Epidemiological and Virological Characterization of 2009 Pandemic Influenza A Virus Subtype H1N1 in Madagascar

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Background. Madagascar was one of the first African countries to be affected by the 2009 pandemic of influenza A virus subtype H1N1 [A(H1N1)pdm2009] infection. The outbreak started in the capital city, Antananarivo, and then spread throughout the country from October 2009 through February 2010.

Methods. Specimens from patients presenting with influenza-like illness were collected and shipped to the National Influenza Center in Madagascar for analyses, together with forms containing patient demographic and clinical information.

Results. Of the 2303 specimens tested, 1016 (44.1%) and 131 (5.7%) yielded A(H1N1)pdm09 and seasonal influenza virus, respectively. Most specimens (42.0%) received were collected from patients <10 years old. Patients <20 years old were more likely than patients >50 years old to be infected with A(H1N1)pdm09 (odds ratio, 2.1; 95% confidence interval, 1.7–2.6; P < .01). Although phylogenetic analyses of A(H1N1)pdm09 suggested multiple introductions of the virus into Madagascar, no antigenic differences between A(H1N1)pdm09 viruses recovered in Madagascar and those that circulated worldwide were observed.

Conclusions. The high proportion of respiratory specimens positive for A(H1N1)pdm09 is consistent with a widespread transmission of the pandemic in Madagascar. The age distribution of cases of A(H1N1)pdm09 infection suggests that children and young adults could be targeted for interventions that aim to reduce transmission during an influenza pandemic.

Influenza pandemics are widespread outbreaks of highly contagious respiratory disease that appear suddenly, infrequently, and at irregular intervals [1]. Influenza pandemics are characterized by the rapid worldwide spread of a novel influenza virus to which humans have had no previous exposure [2]. Influenza symptoms during a pandemic are nonspecific, and therefore laboratory confirmation is required to positively identify a case.

On 11 June 2009, 2 months after the first case of swine-origin 2009 pandemic influenza A virus subtype H1N1 [A(H1N1)pdm2009] infection was detected in Mexico [3, 4], the World Health Organization (WHO) declared a level 6 pandemic alert (defined as sustained, community-wide, human-to-human transmission occurring in at least 2 WHO regions) [5, 6], because of the rapid global spread of the virus [7].

In Madagascar, influenza surveillance has been conducted for several decades. A WHO National Influenza Center was officially recognized in 1978. In September 2007, the Malagasy Ministry of Health, with the support of the Institut Pasteur de Madagascar, established a sentinel surveillance network (SSN).
to monitor febrile illnesses on the basis of daily reports of epidemiological data and weekly virological surveillance [8]. The aim of the network was to facilitate rapid detection of an outbreak and to identify the circulating virus (eg, influenza viruses or arboviruses) responsible for the outbreak.

In this study, we describe the epidemiological and virological characteristics of the 2009 pandemic of A(H1N1)pdm09 infection in Madagascar during the first wave of disease, from August 2009 through February 2010.

MATERIALS AND METHODS

National SSN
The National SSN encompasses private and public primary healthcare centers as part of a global National Integrated Surveillance System that monitors fever syndromes [8]. In August 2009, SSN included 24 sites located in 17 of the 22 health regions in the country. The sites send daily epidemiological reports on influenza-like illness (ILI) cases, while 9 sites ship specimens from up to 5 suspected cases per week.

Surveillance of Study Subjects and Specimen Collection
Samples were received through the SSN and the private health sector, which encompasses general practitioners, private clinics, and hospitals. During the prepandemic period in Madagascar (from April through October 2009), a suspected case of A(H1N1)pdm09 infection was defined as a patient with ILI who met at least one of the following criteria from the WHO case definition [9]: (1) returned from a country or region with an epidemic of A(H1N1)pdm09 infection within the past 7 days, (2) was in close contact with a persons with a confirmed case of A(H1N1)pdm09 infection within the past 7 days, or (3) handled samples suspected of containing A(H1N1)pdm09 in a laboratory or other setting within the past 7 days. When the pandemic was declared by the Malagasy Ministry of Health in October 2009 (calendar week 43), the case definition for suspected A(H1N1)pdm09 infection was changed to the WHO standard case definition for ILI (ie, fever [temperature, ≥38°C] with cough and/or sore throat). Patients with suspected cases were sampled as previously described [10].

Oral and/or nasopharyngeal specimens were placed in universal transport medium (Copan, Italy) and shipped at 4°C to the National Influenza Center at the Institut Pasteur de Madagascar. Specimens were either processed upon reception or stored at −80°C. Demographic and clinical information was collected from each patient with a suspected case.

Virus Detection
Patients with suspected cases were tested using the Centers for Disease Control and Prevention (CDC) real-time reverse-transcription polymerase chain reaction protocol for detection and characterization of human and swine influenza virus [11]. This detection kit includes panels of oligonucleotide primers and dual-labeled hydrolysis (Taqman®) probes for the identification of influenza A virus (subtype H3N2 A(H3N2)s, seasonal subtype H1N1 A(H1N1)s, and A(H1N1)pdm09) and influenza B virus (B).

Phylogenetic Analyses
A(H1N1)pdm09 isolates were sent to the WHO Collaborative Centre (London, United Kingdom) and to the National Institute for Communicable Diseases (Johannesburg, South Africa) for sequencing. Sequences of hemagglutinin (HA) and neuraminidase (NA) genes from a subset of Malagasy viruses were aligned by the ClustalW program, using MEGA 4 software [12]. Phylogenetic trees were reconstructed using the neighbor-joining method of MEGA 4 software. Sequences were deposited into the Global Initiative on Sharing Avian Influenza Database (available at: http://platform.gisaid.org) and GenBank JQ733142 to JQ733145; JQ733151 to JQ733153; JQ733185; JQ733186; JQ733189 to JQ733193 and JQ733196.

Data Analysis
We described the demographic and clinical characteristics of patients with suspected and confirmed cases of A(H1N1)pdm09 infection. We compared the clinical characteristics of A(H1N1)pdm09-positive patients to those of uninfected patients and those of patients infected with seasonal influenza viruses. The χ² test and the Fisher exact test were used for univariate analysis. P values of <.05 were considered to be statistically significant. Variables with a P value of <.20 from univariate analysis were included in multivariate logistic regression analysis. A backward stepwise analysis was performed, and at each step, the new model was compared with the previous one. To confirm whether the model fit, a maximum-likelihood χ² test was used. Analyses were performed using R software, version 2.12.0 (available at: http://www.r-project.org/).

RESULTS

Characteristics of Patients and Specimens
In Madagascar, the first imported case of A(H1N1)pdm09 infection was confirmed on 12 August 2009 in a patient returning from India (Figure 1). Thereafter, several imported cases were detected until October 2009. The first laboratory-confirmed cases of A(H1N1)pdm09 infection in individuals without a history of travel were detected on 8 October 2009. For this study, we selected a period that covered the entire first wave of the pandemic (ie, from 1 August 2009 through 28 February 2010), from the time of the first detected case of A(H1N1)pdm09 infection to the Ministry of Health’s declaration, after 4 consecutive weeks without a new case, that the first wave had ended.
A total of 2353 specimens were received at the National Influenza Center, of which 40.9% (963 of 2353) were collected (Table 1). From the 24 established sentinel sites, specimens were received from 20 sites, and A(H1N1)pdm09 cases were confirmed at 16 sites. The number of samples collected at the sentinel sites ranged from 1 to 182 (median number, 24 samples), and positivity rates ranged from 0% to 76% (median rate, 43%). Specimens received from sites located in the capital, Antananarivo, represented 41.2% of total specimens received from the SSN. Interestingly, of the 59.1% of specimens (1390 of 2353) received from outside of the SSN (eg, from hospitals and private clinics), most came from the capital city during the first weeks of the epidemic.

The age distribution of patients from whom specimens were collected was different from the age distribution of the overall Malagasy population. Indeed, more specimens were collected from patients <20 years old than from patients >20 years old (1608 and 706 specimens, respectively). Overall, we tested 97.9% of specimens (2303) received. A total of 1016 of 2303 patients (44.1%) were confirmed to be infected with A(H1N1)pdm09. Seasonal influenza viruses (A(H1N1)s, A(H3N2)s, and B) were detected in 131 of 2303 patients (5.7%), and in A(H1N1)pdm09 positivities among tested specimens, 2009–2010, Madagascar.

**Figure 1.** Distribution of infections due to 2009 pandemic influenza A virus subtype H1N1 [A(H1N1)pdm2009] and seasonal influenza virus (influenza A virus subtypes H1N1 [A(H1N1)s] and H3N2 [A(H3N2)s] and influenza B virus [FluB]), as well as the rate of A(H1N1)pdm09 positivity among tested specimens, 2009–2010, Madagascar.

<table>
<thead>
<tr>
<th>Region</th>
<th>Specimens Received, No.</th>
<th>Specimens Tested, No.</th>
<th>Positive for A(H1N1)pdm09, No. (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total SSN (24)b</td>
<td>963</td>
<td>955</td>
<td>416 (43.6)</td>
</tr>
<tr>
<td>Antananarivo (4)b</td>
<td>397</td>
<td>393</td>
<td>166 (42.2)</td>
</tr>
<tr>
<td>Provinces (20)b</td>
<td>566</td>
<td>562</td>
<td>250 (44.5)</td>
</tr>
<tr>
<td>Otherc</td>
<td>1390</td>
<td>1348</td>
<td>600 (44.5)</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td><strong>2353</strong></td>
<td><strong>2303</strong></td>
<td><strong>1016 (44.1)</strong></td>
</tr>
</tbody>
</table>

Abbreviation: A(H1N1)pdm09, 2009 pandemic influenza A virus subtype H1N1.

a For clarity, we split results into 2 regions, Antananarivo, the main capital city that represent 10% of the Malagasy population, and provinces that encompass all main cities of all administrative districts.

b Number of sites.

c Other means specimens received outside our SSN (ie, hospital, private clinics, etc).
interval [CI], 1.7–2.6; \( P < .01 \)), and individuals aged 5–19 years were at higher risk of getting infected with A(H1N1)pdm09 (OR range, 2.9 [95% CI, 1.7–4.9] to 5.3 [95% CI, 3.2–8.9]). No significant difference was observed between the 50 nonanalyzed specimens and the analyzed specimens with a high cycle threshold value but were not included in the table.

**Clinical Symptoms of Patients**

To compare clinical symptoms according to the different subtypes of influenza viruses, all 88 patients with unsubtyped influenza A virus were excluded. Complete or partial clinical information was available for the 1016 confirmed pandemic cases. The most frequent symptoms reported were cough (93.9%), fever (78.1%), and rhinorrhea (70.0%) (Table 2). Only 178 patients (17.5%) reported dyspnea and 104 (10.2%) had diarrhea. Overall, 1547 patients who were sampled (69.8%) met the ILI case definition, and in 50.7% (Table 2). Among the 1016 patients with confirmed A(H1N1)pdm09 infection, 785 (77.3%) met the ILI case definition, and in 50.7% (Table 2). Among all analyzed samples, the positivity rate among specimens from patients who met the ILI case definition and presence of 1 or 2 of the following signs: fever, cough, and sore throat. "Missing" was defined as the absence of information about fever, cough, and sore throat.

**Table 2. Sampling Criteria, Age Distribution, and Clinical Symptoms Among Patients With or Without Infection Due to 2009 Pandemic Influenza A Virus Subtype H1N1 A(H1N1)pdm09 or Another Influenza Virus (Seasonal), Madagascar**

<table>
<thead>
<tr>
<th>Variable</th>
<th>A(H1N1)pdm09 (n = 1016)</th>
<th>Other Influenzaa (n = 131)</th>
<th>Negative (n = 1068)</th>
<th>A(H1N1)pdm09 vs Negative</th>
<th>A(H1N1)pdm09 vs Other Influenzaa</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sampling criteria (case definition)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ILI</td>
<td>785 77.3</td>
<td>100 76.3</td>
<td>662 62.0</td>
<td>1.9 1.6–2.4 &lt;.01</td>
<td>1.1 0.7–1.7 &lt;.01</td>
</tr>
<tr>
<td>Non-ILI</td>
<td>177 17.4</td>
<td>25 19.1</td>
<td>293 27.4</td>
<td>Ref ...</td>
<td>Ref ...</td>
</tr>
<tr>
<td>Missingf</td>
<td>54 5.3</td>
<td>6 4.6</td>
<td>113 10.6</td>
<td>... ...</td>
<td>... ...</td>
</tr>
<tr>
<td>Age, y</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0–4</td>
<td>230 22.6</td>
<td>28 21.4</td>
<td>324 30.3</td>
<td>1.8 1.1–3.0 &lt;.01</td>
<td>3.9 1.7–8.6 .02</td>
</tr>
<tr>
<td>5–9</td>
<td>224 22.0</td>
<td>26 19.8</td>
<td>109 10.2</td>
<td>5.3 3.2–8.9 &lt;.01</td>
<td>4.1 1.8–9.1 &lt;.01</td>
</tr>
<tr>
<td>10–14</td>
<td>201 19.8</td>
<td>14 10.7</td>
<td>110 10.3</td>
<td>4.6 2.8–7.9 &lt;.01</td>
<td>6.9 2.8–16.6 &lt;.01</td>
</tr>
<tr>
<td>15–19</td>
<td>138 13.6</td>
<td>13 9.9</td>
<td>121 11.3</td>
<td>2.9 1.7–4.9 &lt;.01</td>
<td>5.1 2.1–12.5 &lt;.01</td>
</tr>
<tr>
<td>20–29</td>
<td>81 8.0</td>
<td>17 13.0</td>
<td>122 11.4</td>
<td>1.7 0.9–2.9 .06</td>
<td>2.3 0.9–5.4 .06</td>
</tr>
<tr>
<td>30–39</td>
<td>57 5.6</td>
<td>11 8.4</td>
<td>120 11.2</td>
<td>1.2 0.7–2.1 .49</td>
<td>2.7 1.0–7.3 .04</td>
</tr>
<tr>
<td>40–49</td>
<td>49 4.8</td>
<td>9 6.9</td>
<td>76 7.1</td>
<td>1.6 0.9–2.9 .09</td>
<td>2.3 0.9–6.3 .08</td>
</tr>
<tr>
<td>≥50</td>
<td>25 2.5</td>
<td>12 9.2</td>
<td>64 6.0</td>
<td>Ref ...</td>
<td>Ref ...</td>
</tr>
<tr>
<td>Missing</td>
<td>11 1.1</td>
<td>1 0.8</td>
<td>22 2.1</td>
<td>... ...</td>
<td>... ...</td>
</tr>
<tr>
<td>Sex</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>505 49.7</td>
<td>57 43.5</td>
<td>496 46.4</td>
<td>Ref ...</td>
<td>Ref ...</td>
</tr>
<tr>
<td>Female</td>
<td>492 48.4</td>
<td>74 56.5</td>
<td>550 51.5</td>
<td>0.9 0.7–1.1 .14</td>
<td>0.8 0.5–1.1 .12</td>
</tr>
<tr>
<td>Missing</td>
<td>19 1.9</td>
<td>0 0.0</td>
<td>22 2.1</td>
<td>... ...</td>
<td>... ...</td>
</tr>
<tr>
<td>Clinical symptom</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Fever</td>
<td>793 78.1</td>
<td>108 82.4</td>
<td>699 65.4</td>
<td>1.7 1.4–2.1 &lt;.01</td>
<td>0.8 0.4–1.3 .36</td>
</tr>
<tr>
<td>Cough</td>
<td>954 93.9</td>
<td>114 87.0</td>
<td>899 84.2</td>
<td>4.4 3.1–6.3 &lt;.01</td>
<td>3.3 1.8–6.0 &lt;.01</td>
</tr>
<tr>
<td>Sore throat</td>
<td>586 57.7</td>
<td>84 64.1</td>
<td>588 55.1</td>
<td>1.1 0.9–1.3 .09</td>
<td>0.8 0.5–1.1 .38</td>
</tr>
<tr>
<td>Asthenia</td>
<td>625 61.5</td>
<td>55 42.0</td>
<td>608 56.5</td>
<td>1.3 1.1–1.5 &lt;.01</td>
<td>2.2 1.5–3.2 &lt;.01</td>
</tr>
<tr>
<td>Headache</td>
<td>675 66.8</td>
<td>72 55.0</td>
<td>629 58.4</td>
<td>1.7 1.4–2.0 &lt;.01</td>
<td>1.8 1.3–2.7 &lt;.01</td>
</tr>
<tr>
<td>Rhinorrhea</td>
<td>711 70.0</td>
<td>91 69.5</td>
<td>678 63.4</td>
<td>1.4 1.1–1.7 &lt;.01</td>
<td>1.0 0.7–1.5 .9</td>
</tr>
<tr>
<td>Dyspnea</td>
<td>178 17.5</td>
<td>12 9.2</td>
<td>196 18.4</td>
<td>0.9 0.7–1.1 .17</td>
<td>1.2 0.7–2.4 .5</td>
</tr>
<tr>
<td>Muscular pain</td>
<td>404 39.8</td>
<td>32 24.4</td>
<td>352 33.0</td>
<td>1.2 0.9–1.4 .06</td>
<td>1.0 0.7–1.7 .9</td>
</tr>
<tr>
<td>Diarrhea</td>
<td>104 10.2</td>
<td>11 8.4</td>
<td>124 11.6</td>
<td>0.8 0.6–1.0 .10</td>
<td>0.7 0.4–1.5 .3</td>
</tr>
</tbody>
</table>

**Abbreviations:** CI, confidence interval; ILI, influenza-like illness; OR, odds ratio; Ref, reference.

a Other influenza are seasonal influenza viruses (ie, influenza A virus subtypes H1N1 and H3N2 and influenza B virus). Some influenza A viruses (88) were detected but unsubtyped because of a high cycle threshold value but were not included in the table.

b Considered statistically significant when \( P < .01 \).

c "ILI" was defined as fever and cough and/or sore throat. "Non-ILI" was defined as nonsatisfaction of the ILI case definition and presence of 1 or 2 of the following signs: fever, cough, and sore throat. "Missing" was defined as the absence of information about fever, cough, and sore throat.

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A total of 552 specimens (23.4%) were received from hospitalized patients. Of these patients, 190 (34.4%) had A(H1N1)pdm09 infection. A total of 53.7% of infected patients were male, 45.3% were children aged <10 years, and 10 (5.3%) were aged >50 years. During the study period, 3 deaths of patients with confirmed A(H1N1)pdm09 occurred. One patient had a history of tuberculosis, a second was a heavy smoker with a history of alcoholism, and a third had congestive heart failure.

When comparing patients with A(H1N1)pdm09 infection to uninfected patients, fever (OR, 1.7; 95% CI, 1.4–2.1), cough (OR, 4.4; 95% CI, 3.1–6.3), asthenia (OR, 1.3; 95% CI, 1.1–1.5), headache (OR, 1.7; 95% CI, 1.4–2.0), and rhinorrhea (OR, 1.4; 95% CI, 1.1–1.7) were more frequent among persons with pandemic influenza (Table 2). In a multivariate analysis that adjusted for age group and clinical symptoms, cough (OR, 4.6; 95% CI, 3.0–7.5), headache (OR, 1.8; 95% CI, 1.5–2.2), fever (OR, 1.6; 95% CI, 1.3–2.0), and asthenia (OR, 1.4; 95% CI, 1.1–1.7) remained associated with pandemic influenza.

When comparing patients with A(H1N1)pdm09 infection to patients with seasonal influenza virus infection, cough (OR, 3.3; 95% CI, 1.8–6.0), asthenia (OR, 2.2; 95% CI, 1.5–3.2), and headache (OR, 1.8; 95% CI, 1.3–2.7) were more common among patients with pandemic influenza (Table 2). In a multivariate analysis that adjusted for age and clinical symptoms, cough (OR, 4.8; 95% CI, 2.2–10.3), asthenia (OR, 3.2; 95% CI, 2.1–4.9), and headache (OR, 1.7; 95% CI, 1.1–2.6) remained associated with A(H1N1)pdm09 infection.

Virological Characteristics of A(H1N1)pdm09 in Madagascar

Antigenic Characteristics of Malagasy Isolates

Malagasy isolates were antigenically closely related to the vaccine strain A/California/7/2009 virus and showed good reactivity against antisera from ferrets immunized with the vaccine strain (J. McCauley, National Institute for Medical Research, personal communication). A set of viruses were analyzed with a wider panel of antisera that included sera raised against viruses from later on in the pandemic (Bayern/69/2009 and A/Lviv/N6/2009). Again, the viruses were homogeneous to these sera, as well as to the older sera. Analyses with different panel of antisera showed that the Malagasy viruses were all homogeneous, except for A/Madagascar/95/2010, which showed a lower level of reactivity with several sera of the panel (J. McCauley, personal communication).

Genetic Characterization of HA Genes From Malagasy Isolates

Sequencing data for the HA gene were available for 26 A(H1N1)pdm09 viruses identified between 2009 and 2010. Phylogenetic analysis revealed 3 amino acid changes in the HA gene, I321V, P83S, and S203T, which were identified in 20 viruses. These changes are similar to the changes identified in viruses isolated worldwide between 2009 and 2010 (Supplementary Figure 1). Among these viruses, 2 subgroups are predominant. The first subgroup showed a unique change (A256T), whereas the second subgroup showed a unique change (D86G). The A256T change is on the head of the HA away from the receptor-binding site in the globular head of the trimer. In the D86G subgroup, we found one isolate, A/Madagascar/95/2010, that showed a lower reactivity against some antisera from immunized ferrets mentioned earlier.

Genetic Characterization of NA Genes From Malagasy Isolates

Phylogenetic analysis of 11 A(H1N1)pdm09 Malagasy viruses isolated between 2009 and 2011 showed 2 amino acid changes, V67I and E398K, in viruses identified between October and December 2009 (Supplementary Figure 2). However, in 2010, different amino acid changes, G77E and R257K, were identified, clustering with viruses isolated in Hong Kong in 2010. Again, these changes were not retained because isolates from 2011 showed different changes (V241I and N369K) as compared to the 2010 isolates from La Reunion Island. The Malagasy viruses did not contain the amino acid change at H275Y associated with oseltamivir resistance (H275Y).

Sensitivity to Sialidase Inhibitors

A subset of 22 A(H1N1)pdm09 viruses were tested for resistance to the sialidase inhibitors oseltamivir and zanamivir, and all were sensitive to both inhibitors (J. McCauley, personal communication).

DISCUSSION

During a 7-month period of the 2009 influenza pandemic, the National Influenza Center received and analyzed 2303 specimens, compared with an average of 432 specimens for the same period during the previous 3 years. The high rate of positivity for A(H1N1)pdm09 among specimens analyzed (45.9%), compared with the average positivity rate for seasonal influenza during the last 3 previous years (38.8%; J. M. Heraud, personal communication), is likely due to the lack of immunity toward this new reassortant virus among the general population. Similar results were observed in several countries [13, 14]. Moreover, data from serological studies suggested a large diffusion of A(H1N1)pdm09 virus among the population [15]. Nevertheless, this rate is quite similar to the rates in some years with active circulation of some seasonal influenza viruses (eg, 45.3% from August 2007 through February 2008) (J. M. Heraud, personal communication). The high number of specimens received might reflect increased media attention and the fear of the population toward this new virus. The real impact of the pandemic within the Malagasy
population might be similar to that of seasonal influenza. Despite some sporadic cases since February 2010, no second wave of A(H1N1)pdm09 infection occurred in Madagascar. As a result, a national serosurvey will be conducted to estimate the incidence of A(H1N1)pdm09 infection in the Malagasy population.

As previously reported, individuals aged 0–4 years accounted for the highest number of cases of A(H1N1)pdm09 infection worldwide [16]. This is probably because mothers are more likely to visit a healthcare center when their children are ill, compared with young adults and adults, who prefer to stay at home and use self-administered medication. Interestingly, our analysis showed that young people and children aged <20 years were significantly more affected than other age groups and that individuals aged 5–19 years had a higher risk of infection with A(H1N1)pdm09. These results are supported by previous studies showing that the highest cumulative incidence of infection with influenza virus occurred in people aged 5–14 years, because of their behavior and because of exposure at school [17, 18]. Thus, to reduce transmission during a pandemic, this population might be a key target for vaccination, both for their own protection (particularly for young children between 6 months and 5 years of age) and to maintain herd immunity. Among people born before 1989 (ie, those ≥20 years), the percentage of A(H1N1)pdm09-positive individuals decreased globally with age. This age distribution in Madagascar is in accordance with a recently published serological study in England, which showed that older age groups seem to be more protected against A(H1N1)pdm09 because of preexisting antibodies directed against other influenza virus subtypes that could induce cross-protection [19]. Among patients who required hospitalization, 10 (5.3%) were aged ≥50 years. This rate is more than the global rate among patients with confirmed A(H1N1)pdm09 infection for the same age groups (2.5%) but similar to recently published data that demonstrated that highest risk of death per capita was among individuals aged ≥50 years [20].

The establishment of the SSN helped in the early detection and efficient monitoring of the pandemic. The network was used as a backbone for other health districts to ship specimens from patients with suspected cases, allowing the National Influenza Center to confirm cases from health districts not directly covered by the network. Moreover, the comparison of positivity rates between specimens collected within and outside of the SSN (43.6% and 44.5%, respectively) indicates that the SSN is representative of the population. In Madagascar, after the first imported case of A(H1N1)pdm09 infection was detected in August 2009, several imported cases were detected until October 2009, similar to other countries [21]. The first laboratory-confirmed A(H1N1)pdm09 cases without a travel history were detected on 8 October 2009 in 3 teenagers from one of the largest schools in Antananarivo [22]. Some of the specimens received did not strictly meet the ILI case definition. Because of the controversy surrounding the ILI case definition, we took the opportunity to study whether the ILI criteria were sensitive and/or specific enough to capture a good proportion of pandemic cases. [23–25]. On the basis of our results, use of “fever” as the only criterion for ILI during the pandemic, which has sometimes been suggested, does not seem to be specific enough to detect true ILI. Indeed, among all analyzed samples, we noticed that the positivity rate among specimens that met the ILI case definition was higher than for samples that did not meet the ILI definition. Interestingly, absence of at least 1 criterion from the ILI case definition (ie, fever, cough, or sore throat) is linked to the lowest detection rate for influenza (34.7%). Consequently, for low-resource countries with limited laboratory capacities, sampling and testing specimens only from individuals who meet the ILI case definition should be considered. We noticed that general practitioners (GPs) outside our SSN collected many specimens from patients who did not meet the ILI case definition. This finding highlights the need to train GPs to use appropriate case definitions when sampling patients for surveillance purposes. Multivariate analysis showed that only fever, cough, and headache were significantly more common among patients with A(H1N1)pdm09 infection, suggesting that these clinical symptoms are more predictive of pandemic infection.

The typical seasonal pattern of influenza activity in Madagascar is January–March and June–October [10, 26, 27]. Thus, the circulation of A(H1N1)pdm09 occurred during the typical period for seasonal influenza within the community in Antananarivo. This may in part explain the intensity and spread of the epidemic. The pandemic virus circulated in Madagascar for approximately 6 months. The pattern of spread of the virus and the observation of epidemic peaks at different times in different regions (data not shown) were probably due to differences in the introduction of viruses, population mobility factors, population density, and bioclimatic factors. Indeed, the capital city is located in a more temperate region of Madagascar, while coastal areas have a tropical, equatorial, or semiarid climate.

During the epidemic, the majority of strains that circulated in Madagascar did not show any antigenic differences from viruses that circulated in other regions of the world, suggesting that a vaccination campaign could have reduced morbidity. Results of phylogenetic analyses of the HA and NA genes of viruses isolated during the study period, especially comparisons of the 2 groups that showed different unique changes (A256T or D86G), favors multiple introductions of A(H1N1) pdm09 strains within the country. Interestingly, sequences of recent 2011 isolates showed that they are more closely related with viruses isolated in La Reunion. This result confirmed that 2009–2010 viruses in Madagascar did not continue to circulate in the country and were replaced in 2011 with new lineages.
Our study has a number of limitations. During the beginning of the epidemic, a large number of specimens received were collected in patients <20 years old, because of outbreaks in schools. Little information was available regarding underlying comorbidities, intensive care unit admissions, and deaths of infected patients. Because only 3 deaths were confirmed, we could not address the severity of or risk factors for pandemic influenza in Madagascar. Another limitation is the lack of sequencing data to better define each season. If we had more viruses sequenced in 2009 and 2010, we might have seen more lineages for the HA gene.

In conclusion, the SSN, which was established for the early detection of outbreaks, proved useful in the early detection and monitoring of the 2009 influenza pandemic in Madagascar. Nevertheless, our system proved to be inefficient to detect an increase in mortality and to estimate the disease burden of the pandemic. Thus, it is important to implement surveillance at the hospital level in the future, to better estimate mortality due to new variants.

Supplementary Data

Supplementary materials are available at The Journal of Infectious Diseases online (http://jid.oxfordjournals.org/). Supplementary materials consist of data provided by the author that are published to benefit the reader. The posted materials are not copyedited. The contents of all supplementary data are the sole responsibility of the authors. Questions or messages regarding errors should be addressed to the author.

Notes

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