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Detection of Pandemic (H1N1) 2009 Virus in Patients Treated with Oseltamivir

To the Editor: In April 2009, an influenza outbreak caused by a novel strain of influenza virus A (H1N1) was identified in Mexico. The rapid spread of this new virus among humans led the World Health Organization to raise the phase of pandemic alert to 6. We report results from the 2 virology laboratories from university hospitals that were involved in the surveillance network of pandemic (H1N1) 2009 in Paris at the beginning of the outbreak in France.

Patients exhibiting influenza-like illness (i.e., fever, sore throat, cough, asthenia, headache, myalgia) and who recently had traveled to countries where the pandemic (H1N1) 2009 outbreak had started (i.e., Mexico, United States, Canada, Japan) were hospitalized. Symptoms began either the day before or the day of hospitalization. Nasal-swab specimens were collected at admission by using the Virocult system (ELITech; Salon-de-Provence, France), and treatment with oseltamivir was started (75 mg, 2×/day). Pandemic (H1N1) 2009 infection was diagnosed by using rapid test QuickVue Influenza A+B (Quidel, San Diego, CA, USA) and real-time reverse transcription–PCR (RT-PCR) assays from the French National Influenza Centers or the US Centers for Disease Control and Prevention (*1*). In the case of a positive result, influenza virus in nasal secretions from patients was monitored daily by RT-PCR until viral genomes became undetectable.

From April 24 through June 7, 2009, nasal swab specimens from 234 persons (132 men; median age of all patients 33 years) were processed; pandemic (H1N1) 2009 infection was confirmed for 17 men and 15 women (median age 33 years) by RT-PCR. Results of the Quidel rapid tests were available for 27 specimens, with positive results for 9 (33% sensitivity). However, no positive result was observed with the Quidel rapid tests among the nasal swab specimens with negative RT-PCR results (100% specificity). Influenza virus detection in nasal secretions was monitored for 16 patients who had laboratory-confirmed pandemic (H1N1) 2009 infection and were treated with oseltamivir. Viral detection by RT-PCR was absent 2 to >5 days after antiviral treatment began (Figure). Significant differences were not found in sex and age of the patients (data not shown).

These preliminary virologic data obtained during the first 6 weeks of pandemic (H1N1) 2009 in France confirm the poor sensitivity of the Quidel test toward this new virus, as recently reported (*2*). Further studies are needed to evaluate the performances of other rapid tests. Hayden et al. (*3*) demonstrated that treatment with oseltamivir significantly reduced duration of viral shedding among patients infected with seasonal influenza virus A (H1N1), in comparison with a placebo group: 1.5–2.5 days vs. 3.5–5.5 days ($p = 0.003$). In our study, surprisingly, PCR results for sequential nasal swab specimens from 16 patients infected by pandemic (H1N1) 2009 and treated with oseltamivir were negative within 3 days after therapy for only 9 (56%); indeed, for 3 (19%) patients, viral genome could be detected >5 days after antiviral treatment began. These data raise questions about potential virus transmission during antiviral treatment and the possible resistance of

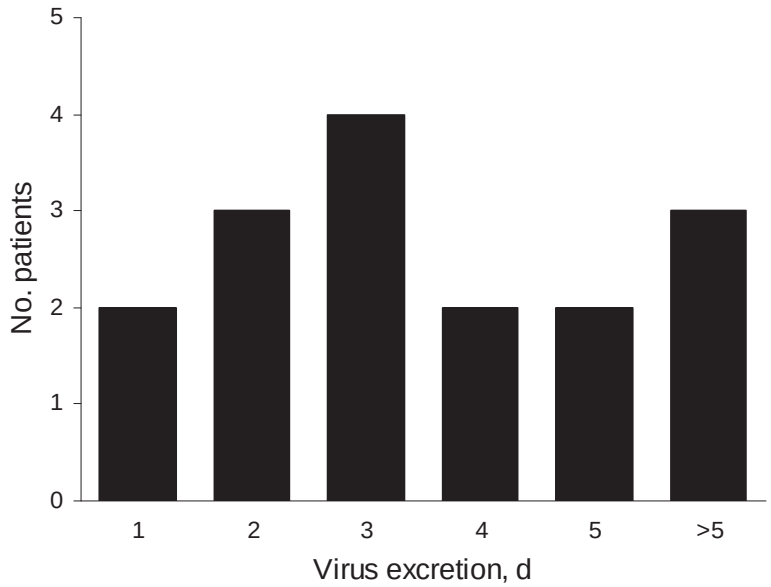

Figure. Duration of pandemic (H1N1) 2009 excretion in nasal swabs from patients treated with oseltamivir. The number of days from start of oseltamivir treatment to achievement of negative results of reverse transcription–PCR (RT-PCR) is indicated for 16 patients. The 3 patients classified in the last group (>5 days) are 1 patient with a negative RT-PCR result on day 7 posttreatment and 2 patients who still had positive results on day 5 posttreatment but provided no additional sample for testing.

pandemic (H1N1) 2009 to oseltamivir. This latter point is now under study.

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Marburg Virus in Fruit Bat, Kenya

To the Editor: Lake Victoria Marburgvirus (MARV) causes severe hemorrhagic fever with a high case-fatality rate in humans. Index cases occurred in Europe during 1967 among laboratory workers who handled tissues and blood samples of nonhuman primates from Africa (*1*). Thereafter, MARV was reported throughout sub-Saharan Africa. Most outbreaks in humans were associated with visits to caves and mines (*2*–*6*). In Kenya, human cases of MARV infection were reported in 1980 and 1987; these occurred after visits to the Kitum Cave at Mount Elgon (*7*,*8*). MARV was detected in tissues of Egyptian fruit bats (*Rousettus aegyptiacus*) and other bat species from the Democratic Republic of Congo (DRC), Gabon, and Uganda (*3*–*6*).

We collected bats from across Kenya during June–July 2007 within the framework of the Global Disease Detection Program, which is dedicated to investigation of emerging pathogens. Collection protocols were approved by the National Museums of Kenya and by the Centers for Disease Control and Prevention (Atlanta, GA, USA). Blood, fecal and oral swab specimens, and selected tissue samples were collected from bats and stored on dry ice.

For MARV detection, total RNA was extracted from pooled or individual liver, spleen, and lung samples from 272 bats. Nested reverse transcription–PCR (RT-PCR) with primers specific for MARV nucleoprotein gene was performed as described (*5*). When a band of the expected size was detected after electrophoresis on an agarose gel, the RT-PCR product was sequenced. Laboratory cross-contamination was not a concern because no work with MARV had been conducted in the facility where the examination was performed.

MARV RNA was detected in pooled liver, spleen, and lung tissue of an apparently healthy, pregnant,