meric medications were encouraged over brand name medications, but medications representing all therapeutic classes for hypertension treatment were available. Clinicians were encouraged to follow evidence-based practice; however, there was no mandate to use a specific agent in the initial treatment of hypertension.

While the patterns of care observed may not be generalizable to other settings, these 3 health care systems care for over 4 million patients in geographically distinct areas and the patient cohort included a clinically and demographically diverse population, approximately 50% female and 17% African American/Hispanic patients. Our findings of a slow but persistent increase in thiazide use suggest that clinical practice guidelines may have an impact on practice within these health care systems.

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Figure. Trends in the prescription of initial antihypertensive medications among patients without compelling indications from 2002 through 2007. ACE indicates angiotensin-converting enzyme inhibitor; CCB, calcium channel blocker; CCB DHP, dihydropyridine calcium channel blocker; CCB non-DHP, nondihydropyridine calcium channel blocker; DIUR KSF ARE, potassium-sparing diuretic.

Clinical and Molecular Evidence for Transmission of Novel Influenza A(H1N1/2009) on a Commercial Airplane

Influenza A(H1N1/2009) has spread rapidly throughout the world by international air travel. However, in-flight transmission of the virus has not been well documented. We report 6 cases of influenza A(H1N1/2009) associated with a single flight from the United States to Asia via Europe (“Flight A”) linked by molecular epidemiological data.

See also pages 861 and 868

Report of Cases. Five passengers and 1 crew member who had traveled on Flight A presented with acute onset of fever, malaise, cough, sore throat, or rhinorrhea, with the first case presenting symptoms while he was in New York, New York, and the rest within 3 days of the flight’s arrival in Singapore. All were discharged well, without se-
Table. Epidemiological Characteristics of Passengers and Crew Members on a Single Flight From the United States to Asia via Europe

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Infected</th>
<th>Not Infected</th>
<th>P Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, mean (SD), y</td>
<td>27.5 (6.1)</td>
<td>37.1 (12.5)</td>
<td>.02</td>
</tr>
<tr>
<td>Sex, M/F, No.</td>
<td>3/3</td>
<td>10/9</td>
<td>&gt;.99</td>
</tr>
<tr>
<td>Passengers/crew, No. (%)</td>
<td>5/1 (83)</td>
<td>14/6 (65)</td>
<td>&gt;.99</td>
</tr>
<tr>
<td>Boarded plane in New York, No. (%)</td>
<td>4/6 (67)</td>
<td>13/20 (65)</td>
<td>&gt;.99</td>
</tr>
<tr>
<td>Total time on plane, mean (SD), h</td>
<td>14.5 (5.0)</td>
<td>15.7 (4.0)</td>
<td>.59</td>
</tr>
<tr>
<td>Carried hand sanitizer, No. (%)</td>
<td>2/6 (33)</td>
<td>6/20 (30)</td>
<td>&gt;.99</td>
</tr>
<tr>
<td>Used mask, No. (%)</td>
<td>0/6</td>
<td>2/20 (10)</td>
<td>&gt;.99</td>
</tr>
<tr>
<td>Sleep time, mean (SD), h</td>
<td>5.0 (3.1)</td>
<td>9.0 (4.1)</td>
<td>.06</td>
</tr>
<tr>
<td>Movie/reading time, mean (SD), h</td>
<td>5.0 (2.1)</td>
<td>5.6 (2.3)</td>
<td>.63</td>
</tr>
<tr>
<td>Used toilet, No. of times</td>
<td>4.8 (1.9)</td>
<td>5.6 (2.9)</td>
<td>.48</td>
</tr>
</tbody>
</table>

For the infected travelers, the attack rate was 4.7% (95% CI 1.9-7.3) on Flight A and 1.3% (95% CI 0.5-2.0) on Flight B. The attack rate was not significantly different between the 2 flights (P=.06; Table). This was consistent with the observation that a higher proportion of infection occurred in younger individuals.

Viral genome sequencing using 1949 bases from segments 4 (HA) and 5 (NP) for 4 of the Flight A cases (A/Sg/case 1-4) revealed that all the sequences closely matched sequences from New York. These were distinct from other viruses identified from Singapore and countries outside the United States from the same period (A/New York/18/2009[H1N1]), and were distinct from other Singapore identified viruses sequenced during the same period (A/Sg/case 1-4) revealed that all the sequences closely matched sequences from New York. These were distinct from other viruses identified from Singapore and countries outside the United States from the same period (A/New York/18/2009[H1N1]).

Figure. Sequence analysis of viruses from cases on a single flight from the United States to Asia via Europe. Case viruses and 1 virus from a contact of case 3 cluster closely to published sequences from the New York region of the United States from the same period (A/New York/18/2009[H1N1]), and were distinct from other Singapore identified viruses sequenced during the same period (A/Sg/case 1-4[H1N1] and A/Sg/contact of case 3[H1N1]).

The phylogenetic tree built from these sequences shows that the crew member was infected by a virus strain virtually identical to other New York strains circulating at the time, while passengers (including the business class passenger [case 2]) were infected by viruses that could be derivatives of this strain. Overall, the molecular and epidemiological data support the evidence of in-flight transmission of influenza A(H1N1)/2009, although the precise mode of transmission is difficult to ascertain with certainty.

Comment. Modern commercial aircraft with high-efficiency particulate filters and frequent recirculation of cabin air have reduced the risk of transmission of airborne respiratory infections. Spread of respiratory viral infections, however, is thought to be related to infectivity of the source patient(s), proximity, and duration of contacts.

Only 2 of the infected passengers on Flight A would have been detected using the WHO criteria for contact tracing. This was also the case with severe acute respiratory syndrome, another emerging viral infection, transmitted predominantly by large particle droplets and direct contact with respiratory secretions or fomites. Perhaps contact tracing all passengers and crew in the same cabin or served by the same crew might be more appropriate in future airline outbreak investigations.

Human activities including onboard interactions may be important in in-flight influenza transmission. Our study showed that the infected passengers slept less on the plane (P=.06; Table). This was also reported in an outbreak of influenza on a delayed Alaskan Airlines flight in 1977. Unfortunately, too few of the passengers we studied used hand sanitizers or masks to assess their impact in reducing transmission of respiratory infections in air travel.

The most important limitation of our study is that we were unable to interview the majority of passengers and crew on Flight A or to do airflow, environmental, or seroepidemiological studies. We also depended on reporting from other international agencies to ascertain all infections. We could thus have underestimated the attack rates.

Our clinical, epidemiological, and molecular evidence are, however, highly suggestive that influenza A(H1N1)/2009 transmission occurred on board Flight A, possibly through human interaction in a crowded cabin. Efforts to contain future emerging respiratory viral in-
Infections spread through international travel will have to include more thorough predeparture screening, perhaps novel decontamination or personal protective technologies, and broader clinical and molecular epidemiologic investigations than currently recommended.

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