Heterogeneous and Dynamic Prevalence of Asymptomatic Influenza Virus Infections

Luis Furuya-Kanamori, Mitchell Cox, Gabriel J. Milinovich, Ricardo J. Soares Magalhaes, Ian M. Mackay, Laith Yakob

Influenza infection manifests in a wide spectrum of severity, including symptomless pathogen carriers. We conducted a systematic review and meta-analysis of 55 studies to elucidate the proportional representation of these asymptomatic infected persons. We observed extensive heterogeneity among these studies. The prevalence of asymptomatic carriage (total absence of symptoms) ranged from 5.2% to 35.5% and subclinical cases (illness that did not meet the criteria for acute respiratory or influenza-like illness) from 25.4% to 61.8%. Statistical analysis showed that the heterogeneity could not be explained by the type of influenza, the laboratory tests used to detect the virus, the year of the study, or the location of the study. Projections of infection spread and strategies for disease control require that we identify the proportional representation of these insidious spreaders early on in the emergence of new influenza subtypes or strains and track how this rate evolves over time and space.

Infection of the respiratory tract with an influenza virus results in symptoms ranging from mild nonfebrile illness to severe disease and complications, including pneumonia, shock, renal failure, encephalopathy, and multiorgan dysfunction (1,2). Influenza viruses infect 5%–15% of the global population annually (3), accounting for ≈500,000 deaths (4) and 19 million disability-adjusted life years (5). The occurrence of asymptomatic influenza viruses infections has been recognized for some time (6), but determinations about their possible role in transmission are largely speculative (7,8). Clarifying the role of these infections in virus transmission requires a solid understanding of their rate of occurrence.

Interest in the contribution of asymptomatic infection to influenza virus transmission has risen in recent years

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Methods

Search Strategy and Selection Criteria
A systematic review and meta-analysis was conducted in accordance with PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-Analyses) guidelines (19). Literature searches were performed on the PubMed and Web of Science databases for the period from the inception of these databases to the beginning of 2015 to identify studies that reported laboratory-confirmed influenza infection (i.e., by culture, PCR, or serologic testing) and the proportion of symptomatic versus asymptomatic presentation. Search terms were chosen to ensure maximum coverage of possible literature and included the terms “influenza,”}

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“carrier,” “carriage,” “shedding,” “asymptomatic,” “influenza AND prophylaxis NOT vaccine” (filtered for randomized control trials), “influenza AND (travel OR migration OR immigrant*) AND (screening OR test OR testing OR detection),” “subclinical,” “serosurvey OR seroprevalence OR seroepidemiology.” Other keywords and connectors were also used (online Technical Appendix 1, http://wwwnc.cdc.gov/EID/article/22/6/15-1080-Techapp1.pdf).

To be eligible for inclusion, studies needed to 1) be peer-reviewed and 2) report the prevalence of asymptomatic influenza virus infections in humans or present the appropriate data from which that prevalence could be calculated. Laboratory confirmation of influenza was a requirement, and it had to be possible to correlate these data to the number of symptomatic patients. We did not impose limitations in terms of study design, influenza virus type, or exposure type (community or experimental inoculation). According to current World Health Organization guidelines, laboratory confirmation consisted of 1) conventional PCR (referred to here as PCR) or real-time reverse transcription PCR (rRT-PCR); 2) virus antigen detection by immunofluorescence or enzyme immunosassay methods; 3) serologic detection of antibodies (hemagglutination inhibition); or 4) virus culture (20). Studies were excluded when the use of antiviral agents without a placebo group was reported. In cases in which a placebo group was used and an asymptomatic proportion could be determined, only this subset was used; otherwise, the study was excluded. Results were restricted to studies published in English; however, no restriction was placed on the publication date of studies that fit these criteria.

Study Selection and Data Extraction
Two authors (L.F-K. and M.C.) independently screened the publications for eligibility in a stepwise fashion. Search results were initially screened based on article titles and abstracts. Then, full-text analysis was performed to identify all studies which either reported asymptomatic prevalence or from which asymptomatic prevalence could be calculated. Any discrepancies that might have affected inclusion or exclusion of a study were resolved through discussion and consensus after independent evaluation by another author (L.Y.). The same 2 authors (L.F-K. and M.C.) assessed the risk for bias of the studies included by using a modified version of the tool developed by Hoy et al. (21) for prevalence studies (online Technical Appendix 2, http://wwwnc.cdc.gov/EID/article/22/6/15-1080-Techapp2.pdf).

The definitions of asymptomatic influenza infection varied considerably between studies. Definitions ranged from a total absence of symptoms to a lack of influenza-like illness (ILI) or acute respiratory illness (ARI). For the sake of clarity, we used the term “asymptomatic” when there was a total absence of symptoms and “subclinical” when the patient did not meet the authors’ criteria for ILI or ARI. Asymptomatic influenza prevalence was considered to be the proportion of all persons with laboratory-confirmed influenza who had no symptoms, whereas subclinical influenza prevalence was the proportion of persons with laboratory-confirmed influenza who failed to meet the study’s definition of symptomatic infection. In addition to collecting data on asymptomatic and subclinical infection prevalence, we collected data on influenza virus type/subtype and study characteristics (e.g., study design, sample size, diagnostic test used to detect influenza virus infection, and the working definition of “symptomatic”).

Statistical Analysis
We used prevalence of asymptomatic versus subclinical carriers among persons with laboratory-confirmed influenza as primary endpoints of interest. We pooled the prevalence estimates of asymptomatic and subclinical influenza across studies by using 2 meta-analytical models, the inverse variance heterogeneity model (22) and the random effects model.

We observed considerable heterogeneity across studies. This heterogeneity was unlikely to be attributable only to random or systematic errors, and actual clinical heterogeneity was deemed to exist. Therefore, we created subgroups by influenza virus type/subtype with the aim of generating more homogeneous groups within which we could anticipate that the differences indeed reflected variability caused by random or systematic error rather than actual clinical heterogeneity. In addition, we built a linear model to examine the variance explained by the influenza virus type/subtype, laboratory test used to detect the virus, year of the study, and geographic location of the study to gain insight into the considerable heterogeneity observed in the prevalence of asymptomatic and subclinical infections. We conducted the meta-analyses by using MetaXL version 2.0 (EpiGear Int Pty Ltd, Brisbane, QLD, Australia), which also included the inverse variance heterogeneity method, and the generalized linear model by using Stata version 12 (StataCorp LP, College Station, TX, USA). All tests were 2-tailed, and a p value <0.05 was deemed statistically significant.

Results

Yield of Search Strategy
A total of 13,219 records were identified from literature searches of the 2 databases. This number was reduced to 9,900 after removal of publications that were either duplicates or not original research papers (e.g., review papers). An additional 3,663 papers were removed based on the title and 5,652 papers more based on the abstract. The full texts of the remaining 585 studies were examined, and 55 articles met the inclusion criteria and were included in the final analysis (Figure; online Technical Appendix 1).
Characteristics of the Studies Included
The 55 articles provided 59 data points because 4 papers reported the prevalence of asymptomatic and subclinical carriers for influenza A and B viruses separately. Overall, 19 studies (22 data points) defined asymptomatic infection as cases in persons lacking symptoms, and 44 studies (46 data points) reported subclinical influenza virus infections.

Infection was confirmed by serologic testing, rRT-PCR, or viral culture; 28 studies reported use of serologic testing alone to confirm infection, 18 used rRT-PCR alone, and the remaining 9 used a combination of methods (5 serologic testing and rRT-PCR, 3 serologic testing and culture, and 1 rRT-PCR and culture). Among the 55 studies, influenza A virus (predominantly H1N1) was the most common type of infection; 5 studies reported influenza B virus infections, and 1 study reported influenza C infections (online Technical Appendix 1 Table 2). Most studies reported on pandemic influenza virus types; 32 of these studies related to the 2009 pandemic influenza A/Mexico/4108/2009 strain. The risk for bias was moderate in 32% of the studies and low in the remaining 68%; no study was found to have a high risk for bias.

Quantitative Synthesis
The overall pooled prevalence for asymptomatic carriers was 19.1% (95% CI 15.2%–35.5%) for any type of influenza, 21.0% (95% CI 4.2%–41.0%) for influenza A, and 22.7% (95% CI 7.7%–39.8%) for influenza A(H1N1) (Table 1; online Technical Appendix 2 Figure 1). For subclinical carriers, the overall pooled prevalence was 43.4% (95% CI 25.4%–61.8%) for any type of influenza, 42.8% (95% CI 22.3%–63.9%) for influenza A, and 39.8% (95% CI 16.4%–64.5%) for influenza A(H1N1) (Table 1; online Technical Appendix 2 Figure 2). However, extensive heterogeneity was immediately evident for reported asymptomatic prevalence ($\tau^2 = 0.31$) and subclinical prevalence ($\tau^2 = 0.45$) that could not be explained by the influenza type/subtype alone. Similar results were obtained with the random effects model (online Technical Appendix 2 Figures 3, 4).

Investigation of Heterogeneity
The considerable heterogeneity observed within asymptomatic and subclinical influenza prevalence could not be explained by the type/subtype of influenza, the laboratory tests used to detect the virus, the location where the study was conducted, or the year of the study. The multivariate regression models could only explain 16.8% and 14.8% of the observed variance for the asymptomatic and subclinical prevalence, respectively. Influenza type/subtype as an independent predictor was found to account for almost the entire variance (16%) found for the prevalence of asymptomatic carriers (Table 2).

Table 1. Heterogeneity within asymptomatic and subclinical influenza infection cases, by virus type/subtype, as determined through a systematic review and meta-analysis of 55 studies

<table>
<thead>
<tr>
<th>Type/subtype</th>
<th>Prevalence (95% CI)</th>
<th>Cochran’s Q</th>
<th>p value (Cochran’s Q)</th>
<th>$I^2$,%</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Asymptomatic</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>All types of influenza</td>
<td>19.1 (5.2–35.5)</td>
<td>752.40</td>
<td>&lt;0.001</td>
<td>97</td>
</tr>
<tr>
<td>Influenza A</td>
<td>21.0 (4.2–41.0)</td>
<td>692.94</td>
<td>&lt;0.001</td>
<td>98</td>
</tr>
<tr>
<td>Influenza A(H1N1)</td>
<td>22.7 (7.7–39.8)</td>
<td>561.14</td>
<td>&lt;0.001</td>
<td>97</td>
</tr>
<tr>
<td><strong>Subclinical</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>All types of influenza</td>
<td>43.4 (25.4–61.8)</td>
<td>1768.24</td>
<td>&lt;0.001</td>
<td>97</td>
</tr>
<tr>
<td>Influenza A</td>
<td>42.8 (22.3–63.9)</td>
<td>1689.78</td>
<td>&lt;0.001</td>
<td>98</td>
</tr>
<tr>
<td>Influenza A(H1N1)</td>
<td>39.8 (16.4–64.5)</td>
<td>1388.54</td>
<td>&lt;0.001</td>
<td>98</td>
</tr>
</tbody>
</table>

*The $I^2$ statistic describes the percentage of variation across studies that is attributable to heterogeneity rather than chance.
temporal changes in this rate.

the asymptomatic rate of influenza virus infection would
sensitive diagnostic testing and standardized reporting of
per–influenza type rate simply does not exist. Employing
tomatic infection mutate so rapidly that a meaningful single
cluded). Alternatively, influenza viruses conferring asymp
clinical studies and data on sex and age of patients were ex
and these have been missed (e.g., details of patient vaccina
underlie the asymptomatic rates of influenza virus infection
one being that generally applicable biologic mechanisms
explanations for the extreme heterogeneity are plausible,
treme heterogeneity in this reported rate. Some alternative
to 65%, resulting in an overall failure to explain the ex
asymptomatic influenza A(H1N1) virus ranged from 0%
influenza virus subtypes. For example, the prevalence of
rate (or even an informative range) between or even within
health bodies and researchers.

We found no evidence to support a fixed asymptomatic
rate (or even an informative range) between or even within
influenza virus subtypes. For example, the prevalence of
asymptomatic influenza A(H1N1) virus ranged from 0% to
65%, resulting in an overall failure to explain the ex-
treme heterogeneity in this reported rate. Some alternative
explanations for the extreme heterogeneity are plausible,
one being that generally applicable biologic mechanisms
underlie the asymptomatic rates of influenza virus infection
and these have been missed (e.g., details of patient vaccina-
oration or infection history were not routinely described in the
clinical studies and data on sex and age of patients were ex-
cluded). Alternatively, influenza viruses conferring asym-
tomatic infection mutate so rapidly that a meaningful single
per–influenza type rate simply does not exist. Employing
sensitive diagnostic testing and standardized reporting of
the asymptomatic rate of influenza virus infection would
elucidate any underlying mechanisms or demonstrate any
temporal changes in this rate.

Publication Bias
For both asymptomatic and subclinical carrier prevalence,
the funnel plots showed no indication of publication bias.
This result was confirmed by Doi plots (data not shown).

Discussion
Studies of laboratory-confirmed influenza typically do
not include details of the symptomatic versus asympto-
matic rate of infection. Of the few that do include this
information, ambiguity exists between definitions of as-
ymptomatic versus subclinical infections. This has per-
PETuated the ubiquitous issue of absent denominators in
documented influenza rates and has caused substantial
aberrations in initial reports of newly emerging subtypes
and strains (23). We propose that the term “asymptom-
ic” be used exclusively to describe the complete absence
of symptoms associated with influenza virus infection
in patients with laboratory-confirmed cases. Given that
reporting of this rate in the clinical literature would re-
quire little to no additional effort for most study designs,
we also propose that the asymptomatic rate of laboratory
test–positive persons be declared explicitly by public
health bodies and researchers.

This lack of a convenient asymptomatic rate poses a
considerable obstacle to public health planning. Disease
surveillance and control strategy is contingent on reliable
estimates for the asymptotic rate and the contribution
that asymptomatic persons have on transmissibility. For
example, a low asymptomatic rate improves the utility
of passive (i.e., symptom-based) surveillance, whereas a
higher asymptomatic rate might prompt presumptive travel
restrictions to curb the spread of newly emerging subtypes
and strains, especially if a high mortality rate is evident ear-
ly in the outbreak. Future analyses correlating asymptom-
ic rates with mortality rates are also required; although one
could easily speculate that influenza subtypes and strains
eliciting high asymptomatic rates probably incur corre-
pondingly low mortality rates, no evidence supporting this
assumption currently exists.

Our study clearly demonstrates the inappropriateness
of a one-size-fits-all approach to mitigating the spread
of human influenza viruses. As new subtypes and strains
emerge, actively surveying infection status of local popu-
lations and tracking any changes in asymptomatic rates of
infection should increasingly become a global health pri-
ority, possibly necessitating the provision of international
resources and the deployment of dedicated rapid-response
teams who are guided by standardized protocols.

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arship (no. 3781_2014), an Australia National University Higher
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Tecnología Scholarship (no. 095-FINCyT-BDE-2014) to L.F.K.
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Mr. Furuya-Kanamori is an infectious disease epidemiologist. He
is enrolled in a PhD program at the Australian National University
where he uses modern quantitative methods to better understand
risk factors associated with different infectious diseases.

References
1. Taubenberger JK, Morens DM. The pathology of influenza virus
10.1146/annurev.pathmechdis.3.121806.154316
etymology is concerned with the origin of words, how they've evolved over time, and changed in form and meaning as they were translated from one language to another. Every month, EID publishes a feature highlighting the etymology of a word from medicine or public health.

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Technical Appendix 1

Search Strategies

First Search

Influenza AND ((Asymptomatic OR Carrier OR carriage OR shedding OR symptomatic OR Subclinical OR serosurvey OR seroprevalence OR seroepidemiology) OR ((travel OR migration OR immigra*) AND (screening OR test OR testing OR detection)) OR ((“Cohort Studies”[Mesh] OR “Case-Control Studies”[Mesh]) AND “Influenza A virus”[Mesh]))

Second Search


Manually filtered for randomized controlled trials.
**Technical Appendix Table 1.** Characteristics of the 55 studies included in systematic review and meta-analysis of asymptomatic and subclinical influenza infection prevalence

<table>
<thead>
<tr>
<th>Authors, year</th>
<th>Location of the study</th>
<th>Influenza type or subtype</th>
<th>Seasonal / Pandemic</th>
<th>Exposure type</th>
<th>Diagnosis test</th>
<th>Definition of asymptomatic</th>
<th>Definition of subclinical</th>
<th>Asymptomatic prevalence, %</th>
<th>Subclinical prevalence, %</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aho M, et al., 2010</td>
<td>Finland</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Military garrison</td>
<td>HI ≥10</td>
<td>No symptoms of URT infection</td>
<td>—</td>
<td>40.7</td>
<td>—</td>
</tr>
<tr>
<td>Belderok SM, et al., 2013</td>
<td>Netherlands</td>
<td>A, and B</td>
<td>Seasonal</td>
<td>Travel to tropical and subtropical countries</td>
<td>HI ≥40 and ≥4-fold increase above pre-travel titer</td>
<td>—</td>
<td>—</td>
<td>90.83</td>
<td></td>
</tr>
<tr>
<td>Bone A, et al., 2012</td>
<td>France</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Community</td>
<td>HI ≥40</td>
<td>—</td>
<td>—</td>
<td>29.52</td>
<td>—</td>
</tr>
<tr>
<td>Buescher, et al., 1969</td>
<td>Thailand and Panama</td>
<td>A (H3N1)</td>
<td>Pandemic</td>
<td>Military garrison</td>
<td>HI ≥32</td>
<td>—</td>
<td>—</td>
<td>77.5</td>
<td>—</td>
</tr>
<tr>
<td>Carey DE, et al., 1958</td>
<td>USA</td>
<td>A (H2N2)</td>
<td>Pandemic</td>
<td>Parish</td>
<td>HI ≥10</td>
<td>—</td>
<td>No ILI</td>
<td>90.83</td>
<td>—</td>
</tr>
<tr>
<td>Ceyhan M, et al., 2010</td>
<td>Turkey</td>
<td>A (H5N1)</td>
<td>Community, poultry exposure and healthcare workers</td>
<td>HI ≥21</td>
<td>—</td>
<td>No symptoms of avian influenza infection</td>
<td>—</td>
<td>81.25</td>
<td>—</td>
</tr>
<tr>
<td>Clover RD, et al., 1986*</td>
<td>USA</td>
<td>A (H1N1)</td>
<td>Seasonal</td>
<td>Community</td>
<td>Positive culture or HI ≥4-fold increase</td>
<td>—</td>
<td>No ILI</td>
<td>60</td>
<td>—</td>
</tr>
<tr>
<td>Cui F, et al., 2011</td>
<td>China</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Train</td>
<td>rRT-PCR</td>
<td>—</td>
<td>No ARI</td>
<td>13.64</td>
<td>—</td>
</tr>
<tr>
<td>Botan A, et al., 2014</td>
<td>Israel</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Hospital</td>
<td>rRT-PCR</td>
<td>—</td>
<td>No URI</td>
<td>30.77</td>
<td>—</td>
</tr>
<tr>
<td>Du Ry van Beest Holle M, et al., 2005</td>
<td>Netherlands</td>
<td>A (H7N7)</td>
<td>Pandemic</td>
<td>Poultry</td>
<td>HI ≥10</td>
<td>—</td>
<td>No ILI</td>
<td>93.94</td>
<td>—</td>
</tr>
<tr>
<td>Foy HM, et al., 1987</td>
<td>USA</td>
<td>B</td>
<td>Seasonal</td>
<td>Community</td>
<td>HI ≥10</td>
<td>—</td>
<td>No ILI</td>
<td>32.43</td>
<td>—</td>
</tr>
<tr>
<td>Gray GC, et al., 2014</td>
<td>Cambodia</td>
<td>A (H1N1), A (H3N2), and B</td>
<td>Seasonal and pandemic</td>
<td>Community</td>
<td>HI ≥4-fold increase</td>
<td>—</td>
<td>No ILI</td>
<td>64.44</td>
<td>—</td>
</tr>
<tr>
<td>Guinard A, et al., 2009</td>
<td>France</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>School</td>
<td>rRT-PCR</td>
<td>—</td>
<td>No ILI</td>
<td>53.33</td>
<td>—</td>
</tr>
<tr>
<td>Hayden FG, et al., 1999*</td>
<td>USA</td>
<td>A (H1N1)</td>
<td>Seasonal</td>
<td>Experimental inoculation</td>
<td>Positive culture and/or HI ≥4-fold increase</td>
<td>—</td>
<td>No URT illness</td>
<td>46.15</td>
<td>—</td>
</tr>
<tr>
<td>Hayward AC, et al., 2014</td>
<td>UK</td>
<td>A (H1N1), A (H3N2), and B</td>
<td>Seasonal and pandemic</td>
<td>Community</td>
<td>rRT-PCR</td>
<td>—</td>
<td>No ILI</td>
<td>46.22</td>
<td>—</td>
</tr>
<tr>
<td>Hsieh YH, et al., 2014</td>
<td>Taiwan</td>
<td>A (H1N1)</td>
<td>Seasonal</td>
<td>Community and school</td>
<td>HI ≥4-fold increase</td>
<td>No symptoms</td>
<td>No ILI</td>
<td>45.15</td>
<td>33.33</td>
</tr>
<tr>
<td>Hudson L, et al., 2013</td>
<td>New Zealand</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Healthcare workers</td>
<td>HI ≥40</td>
<td>None influenza symptoms</td>
<td>—</td>
<td>25.44</td>
<td>—</td>
</tr>
<tr>
<td>Ison MG, et al., 2012*</td>
<td>Belgium, Estonia, France, Germany, Hungary, Israel, Italy, Lithuania, Spain, UK, USA</td>
<td>A (H1N1), A (H3N2), and B</td>
<td>Transplant recipients</td>
<td>Positive culture and/or HI ≥4-fold increase</td>
<td>—</td>
<td>No symptoms</td>
<td>—</td>
<td>25</td>
<td>—</td>
</tr>
<tr>
<td>Jackson ML, et al., 2011</td>
<td>USA</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>School</td>
<td>HI ≥20 and ≥4-fold increase</td>
<td>No symptoms</td>
<td>No ILI</td>
<td>81.25</td>
<td>—</td>
</tr>
<tr>
<td>Authors, year</td>
<td>Location of the study</td>
<td>Influenza type or subtype</td>
<td>Seasonal / Pandemic</td>
<td>Exposure type</td>
<td>Diagnosis test</td>
<td>Definition of asymptomatic</td>
<td>Definition of subclinical</td>
<td>Asymptomatic prevalence, %</td>
<td>Subclinical prevalence, %</td>
</tr>
<tr>
<td>---------------</td>
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<td>--------------------------</td>
</tr>
<tr>
<td>Jaeger JL, et al., 2011</td>
<td>USA</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Hospital</td>
<td>HI ≥20</td>
<td>—</td>
<td>No ARI or ILI</td>
<td>—</td>
<td>66.66</td>
</tr>
<tr>
<td>Johnson S, et al., 2011</td>
<td>UK</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Boarding school</td>
<td>HI ≥8</td>
<td>—</td>
<td>No ILI</td>
<td>—</td>
<td>68.35</td>
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<tr>
<td>Khakpour M, et al., 1969</td>
<td>Iran</td>
<td>A (H3N2)</td>
<td>Pandemic</td>
<td>Prisoners</td>
<td>HI</td>
<td>—</td>
<td>No ILI</td>
<td>—</td>
<td>23.53</td>
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<tr>
<td>Khaotham CB, et al., 2013</td>
<td>USA</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Navy vessel</td>
<td>rRT-PCR or HI ≥4-fold increase</td>
<td>No symptoms</td>
<td>No ILI</td>
<td>82.11</td>
<td>88.03</td>
</tr>
<tr>
<td>Khuntirat B, et al., 2014</td>
<td>Thailand</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Community</td>
<td>rRT-PCR and HI ≥4-fold increase</td>
<td>—</td>
<td>No ILI</td>
<td>—</td>
<td>83.33</td>
</tr>
<tr>
<td>Kumar S, et al., 2010</td>
<td>USA</td>
<td>A (H1N1)</td>
<td>Pandemic</td>
<td>Community</td>
<td>rRT-PCR</td>
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<td>Lau LLH, et al., 2010</td>
<td>Hong Kong</td>
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<td>Levy JW, et al., 2013</td>
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<td>Mikulska M, et al., 2013</td>
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<td>Finland</td>
<td>A (H3N2)</td>
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<td>Pascalis H, et al., 2012</td>
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<td>Paton NI, et al., 2011</td>
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<td>New Zealand</td>
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<td>Qi W, et al., 2014</td>
<td>China</td>
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<td>Redlberger-Fritz M, et al., 2014</td>
<td>Austria</td>
<td>A (H1N1)</td>
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<td>Attended hospital</td>
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<td>Definition of subclinical</td>
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<td>Subclinical prevalence, %</td>
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<td>Robinson JL, et al., 2007</td>
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<td>Salez N, et al., 2014</td>
<td>France, Reunion Island, UK</td>
<td>C</td>
<td>Community</td>
<td>HI, ELISA and rRT-PCR</td>
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<td>No ILI</td>
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<td>University campus</td>
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<td>Healthcare workers</td>
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<td>Suess T, et al., 2012</td>
<td>Germany</td>
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<td>Community</td>
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<td>No ILI</td>
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<td>Pandemic</td>
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<td>Toyokawa T, et al., 2011</td>
<td>Japan</td>
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<td>Pandemic</td>
<td>Healthcare workers</td>
<td>rRT-PCR</td>
<td>No symptoms</td>
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<td>Vilella A, et al., 2012</td>
<td>Dominican Republic</td>
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<td>School</td>
<td>rRT-PCR</td>
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<td>Wang TE, et al., 2010</td>
<td>Taiwan</td>
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<td>62.5</td>
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<td>Woods CW, et al., 2013</td>
<td>USA and UK</td>
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<td>Seasonal</td>
<td>Experimental inoculation</td>
<td>Positive culture or rRT-PCR</td>
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<td>Jackson score &lt;6</td>
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<td>Yan L, et al., 2012</td>
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<td>Pandemic</td>
<td>School</td>
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<td>No ARI</td>
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<td>56.1</td>
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<td>Zaman M, et al., 2011</td>
<td>Pakistan</td>
<td>A (H5N1)</td>
<td>Pandemic</td>
<td>Hospital</td>
<td>rRT-PCR</td>
<td>No symptoms</td>
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*Only control or placebo group included; ARI, acute respiratory illness; HI, hemagglutination inhibition; ILI, influenza-like illness; LRT, lower respiratory tract; rRT-PCR, real-time reverse transcription PCR; URT, upper respiratory tract.*
Technical Appendix 2 Table. Included studies (N = 55), by influenza type/subtype

<table>
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<th>Type</th>
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<td>A</td>
<td>H10N8</td>
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<td>H7N7</td>
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<td>2</td>
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<td>H3N2</td>
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<td>H2N2</td>
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<td>16</td>
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<tr>
<td></td>
<td>H1N1</td>
<td>38</td>
<td>5,8,9,12–15,17–47</td>
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<tr>
<td>B</td>
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<td>5</td>
<td>5,8,12,48,49</td>
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<tr>
<td>C</td>
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<tr>
<td>Mixed</td>
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<td>6</td>
<td>49.51–55</td>
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</table>

References


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   http://dx.doi.org/10.2188/jeaJE20100119


   http://dx.doi.org/10.1001/jama.282.13.1240


   http://dx.doi.org/10.1093/cid/cir437


   http://dx.doi.org/10.1111/irv.12100

   http://dx.doi.org/10.3390/v2040782


Heterogeneous and Dynamic Prevalence of Asymptomatic Influenza Virus Infections

Technical Appendix 2

Risk for Bias Assessment

Risk for bias of the studies was assessed by using a modified version of the tool developed by Hoy et al. for prevalence studies. The modified tool assessed the external and internal validity of the studies by 9 criteria: 1) the targeted population was a close representation of the national population; 2) the sampling frame was a true or close representation of the general population; 3) random selection was used to select the study population; 4) the likelihood of nonresponse bias was minimal; 5) the case definition of influenza infection was based on laboratory tests; 6) the data collected were reliable; 7) the method used to collect the data was the same for all subjects; 8) the numerator and denominator of the prevalence were based on all the study participants; and 9) the data were largely recorded directly from the participants.

Statistical Analysis

All prevalence estimates were pooled after double arcsine square root transformation and back-transformed for reporting (1). We did not use the standard random effects (RE) model (2) to pool because the latter is known to underestimate the statistical error and exacerbate publication bias (3–5). Therefore, the prevalence rates of asymptomatic and subclinical influenza across studies within the subgroups were pooled using the inverse variance heterogeneity (IVhet) model (6). This method uses a quasi-likelihood based variance structure without distributional assumptions and thus has coverage probabilities for the CI well within the 95% nominal level and has been documented to have better performance (lower mean squared error) when compared to the RE method (7). The results from the RE model have nevertheless been reported (Technical Appendix 2 Figures 3 and 4) for comparison purposes. Publication bias was assessed through Egger’s linear regression and visual inspection of funnel and Doi plots (8).
References


Technical Appendix 2 Figure 1. Forest plots for asymptomatic prevalence of A) influenza overall, B) influenza A, and C) influenza A(H1N1) virus infections generated by using the inverse variance heterogeneity model for 55 studies included in systematic review and meta-analysis of asymptomatic and subclinical influenza infection prevalence. Details on these studies are provided in Technical Appendix 1 (http://wwwnc.cdc.gov/EID/article/22/6/15-1080-Techapp1.pdf).

Technical Appendix 2 Figure 2. Forest plots for subclinical prevalence of A) influenza overall, B) influenza A, and C) influenza A(H1N1) virus infections generated by using the inverse variance
heterogeneity model for 55 studies included in systematic review and meta-analysis of asymptomatic and subclinical influenza infection prevalence.

Technical Appendix 2 Figure 3. Forest plots for asymptomatic prevalence of A) influenza overall, B) influenza A, and C) influenza A(H1N1) virus infections generated by using the random effects model for 55 studies included in systematic review and meta-analysis of asymptomatic and subclinical influenza infection prevalence.
Technical Appendix 2 Figure 4. Forest plots for subclinical prevalence of A) influenza overall, B) influenza A, and C) influenza A(H1N1) virus infections generated by using the random effects model for 55 studies included in systematic review and meta-analysis of asymptomatic and subclinical influenza infection prevalence.