product after 1 July 2023.

Laboratory Methods

Participants had nasal and oropharyngeal swab specimens obtained (nasal only for children <2 years of age). Specimens were tested for influenza (including type and influenza A subtype) and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) viruses by means of reverse-transcriptase polymerase chain reaction (RT-PCR) molecular assays at site laboratories. Participants who tested positive for influenza were designated as case patients and participants who tested negative for influenza and SARS-CoV-2 were designated non-case patients (controls). Influenza-positive specimens were genetically characterized using next-generation sequencing locally (1 site, in Arizona) or at CDC (6 sites). Each sample's hemagglutinin clade was based on its consensus sequence [12].

Statistical Analysis

We excluded the following from the primary analyses: participants with inconclusive influenza test results, participants who tested positive for SARS-CoV-2 [13], and participants who had been vaccinated <14 days before illness onset. Influenza VE was estimated with a test-negative design comparing odds of testing positive for influenza among vaccinated versus unvaccinated participants [14]. VE is expressed as $(1 - OR) \times 100$, where OR is the adjusted odds ratio for influenza among vaccinated persons versus unvaccinated persons from logistic regression models. Models were adjusted a priori for study site, participant age (group for all-age estimates and year of age for age group-specific estimates) at enrollment, presence of ≥ 1 underlying health condition, and month of illness onset. Additional covariates (ie, sex, race and ethnicity, self-rated general health status, and interval between onset and enrollment) were considered using a threshold for inclusion of $\geq 5\%$ change in the OR. Estimates include 95% confidence intervals (CIs) where exclusion of 0% indicates statistically significant VE.

We estimated VE by influenza type/subtype and by age group (8 months to 8 years, 9–17 years, 18–49 years, 50–64 years, or ≥ 65 years). Age group-specific estimates were combined when models did not converge. We also examined VE against A(H1N1)pdm09 among people born in 1958–1979 (aged 45–65 years) because this cohort has been associated with lower effectiveness against A(H1N1)pdm09 in prior seasons [15]. We estimated age group-specific VE against any influenza by time since vaccination using intervals of 14–60, 60–120, and >120 days since vaccination compared with unvaccinated participants.

RESULTS

Participant Characteristics

From 1 October 2023 through 30 April 2024, we enrolled 9061 participants who presented to outpatient and urgent care clinics and emergency departments for acute respiratory illness. We excluded 2432 participants from primary analyses; more than half of excluded participants (1294 [52%]) tested positive for SARS-CoV-2 (Supplementary Figure 1). Of the included 6629 participants, 1780 (27%) tested positive for influenza (Table 1): 806 (45%) for A(H1N1)pdm09, 567 (32%) for influenza B/Victoria, 328 (18%) for A(H3N2), and 104 (6%) for influenza A viruses of undetermined subtype; 20 participants (1%) had influenza A and B virus coinfections, and 5 (<1%) had influenza A(H1N1)pdm09

and A(H3N2) coinfections. Notably, a smaller proportion of B/Victoria cases occurred in participants aged ≥ 50 years compared with influenza A subtype viruses (Supplementary Figure 2). The number of influenza-positive participants enrolled per week peaked in late January 2024 (Supplementary Figure 3). A total of 2432 participants (37%) were considered vaccinated for influenza for the 2023–2024 season. Of these, 346 (14%) had no documented immunization record of 2023–2024 influenza vaccine but had plausible self-reported receipt.

Influenza-positive case patients were more likely to be male, be younger, identify themselves as black or African American, report better general health, and seek care earlier compared with test-negative controls; case patients were also less likely to have an underlying health condition than controls (Table 1). The proportion of participants vaccinated differed by study site, sex, age, race and ethnicity, general health status, presence of an underlying health condition, and number of days between illness onset and enrollment (Table 1). A total of 1513 vaccinated participants (62%) had a documented vaccine type. Of those with known vaccine type, 1362 (90%) received egg-based vaccines and 151 (10%) received non-egg-based vaccines (123 ccIV4 and 28 RIV4). Among 654 vaccinated adults aged ≥ 65 years, 492 (75%) had a known vaccine type. Of those, 467 (95%) received a preferentially recommended vaccine: 281 (57%) received high-dose inactivated influenza vaccine, and 186 (38%) received adjuvanted influenza vaccine; none received RIV4.

Genetic Characterization

A total of 1193 viruses were successfully sequenced: 616 A(H1N1)pdm09, 344 B/Victoria, and 233 A(H3N2). A(H1N1) pdm09 viruses belonged to 2 genetic subclades: 477 (77%) to 6B.1A.5a.2a.1 (2a.1), the same genetic subclade as the 2023–2024 A(H1N1)pdm09 vaccine reference virus, and 139 (23%) to 6B.1A.5a.2a (2a). The 2a.1 genetic subclade predominated among sequenced A(H1N1)pdm09 viruses throughout the enrollment period (Supplementary Figure 4). The distribution of A(H1N1)pdm09 genetic subclades was similar at 6 sites where 2a.1 genetic subclade viruses comprised 76%–86% of sequenced A(H1N1)pdm09 viruses; at the Missouri site, 57% of sequenced A(H1N1)pdm09 viruses belonged to the 2a genetic subclade. All B/Victoria viruses belonged to genetic clade V1A.3a.2, and all A(H3N2) viruses belonged to genetic subclade 2a.3a.1.

VE Results

From October 2023 through April 2024, the overall adjusted VE against medically attended outpatient influenza A and B viruses was 44% (95% CI, 36%–51%) (Table 2). Estimated VE was 29% (95% CI, 15%–41%) against influenza A(H1N1)pdm09, 74% (65%–81%) against influenza B/Victoria, and 30% (8%–47%) against A(H3N2). VE against A(H1N1)pdm09 varied by age group; VE was lowest, offering no protection against medically attended outpatient illness, among adults aged 50–64 years (–8% [95% CI, –62% to 28%]) and was highest among children aged 8 months to 8 years (72% [49%–86%]). Among adults born in a specific birth cohort (birth years 1958–1979), we observed no protection in terms of medically attended illness against A(H1N1)pdm09-associated influenza (2% VE [95% CI, –38% to 30%]). Among participants of all ages, VE was higher against influenza A(H1N1)pdm09 genetic subclade 2a viruses (57% [95% CI, 32%–74%]) compared with genetic subclade 2a.1 viruses (26% [7%–41%]) (Figure 1). When stratified by age group, the

greatest difference in VE between the 2 genetic subclade was observed among participants aged 18–64 years. VE against A(H1N1)pdm09 genetic subclade 2a.1 viruses in this age group was 13% (95% CI, –16% to 35%) versus 61% (30%–80%) against viruses in the 2a genetic subclade.

The median time between vaccination and illness onset was 94.5 days (interquartile range, 58–134 days). The interval was shorter among children aged 8 months to 17 years (median [interquartile range], 83 [51–128] days) than among adults aged 18–64 years (95 [56–134] days) and adults aged ≥65 years (99.5 [64.5–142] days). Half of vaccinated adults aged ≥65 years were vaccinated by 4 October 2023, compared with 12 October 2023 for adults aged 18–49 years and 21 October 2023 for children and adolescents aged 8 months to 17 years. Overall and for each age group, VE point estimates were highest among people vaccinated 14–59 days before illness onset compared with those with longer intervals, although CIs largely overlapped (Supplementary Table 2). We observed statistically significant VE against outpatient influenza through ≥120 days after vaccination among both children and adults aged <64 years. Among adults aged ≥65 years, statistically significant VE was not observed ≥60 days after vaccination.

Sensitivity Analyses

VE calculated using different sources of influenza vaccination data was within 10% points of overall adjusted VE against any influenza combining data sources. VE against any influenza based on self-reported or parent/guardian-reported influenza vaccination was 32% (95% CI, 21%–41%); VE based on EHR-documented data only was 44% (35%–52%) (Supplementary Table 3). Sensitivity analyses varying inclusion criteria for analysis were all within 6% points of the overall adjusted VE against any influenza reported in the primary analysis.

DISCUSSION

In a season with cocirculation of A(H1N1)pdm09, A(H3N2), and B/Victoria influenza viruses, we estimated that influenza vaccination reduced the risk of outpatient medically attended influenza by 44%. We found significant protection overall against A(H1N1)pdm09, B/Victoria, and A(H3N2) viruses. Observed vaccine protection varied against the 2 A(H1N1)pdm09 genetic subclades that circulated in the United States; lower protection was observed against the predominant A(H1N1)pdm09 virus (genetic subclade 2a.1) that was included in the 2023–2024 vaccine. Protection against any influenza was greatest 14–59 days after vaccination. Protection was observed >120 days after vaccination for participants aged <65 years.

We report differences in effectiveness by age group and influenza A virus subtype, that may contribute to our understanding of antigenic imprinting with A(H1N1) viruses. Specifically, we observed no significant protection against medically attended influenza A(H1N1)pdm09-related illness among adults aged 18–64 years. Reduced protection in this age category appeared limited to A(H1N1)pdm09 viruses in the 2a.1 genetic subclade. Restricting further by birth cohort, we observed no protection among participants born in 1958–1979, the same birth cohort previously associated with reduced VE against A(H1N1)pdm09 viruses [15–17].

Individuals in this birth cohort were likely exposed to influenza A(H2N2) or A(H3N2) before A(H1N1) and were first exposed to A(H1N1) viruses after this subtype reemerged in 1977 [18]. This birth cohort has experienced lower VE against A(H1N1)pdm09 clade 6B.1 viruses compared to other cohorts [15, 16]. Serologic studies of vaccine response would help to understand potential birth cohort effects and inform development of improved influenza vaccines that might overcome these effects. The A(H1N1)pdm09 vaccine antigen will continue to be an A/Wisconsin/67/2022-like virus antigen from the 2a.1 genetic subclade for the 2024–2025 Northern Hemisphere season [19].

Results from this study of VE against medically attended acute respiratory illness in outpatient or ambulatory settings are consistent with findings from active enrollment and EHR-based surveillance platforms in different populations and settings in the 2023–2024 season. While the US Flu VE Network estimates VE against medically attended outpatient illness, some evidence suggests that influenza vaccination could attenuate influenza disease severity [20]. Midseason estimates of VE from 4 US VE studies conducted in outpatient and inpatient settings demonstrated early protection against illness and hospitalizations; overall VE against any influenza ranged from 52% to 67% among children and adolescents and from 33% to 49% among adults [8]. Estimates were similar against both mild-to-moderate outpatient illness and influenza-associated hospitalizations. A previous analysis comparing 25 paired VE estimates in outpatient and inpatient settings found similar levels of protection against mild-to-moderate and more severe influenza [21].

Furthermore, estimates from the US-based VISION EHR-based surveillance platform [22] found similar VE against influenza A and B in outpatient (emergency department and urgent care clinics) and inpatient settings, consistent with US Flu VE Network estimates among enrolled outpatients. Among VE studies conducted outside the United States, midseason estimates from Canada reported higher overall effectiveness against A(H1N1)pdm09 (63% [95% CI, 51%–72%]) in a setting of approximately equal detections of genetic subclades 2a.1 and 2a [23]. VE was lower against 2a.1 viruses (56% [95% CI, 33%–71%]) than against 2a viruses (67% [48%–80%]), though CIs overlapped. Similar trends were reported from European outpatient and inpatient studies [24] and an health administration data-based study in Alberta, Canada [25].

Like other observational studies, the current study is subject to several limitations. First, some misclassifications of exposure may have occurred. In a small proportion (14%) of vaccinated participants, we relied on self-reported influenza vaccine receipt that was not documented in immunization records. It has been reported that the number of influenza vaccines administered in medical offices has declined by about 32% since the coronavirus disease 2019 pandemic as people increasingly seek vaccinations from pharmacies [4]. This shift may affect availability of vaccination data in EHRs. VE estimates in sensitivity analyses varying source of vaccination status data were comparable, however. We also report VE of receipt of ≥ 1 dose of 2023–2024 vaccine, although some children aged < 9 years are recommended to receive 2 seasonal doses to be considered fully vaccinated [1]. Second, analyses of VE by virus genetic clade/subclade, birth cohort, participant age, and time since vaccination were limited by the number of patients enrolled during the influenza season.

Third, while the test-negative design reduces potential bias due to differences in healthcare seeking, unmeasured confounding related to study enrollment may have affected VE estimates. However, our findings were robust to changes in inclusion criteria and definitions of exposure status. Finally, while we systematically tested participants for influenza and SARS-CoV-2, we did not conduct systematic testing for respiratory syncytial virus, for which vaccines are currently being administered to certain populations. As vaccine uptake increases, testing for respiratory syncytial virus in test-negative design studies of influenza VE may become important to minimize bias due to potential violation of the control exchangeability assumption [26].

The results presented in this study demonstrate an overall benefit of receiving the 2023–2024 influenza vaccine in the United States. As influenza vaccine components are updated, annual studies are needed to assess protections against circulating strains and emergent genetic clades. VE studies may contribute to future vaccine strain selection and improvements in influenza vaccines.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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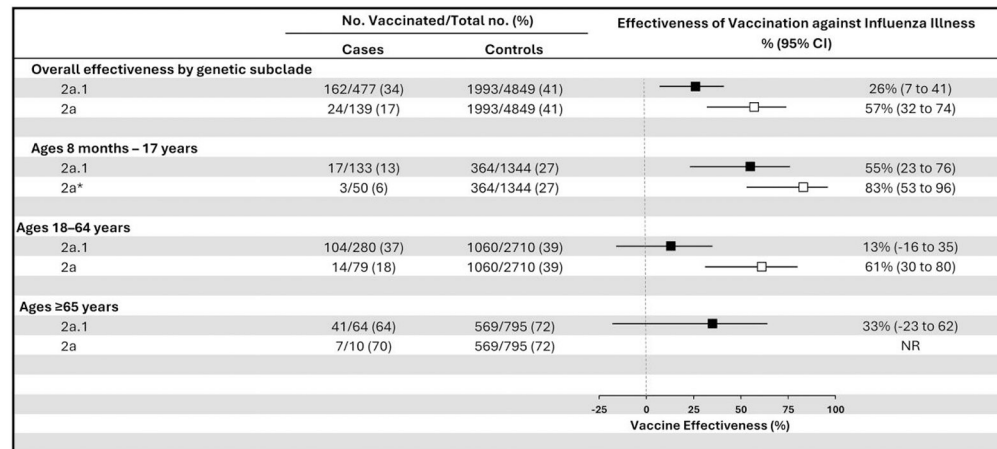
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**Figure 1.**

Adjusted vaccine effectiveness (VE) against outpatient influenza A(H1N1)pdm09 genetic subclade-associated illness visits among patients aged ≥ 8 months enrolled at US Flu VE Network sites, October 2023 through April 2024; models were adjusted for study site, age, presence of ≥ 1 underlying health condition, and month of illness onset (data in the 2a group in children [aged 8 months to 17 years] were unadjusted due to small sample size). Note that 95% confidence intervals (CIs) that exclude 0% are considered statistically significant. Abbreviation: NR, not reported due to small sample size.

Characteristics of Participants Enrolled in the US Flu VE Network for the 2023–2024 Influenza Season^a

Table 1.

Characteristic	RT-PCR Status						Vaccinated Against Influenza		
	Total No. (N = 6629)	Influenza Positive		Influenza Negative		P Value			
		No. (n = 1780)	Column %	No. (n = 4849)	Column %		No. (n = 2432)	Row %	P Value
Study site									
Arizona	584	207	12	377	8	<.01	72	12	<.01
Michigan	368	82	5	286	6		183	50	
Missouri	791	346	19	445	9		201	25	
Ohio	773	260	15	513	11		214	28	
Pennsylvania	1189	358	20	831	17		504	42	
Texas	1800	351	20	1449	30		731	41	
Washington	1124	176	10	948	20		527	47	
Sex ^b									
Female	3990	1034	58	2956	61	.03	1540	39	<.01
Male	2623	744	42	1879	39		889	34	
Age group									
8 m to 8 y	1367	407	23	960	20	<.01	286	21	<.01
9–17 y	613	229	13	384	8		147	24	
18–49 y	2699	774	43	1925	40		859	32	
50–64 y	1013	228	13	785	16		486	48	
≥65 y	937	142	8	795	16		654	70	
Race and ethnicity ^c									
American Indian or Alaska Native	121	22	1	99	2	.03	32	26	.02
Asian	346	107	6	239	5	.08	141	41	.11
Black or African American	1881	609	34	1272	26	<.01	449	24	<.01
Native Hawaiian or Other Pacific Islander	70	22	1	48	1	.39	15	21	.01
White	4247	1018	57	3229	67	<.01	1798	42	<.01
Hispanic or Latino	1023	285	16	738	15	.45	284	28	<.01
Self-rated general health status ^d									

Characteristic	RT-PCR Status							
	Total No. (N = 6629)	Influenza Positive		Influenza Negative		Vaccinated Against Influenza		
		No. (n = 1780)	Column %	No. (n = 4849)	Column %	No. (n = 2432)	Row %	P Value
Excellent	1671	536	30	1135	23	477	29	<.01
Very good	2275	618	35	1657	34	842	37	
Good	1855	462	26	1393	29	778	42	
Fair/poor	811	161	9	650	13	332	41	
Underlying chronic health conditions ^e								
None	3851	1230	69	2621	54	1044	27	<.01
≥1	2778	550	31	2228	46	1388	50	
Time from illness onset to enrollment								
<3 d	2250	729	41	1521	31	742	33	<.01
3–4 d	2047	610	34	1437	30	683	33	
5–7 d	1207	264	15	943	19	482	40	

Abbreviation: RT-PCR, reverse-transcriptase polymerase chain reaction.

^aIncluded patients with medically attended acute respiratory illness enrolled in the US Influenza Vaccine Effectiveness network between October 2023 through April 2024.

^bSex was missing for 16 participants.

^cParticipants self-identified all options that applied and could have chosen >1. Race and ethnicity were missing for 54 participants.

^dSelf-rated general health status was missing for 17 participants.

^eUnderlying chronic health conditions included chronic cardiac diseases and circulatory diseases, chronic pulmonary diseases, diabetes mellitus, chronic renal disease, hemoglobinopathies, immunosuppressive disorders, cancer, metabolic diseases, liver diseases, neurological or musculoskeletal conditions, cerebrovascular disease, morbid obesity, and endocrine disorders.

Table 2.
Adjusted Vaccine Effectiveness Against Outpatient Influenza-Associated Illness Visits Among Patients Aged ≥8 Months Enrolled at US Flu VE Network Sites, October 2023 to April 2024

Influenza Virus by Age Group	Influenza Positive (Case Patients)		Influenza Negative (Controls)		VE, % (95% CI) ^a
	No. Vaccinated/Total	% Vaccinated	No. vaccinated/Total	% Vaccinated	
All influenza viruses					
All ages ≥8 m	439/1780 ^b	25	1993/4849	41	44 (36–51)
8 mo to 8 y	33/407	8	253/960	26	68 (51–79)
9–17 y	36/229	16	111/384	29	59 (35–75)
18–49 y	183/774	24	676/1925	35	38 (24–50)
50–64 y	102/228	45	384/785	49	16 (–11 to 41)
≥65 y	85/142	60	569/795	72	37 (5–58)
Influenza A(H1N1)pdm09					
All ages ≥8 m	248/806	31	1993/4849	41	29 (15–41)
8 mo to 8 y	12/177	7	253/960	26	72 (49–86)
9–17 y	13/67	19	111/384	29	42 (–20 to 73)
18–49 y	93/316	29	676/1925	35	21 (–6 to 41)
50–64 y	71/148	48	384/785	49	–8 (–62 to 28)
≥65 y	59/98	60	569/795	72	39 (2–62)
Influenza B/Victoria					
All ages ≥8 m	62/567	11	1993/4849	41	74 (65–81)
8 mo to 8 y	8/179	4	253/960	26	81 (61–92)
9–17 y	13/125	10	111/384	29	77 (55–89)
18–49 y	34/235	15	676/1925	35	67 (51–78)
≥50 y	7/28	25	953/1580	60	79 (50–92)
Influenza A(H3N2)					
All ages ≥8 m	98/328	30	1993/4849	41	30 (8–47)
8 mo to 17 y	20/68	29	364/1344	27	–5 (–90 to 43)
18–49 y	46/194	23	676/1925	35	35 (5–57)
≥50 y	32/63	51	953/1580	60	23 (–37 to 56)

Abbreviations: CI, confidence interval; VE, vaccine effectiveness.

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Models adjusted for study site, age, presence of ≥ 1 underlying health condition, and month of illness onset; 95% CIs that exclude 0% are considered statistically significant.

Total influenza case patients include 112 positive for influenza A of undetermined subtype, 20 with influenza A and B coinfections, and 5 with influenza A(H1N1)pdm09 and A(H3N2) coinfections. Coinfections are included as cases of both detected viruses in the table.