Oseltamivir-Resistant Influenza A(H1N1)pdm09 Viruses, United States, 2013–14

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We report characteristics of oseltamivir-resistant influenza A(H1N1)pdm09 viruses and patients infected with these viruses in the United States. During 2013–14, fifty-nine (1.2%) of 4,968 analyzed US influenza A(H1N1)pdm09 viruses had the H275Y oseltamivir resistance–conferring neuraminidase substitution. Our results emphasize the need for local surveillance for neuraminidase inhibitor susceptibility among circulating influenza viruses.

During the 2013–14 influenza season, influenza A(H1N1)pdm09 virus was the predominant circulating virus (~80%) in the United States for the first time since the 2009 pandemic (1). We report and describe characteristics of oseltamivir-resistant influenza A(H1N1)pdm09 viruses and patients infected with these viruses in the United States.

The Study

We requested that all US state public health laboratories submit influenza-positive specimens for virologic surveillance, including antiviral susceptibility testing, as described (2). In brief, every 2 weeks each laboratory was asked to send ≤5 specimens for all virus types for virus isolation and neuraminidase (NA) inhibition assay for oseltamivir, zanamivir, and, in a subset, laninamivir and peramivir (3). All oseltamivir-resistant viruses were tested for the H275Y substitution in NA by pyrosequencing (4). Unpropagated influenza A(H1N1)pdm09 virus–positive clinical specimens were screened for the H275Y substitution by pyrosequencing (online Technical Appendix, http://wwwnc.cdc.gov/EID/article/21/1/14-1006-Techapp1.pdf). If a cluster (>2 viruses) of oseltamivir-resistant A(H1N1)pdm09 viruses was detected, the state was asked to submit additional influenza A(H1N1)pdm09 virus specimens for testing.

We attempted to collect information by using a standard form from all patients with oseltamivir-resistant virus infection and from a sample of patients with oseltamivir-susceptible virus infection. A 2:1 (susceptible:resistant) sample was randomly selected from the list of tested specimens from the same age group in each state (<5, 5–17, 18–64, and ≥65 years). Patients with oseltamivir-resistant or -susceptible virus infections were compared by using conditional logistic regression models that controlled for age. Full NA and hemagglutinin sequence analysis was performed on all resistant viruses and a subset of susceptible viruses.

During October 1, 2013–April 30, 2014, a total of 4,968 influenza A(H1N1)pdm09 virus specimens collected from 50 US states and 2 territories were tested for antiviral susceptibility (1,811 virus isolates and 3,157 clinical specimens). A total of 59 (1.2%) influenza A(H1N1)pdm09 viruses from 20 states had the H275Y NA substitution conferring resistance to oseltamivir and peramivir (Figure 1; Table 1). None of 1,811 virus isolates was resistant to zanamivir.

Viruses with the H275Y substitution were detected in patient specimens collected during October 7, 2013–March 25, 2014; monthly prevalence ranged from 0.8% to 2.5%. Among 49 (83.0%) patients with a resistant virus infection and available information, 15 (30.6%) received oseltamivir before specimen collection (Table 2). Prior oseltamivir use was more frequent among hospitalized patients and patients with resistant virus infections than those with susceptible virus infections. Among those with prior exposure, 6 (40.0%) patients with oseltamivir-resistant and none with oseltamivir-susceptible virus infections were immunocompromised (p = 0.03). No differences were found between patients with oseltamivir-resistant or -susceptible virus infections.

Most resistant viruses were clustered in 5 states (California, Hawaii, Louisiana, Mississippi, and Pennsylvania) (Figure 1). Among patients with oseltamivir-resistant virus infection, only 1/4 from California, 0/4 from Hawaii, 3/11 from Louisiana, 1/3 from Mississippi, and 0/4 from Pennsylvania had exposure to oseltamivir before specimen collection. All patients from Pennsylvania except 1 attended 1 of 2 universities (among 7 participating students, none shared classes, residences, or social events). There were no epidemiologic links between other patients.

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DISPATCHES

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Limited information was available for oseltamivir-treated patients with resistant and susceptible virus infections (online Technical Appendix Table).

Most hemagglutinin sequences from US influenza A(H1N1)pdm09 viruses collected since October 1, 2013, belonged to the 6B genetic group, and there was minimal separate clustering between susceptible and resistant viruses (online Technical Appendix Figure 1). Similar results were observed for the phylogenetic tree of the NA gene (Figure 2). NA sequences from resistant viruses in the United States with the H275Y substitution were generally scattered among other susceptible viruses from genetic group 6B viruses. Most (>99%) influenza A(H1N1)pdm09 viruses currently in circulation have NA substitutions V241I and N369K (online Technical Appendix Figure 2). There was >1 cluster of NA sequences with the N386K substitution; each cluster contained susceptible and resistant viruses. Most (>89%) resistant viruses from the United States do not have the N386K mutation.

**Conclusions**

During the 2013–14 influenza season, prevalence of oseltamivir-resistant influenza A(H1N1)pdm09 viruses was low (∼1%) in the United States, although prevalence was higher in a few states. Most patients infected with an oseltamivir-resistant influenza A(H1N1)pdm09 virus had no

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**Table 1. Neuraminidase inhibitor susceptibility for influenza A(H1N1)pdm09 viruses, United States, October 1, 2013–April 30, 2014**

<table>
<thead>
<tr>
<th>Method of testing</th>
<th>Neuraminidase inhibitor</th>
<th>Neuraminidase inhibition assay†</th>
<th>Neuraminidase inhibition assay‡</th>
<th>Neuraminidase inhibition assay§</th>
</tr>
</thead>
<tbody>
<tr>
<td>Neuraminidase inhibition assay†</td>
<td>Oseltamivir</td>
<td>1,811</td>
<td>1,811</td>
<td>1,431</td>
</tr>
<tr>
<td>No. virus isolates tested‡</td>
<td></td>
<td>1,792</td>
<td>1,811</td>
<td>1,412</td>
</tr>
<tr>
<td>No. oseltamivir susceptible (mean IC(_{50}) ± SD), nmol/L</td>
<td></td>
<td>(0.19 ± 0.14)</td>
<td>(0.18 ± 0.06)</td>
<td>(0.06 ± 0.02)</td>
</tr>
<tr>
<td>No. oseltamivir resistant (mean IC(_{50}) ± SD), nmol/L</td>
<td></td>
<td>19</td>
<td>0</td>
<td>19</td>
</tr>
<tr>
<td>Resistance, %</td>
<td></td>
<td>(181.31 ± 67.63)</td>
<td>(17.71 ± 6.83)</td>
<td>1.1</td>
</tr>
<tr>
<td>Pyrosequencing§</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No. clinical specimens tested</td>
<td>3,157</td>
<td>NA</td>
<td>3,157</td>
<td>NA</td>
</tr>
<tr>
<td>No. H275 wild-type</td>
<td>3,117</td>
<td>NA</td>
<td>3,117</td>
<td>NA</td>
</tr>
<tr>
<td>No. H275 variants</td>
<td>40</td>
<td>NA</td>
<td>40</td>
<td>NA</td>
</tr>
<tr>
<td>Resistance, %</td>
<td>1.3</td>
<td>NA</td>
<td>1.3</td>
<td>NA</td>
</tr>
<tr>
<td>Total</td>
<td>4,968</td>
<td>1,11</td>
<td>4,588</td>
<td>352</td>
</tr>
<tr>
<td>No. resistant viruses</td>
<td>59</td>
<td>0</td>
<td>59</td>
<td>0</td>
</tr>
<tr>
<td>Resistance, %</td>
<td>1.2</td>
<td>0</td>
<td>1.3</td>
<td>0</td>
</tr>
</tbody>
</table>

*IC\(_{50}\), 50% inhibitory concentration; NA, not applicable.
†H275Y confirmed in virus isolate by pyrosequencing and full neuraminidase sequencing.
‡Most (99.8%) influenza A(H1N1)pdm09 virus isolates were characterized as A/California/7/2009-like, the influenza A (H1N1) component of the 2013–2014 Northern Hemisphere influenza vaccine.
§Includes pyrosequencing data from New York contract laboratory and data submitted by 19 state public health laboratories in Arizona, California, Colorado, Delaware, Florida, Georgia, Hawaii, Idaho, Maine, Maryland, Massachusetts, Michigan, Minnesota, New York, Pennsylvania, Texas, Utah, Washington, and Wisconsin.
prior exposure to oseltamivir. These findings are consistent with a low, and locally variable, level of circulation of resistant viruses. In our study, exposure to oseltamivir before specimen collection was more common among hospitalized patients with resistant virus infections than before specimen collection was more common among patients without prior oseltamivir exposure, suggesting community transmission. These H275Y viruses had permissive mutations, V241I and N369K, in addition to N386S substitutions, which was similar to H275Y viruses isolated in 2012 from Dutch travelers returning from Spain (11). These mutations were believed to offset the destabilizing effect of H275Y and possibly enhance virus transmissibility. The substitutions V241I, N369K, or N386S were not present in influenza A(H1N1)pdm09 virus when it emerged in 2009. However, since 2011, circulating influenza A(H1N1)pdm09 H275Y viruses have acquired these substitutions, coinciding with increasing evidence for community transmission. These H275Y viruses in the United States and other countries (2,12).

All influenza A(H1N1)pdm09 viruses circulating in the United States in 2013–14 had V241I and N369K substitutions, and ≈10% of resistant viruses and ≈20% of susceptible viruses had an additional substitution (N386K). All influenza A(H1N1)pdm09 H275Y viruses detected in China and Japan in 2013–14 had 3 substitutions (13). In combination with the H275Y substitution, V241I or N369K enhances surface expression and activity of NA (14). The N386S substitution and the recently detected N386K substitution result in loss of a glycosylation site (15). The N386S substitution and the recently detected N386K substitution result in loss of a glycosylation site (15). The N386S substitution and the recently detected N386K substitution result in loss of a glycosylation site (15). The N386S substitution and the recently detected N386K substitution result in loss of a glycosylation site (15). The N386S substitution and the recently detected N386K substitution result in loss of a glycosylation site (15). The N386S substitution and the recently detected N386K substitution result in loss of a glycosylation site (15).
Close monitoring for the N386K/S substitution may provide information needed to delineate its role in virus spread. In addition to permissive NA mutations, other properties, such as antigenic novelty, which might provide an advantage to oseltamivir-resistant viruses and facilitate their spread, should also be monitored.

The potential for emergence and spread of oseltamivir-resistant influenza A(H1N1)pdm09 viruses, coupled with limited pharmaceutical options against influenza, emphasizes the need for local surveillance for NA inhibitor susceptibility among circulating influenza viruses. Studies on biologic characteristics (e.g., replication in and transmissibility from ferrets) of influenza A(H1N1)pdm09 virus community isolates with H275Y and other permissive mutations are ongoing.

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References


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Technical Appendix

Supplemental Methods for Analysis of Oseltamivir-Resistant Influenza A(H1N1)pdm09 Viruses, United States, 2013–14

Neuraminidase inhibition (NI) assays (1) and pyrosequencing (2) were performed according to standard protocols of the Centers for Disease Control and Prevention (CDC) (Atlanta, GA, USA) (fluantiviral@cdc.gov). For national virologic surveillance, NI testing for most (80%) virus isolates (n = 1,811) was performed by public health laboratories in California, Wisconsin, and Utah that were contracted by the Association for Public Health Laboratories (Silver Spring, MD, USA). The remaining (20%) NI testing was performed by CDC. Results of the NI assay (50% inhibitory concentration) were interpreted and reported in accordance with recommendations of the Influenza Antiviral Working Group of the World Health Organization (3), in which influenza A viruses with <10-fold change in 50% inhibitory concentration are characterized as exhibiting normal inhibition by the respective neuraminidase inhibitor, and those with 10–100-fold and >100-fold change as exhibiting reduced and highly reduced inhibition, respectively. Viruses showing reduced and highly reduced inhibition are genetically analyzed to detect molecular markers of neuraminidase inhibitor resistance. In this study, virus isolates showing highly reduced inhibition by oseltamivir were tested by pyrosequencing at CDC to confirm the presence of the H275Y marker of resistance.

Of 3,157 clinical specimens tested primarily by pyrosequencing to detect the H275Y marker, 40% were tested for national surveillance by the Wadsworth Center, New York State Department of Health (Albany, NY, USA), which was also contracted by the Association for Public Health Laboratories, and 60% were tested for individual state surveillance by 19 other public health laboratories, who then shared their data with CDC. Further comprehensive genetic analysis was performed on drug-resistant viruses detected by NI assay or pyrosequencing. Antiviral susceptibility data from all above testing sources were consolidated for publication in the weekly CDC FluView report (4) on national virologic surveillance. When necessary, surveillance was enhanced by increasing
sampling and testing in specific regions exhibiting higher than the national frequency of neuraminidase inhibitor resistance.

References


Technical Appendix Figure 1. Evolutionary relationships among influenza A (H1N1)pdm09 hemagglutinin (HA) genes, United States, 2013–14. Phylogenetic tree was generated by using the MEGA software package v5.2 (http://www.megasoftware.net/) and the neighbor-joining method. Evolutionary distances were computed by using the maximum composite likelihood model. Analysis included 193 representative A(H1N1)pdm09 HA gene sequences. Scale bar indicates nucleotide substitutions per site. Solid circles indicate oseltamivir-resistant H275Y markers. A/California/07/2009 (current Northern Hemisphere vaccine strain) virus was used as a reference for ancestry (root) and numbering. F, Centers for Disease Control and Prevention reference antigen; Oct, October 2013; Nov, November 2013; Dec, December 2013; Jan, January 2014; Feb, February 2014; GLY, glycosylation.
Technical Appendix Figure 2. Evolutionary relationships among influenza A (H1N1)pdm09 neuraminidase (NA) genes, United States, 2013–14. Phylogenetic tree was generated by using the MEGA software package v5.2 (http://www.megasoftware.net/) and the neighbor-joining method. Evolutionary distances were computed by using the maximum composite likelihood model. Analysis included 193 representative A(H1N1)pdm09 NA gene sequences. Scale bar indicates nucleotide substitutions per site. Solid circles indicate oseltamivir-resistant H275Y markers. A/California/07/2009 (current Northern Hemisphere vaccine strain) virus was used as a reference for ancestry (root) and numbering. F, Centers for Disease Control and Prevention reference antigen; Oct, October 2013; Nov, November 2013; Dec, December 2013; Jan, January 2014; Feb, February 2014; GLY, glycosylation.