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In February 2016, three influenza B/Victoria/2/87 lineage viruses exhibiting 4- to 158-fold reduced inhibition by neuraminidase inhibitors were detected in Laos. These viruses had an H134N substitution in the neuraminidase and replicated efficiently in vitro and in ferrets. Current antiviral drugs may be ineffective in controlling infections caused by viruses harboring this mutation.

Influenza B viruses cause annual epidemics and contribute to ≈30% of influenza-associated deaths among children in the United States (1). Two lineages, B/Victoria/2/87 and B/Yamagata/16/88, have been co-circulating globally in recent years (2,3). Neuraminidase (NA) inhibitors (NAIs) are the only drugs available for treating influenza B virus infections, but NA mutations that emerge during treatment or due to natural variance can diminish the usefulness of NAIs.

The Study

For this study, the National Center for Laboratory and Epidemiology in Vientiane, Laos, a member of the World Health Organization Global Influenza Surveillance and Response System, provided influenza A and B viruses to the World Health Organization Collaborating Center at the Centers for Disease Control and Prevention (CDC) in Atlanta, Georgia, USA; the viruses had been collected during October 1, 2015–February 29, 2016. We propagated the viruses and then used the CDC standardized NA inhibition assay to assess their susceptibility to NAIs (4). Compared with the median 50% inhibitory concentration (IC$_{50}$) values for B-Victoria lineage viruses, IC$_{50}$ values for 2 of the 24 B-Victoria lineage viruses, B/Laos/0406/2016 and B/Laos/0525/2016, were elevated for zanamivir (129- to 158-fold), oseltamivir (4-fold), peramivir (72- to 74-fold), and laninamivir (41- to 42-fold) (Table 1). These results were interpreted as highly reduced inhibition by zanamivir, normal inhibition by oseltamivir, and reduced inhibition by peramivir and laninamivir (Table 1) (5).

This interpretation is useful but obscures the higher median oseltamivir IC$_{50}$ value (9.67 nmol/L vs. 0.42–1.47 nmol/L for other NAIs; Table 1) and the lower potency of oseltamivir in inhibiting NA activity of influenza B viruses (4,7). Moreover, reports from clinical studies indicate a lesser susceptibility of influenza B viruses to oseltamivir than to zanamivir (7–9). Although the laboratory criteria defining clinically relevant NAI resistance are not established, the inhibitory profiles of these 2 viruses suggest resistance to ≥1 antiviral drugs. NA sequence analysis revealed that both viruses had an amino acid substitution, histidine (H)→asparagine (N), at the highly conserved residue 134 (NA-H134N) (6); the presence of H134N in the respiratory specimens was confirmed by pyrosequencing (Figure 1) (10). NA-H134Y was previously reported in influenza B virus displaying reduced inhibition by peramivir (11). The inhibition profile of influenza B viruses bearing NA-H134N resembles that of influenza A(H1N1) viruses carrying NA-Q136R (residue 134 in influenza B NA corresponds to 136 in N1 numbering) (12). Residue 134 (136) has been implicated in the conformational change of the 150-loop, which may adversely affect the interaction between the NA active site and NAIs, especially those containing the guanidyl group (online Technical Appendix Figure, https://wwwnc.cdc.gov/EID/article/23/4/16-1876-Techapp1.pdf).

To expand testing, the Laos National Center for Laboratory and Epidemiology provided 40 additional specimens

DISPATCHES

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that were positive for B-Victoria lineage virus by real-time reverse transcription PCR (13), bringing the total number tested to 64. The specimens were collected during October 2015–April 2016 in Champasack (n = 41), Vientiane (n = 12), Luangprabang (n = 7), and Saravanh (n = 5) Provinces from 28 male and 37 female patients (median age 7 [range 0–67] years). Pyrosequencing revealed NA-H134N in 1 specimen; the respective isolate, B/Laos/0654/2016, displayed the expected NA inhibition profile (Table 1). In total, we found the NA-H134N substitution in 3 (4.6%) of the 65 tested B-Victoria viruses. Analysis of NA sequences deposited to the GISAID database (http://www.gisaid.org) revealed that among 8,601 sequences of influenza B virus collected worldwide during October 2014–September 2016, only 3 other sequences contained a substitution at H134 (2 harbored H134Y and 1 H134L); the 3 sequences were for B-Victoria lineage viruses.

Epidemiologic data revealed that the NA-H134N viruses were collected from a young woman, a young man, and a 3-year-old girl residing in 2 distant provinces (Table 2). The 3 infections occurred 6–10 days apart in February 2016, and 1 of the patients received medical care for severe acute respiratory illness. No epidemiologic links were identified among the 3 patients infected with the drug-resistant viruses, and patients had no documented exposure to NAIs.

**Table 1. Neuraminidase inhibitor susceptibility of influenza B viruses isolated from human respiratory specimens, Laos, 2016**

<table>
<thead>
<tr>
<th>Virus isolate</th>
<th>NA amino acid change</th>
<th>Zanamivir IC_{50} ± SD (Inhibitor concentration needed to reduce NA activity by 50%)</th>
<th>Oselaltamivir IC_{50} ± SD (Inhibitor concentration needed to reduce NA activity by 50%)</th>
<th>Peramivir IC_{50} ± SD (Inhibitor concentration needed to reduce NA activity by 50%)</th>
<th>Laninamivir IC_{50} ± SD (Inhibitor concentration needed to reduce NA activity by 50%)</th>
<th>Date specimen collected</th>
<th>GISAID accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>B/Laos/0080/2016</td>
<td>H134</td>
<td>1.09 ± 0.16 (1)</td>
<td>14.48 ± 1.76 (1)</td>
<td>0.36 ± 0.05 (1)</td>
<td>1.15 ± 0.02 (1)</td>
<td>14 Jan</td>
<td>EPIISL 222862</td>
</tr>
<tr>
<td>B/Laos/0406/2016</td>
<td>H134N</td>
<td>148.36 ± 14.40</td>
<td>37.87 ± 1.96 (4)</td>
<td>31.09 ± 3.70 (74)</td>
<td>62.43 ± 4.66 (42)</td>
<td>15 Feb</td>
<td>EPIISL 230599</td>
</tr>
<tr>
<td>B/Laos/0525/2016</td>
<td>H134N</td>
<td>176.03 ± 11.14</td>
<td>37.55 ± 5.60 (4)</td>
<td>30.25 ± 2.90 (72)</td>
<td>60.12 ± 2.38 (41)</td>
<td>25 Feb</td>
<td>EPIISL 230600</td>
</tr>
<tr>
<td>B/Laos/0654/2016</td>
<td>H134N</td>
<td>151.95 ± 16.30</td>
<td>35.06 ± 5.08 (4)</td>
<td>31.29 ± 0.24 (75)</td>
<td>61.53 ± 1.03 (42)</td>
<td>25 Feb</td>
<td>EPIISL 230600</td>
</tr>
</tbody>
</table>

*Viruses were isolated and propagated on MDCK cells. Susceptibility was determined using a fluorescence-based neuraminidase (NA) inhibition assay. †Fold change compared with the median IC_{50} value determined for influenza B-Victoria lineage viruses (n = 430) that were circulating worldwide during the 2015–16 influenza season. Median IC_{50} values were 1.11, 9.67, 0.42, and 1.47 nm for zanamivir, oseltamivir, peramivir, and laninamivir, respectively. Bold indicates fold increases that correspond to reduced inhibition (5- to 50-fold) or to highly reduced (>50-fold) inhibition by a NAI, as outlined by the World Health Organization Expert Working Group of the Global Influenza Surveillance and Response System for Surveillance on Antiviral Susceptibility (5). §Amino acid residue 134 in influenza type B NA corresponds to residue Q136 in N1 and N2 NA amino acid numbering (6). ¶Oselaltamivir carboxylate was used in NA inhibition assay.

**Figure 1. Neuraminidase gene segment (nts 399–497) of influenza B/Laos/0080/2016 virus carrying NA-H134 (A) and B/Laos/0654/2016, NA-N134 (B). RNA extracted from respiratory specimens was used for reverse transcription PCR (RT-PCR) amplification. Two primers, NA-B-242F (5'-CATACCCCGCTTAT CTTGC-3', forward primer) and NA-B-426Rb (biotin-5'-CTGTCTCCCTTGTTCC ATTGTAG-3'; reverse biotinylated primer) were used in RT-PCR, essentially as described previously (10); primer NA-B-378Fs (5'-TGCAAAACACTTGG CTTAACC-3') was used for pyrosequencing. Underlining indicates nucleotide triplet encoding amino acid residue 134. Shading indicates the nucleotides used to determine the proportion of H134 and N134 neuraminidase variants. Pyrosequencing dispensation order: E-Enzyme mixture; S-substrate mixture; G, C, A and T – nucleotides dGTP, dCTP, dATPoS and dTTP, correspondingly.
The 3 drug-resistant viruses were genetically similar to other B-Victoria lineage viruses circulating in Laos during 2015–2016. Besides having the NA-H134N amino acid substitution, these viruses also shared the M1-H159Q amino acid substitution not identified in other virus sequences (Table 2). Also, these viruses have 3 synonymous nucleotide mutations: PB1-c93t, PB1-g1930a, and HA-g1520a. In addition, NA-H134N viruses differed from each other by the following synonymous nucleotide mutations: B/Laos/0406/2016 possessed NS1-g345a, B/Laos/0525/2016 possessed NA-V220I, and B/Laos/0654/2016 possessed NS2-g186a.

Table 2. NA-H134N substitution—containing influenza B viruses that caused confirmed infection among 3 persons, Laos, February 2016

<table>
<thead>
<tr>
<th>Virus name, passage history§</th>
<th>Amino acid change in virus genes†</th>
<th>Patient information</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>NA H134</td>
<td>D390</td>
</tr>
<tr>
<td>B/Laos/0406/2016 Original</td>
<td>N</td>
<td>D/E</td>
</tr>
<tr>
<td>C2</td>
<td>N</td>
<td>D/E</td>
</tr>
<tr>
<td>B/Laos/0525/2016 Original</td>
<td>N</td>
<td>–</td>
</tr>
<tr>
<td>C2</td>
<td>N</td>
<td>–</td>
</tr>
<tr>
<td>B/Laos/0654/2016 Original</td>
<td>N</td>
<td>–</td>
</tr>
<tr>
<td>C1</td>
<td>N</td>
<td>–</td>
</tr>
</tbody>
</table>

*HA, hemagglutinin; ILI, influenza-like illness; M1, matrix protein 1; NA, neuraminidase; NS1, nonstructural protein 1; Pres., presentation; SARI, severe acute respiratory illness; –, indicates same amino acid residue as in the consensus sequence of B-Victoria viruses that were circulating in Laos during the 2015–16 influenza season.

†Strain-specific amino acid sequence numbering is used. Sequences for all 8 gene segments were generated using the MiSeq sequencing system (Illumina Inc., San Diego, CA, USA) (14) (online Technical Appendix Table 1, https://wwwnc.cdc.gov/EID/article/23/4/16-1876-Techapp1.pdf). Data are amino acid differences in protein-coded regions of NA, HA, M1, and NS1 genes compared with the consensus sequence. Not shown: synonymous nucleotide mutations that were common for the NA-H134N viruses: PB1-c93t, PB1-g1930a, and HA-g1520a. In addition, NA-H134N viruses differed from each other by the following synonymous nucleotide mutations: B/Laos/0406/2016 possessed NS1-g345a, B/Laos/0525/2016 possessed NA-V220I, and B/Laos/0654/2016 possessed NS2-g186a.

‡Corresponds to position 219 in NS1 protein numbering used by Ma et al. (15).

§Original indicates specimen collected from patient; C1 and C2 indicates virus propagated 1 or 2 times on MDCK cells.

¶Presence of the NA-H134N substitution in the original respiratory specimens was confirmed by a pyrosequencing assay (Figure 1; online Technical Appendix Table 2).

Conclusions

In February 2016, we detected 3 influenza B viruses in Laos bearing a rare NA-H134N substitution. Current antiviral medications may not effectively control infections...
Antiviral Drug–Resistant Influenza B Viruses

causethesuchviruses.VirusharboringNA-H134NandNS1-V220IreplicatedefficientlyinNHBEcellsandin
theferretupperrespiratorytract.Studiestoascertainthe
effectofNA-H134NandNS1-V220IoinfluenzaBvi
rusvirulenceandtransmissibilityinamanimalianhost
areneeded.

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Australia, for providing laninamivir.

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Dr. Baranovich worked in the Influenza Division, National
Center for Immunization and Respiratory Diseases, Centers for
Disease Control and Prevention, during the conduct of this study.
Her research interests include the molecular mechanisms of
influenza virus resistance to antiviral medications and the effect
of resistance mutations on viral fitness and evolution.

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alignment of paramyxovirus hemagglutinin-neuraminidase with

Figure 2. Characterization of influenza B viruses detected in
Laos, February 2016. A) Thermostability of neuraminidase
(NA) determined after viruses were incubated for 15 min at
4°C or at 30°C–57°C. NA enzyme activity was determined
by a fluorescence-based assay (4). B) Replication kinetics
of influenza B viruses in fully differentiated human primary
NHBE cells that were inoculated with the designated viruses
(multiplicity of infection 0.001). Apical washes were taken
at indicated times after inoculation, and virus titers were
determined on MDCK cells. The area under the virus titer curve
from 2 to 72 h after inoculation (AUC 2–72) was determined
and compared with that of the control virus by repeated-measures
analysis of variance with the Dunnett posttest, using GraphPad
Prism 5 software (GraphPad Software, La Jolla, CA, USA).
Dashed line represents the limit of detection of the assay (1.75
log 50 tissue culture infectious dose [TCID 50/mL]). Values
shown are means and SDs from 2 independent experiments
performed in duplicates (n = 4). Error bars represent SDs. NS,
not significant.


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