CHARACTERIZATION OF SEASONAL INFLUENZA VIRUSES FROM AMERICAS, SEPT. 2016 TO PRESENT

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Centers for Disease Control and Prevention
Atlanta, GA 30333
Specimen Received at CDC from PAHO Countries

Count of Specimens

INFLUENZA SEASON

2012-13: 291 (H3: 229, H1PDM09: 18, B: 26, A: 26)
2013-14: 314 (H3: 226, H1PDM09: 22, B: 60, A: 0)
2014-15: 347 (H3: 227, H1PDM09: 6, B: 114, A: 0)
2015-16: 651 (H3: 305, H1PDM09: 346, B: 30, A: 0)
2016-17: 140 (H3: 89, H1PDM09: 56, B: 72, A: 5)
### Weeks between Specimens Collection and Receipt at CDC By Season For PAHO countries

<table>
<thead>
<tr>
<th>Season</th>
<th>2013</th>
<th>2014</th>
<th>2015</th>
<th>2016</th>
<th>2017</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>AVG</td>
<td>Min</td>
<td>Max</td>
<td>AVG</td>
<td>Min</td>
</tr>
<tr>
<td>Wks</td>
<td>17.60</td>
<td>3</td>
<td>37</td>
<td>15.38</td>
<td>2</td>
</tr>
<tr>
<td>Weeks</td>
<td>2013</td>
<td>2014</td>
<td>2015</td>
<td>2016</td>
<td>2017</td>
</tr>
<tr>
<td>One to Four weeks</td>
<td>1.18%</td>
<td>2</td>
<td>8.47%</td>
<td>15</td>
<td>3%</td>
</tr>
<tr>
<td>Five to Eight weeks</td>
<td>11.83%</td>
<td>20</td>
<td>27.12%</td>
<td>48</td>
<td>20%</td>
</tr>
<tr>
<td>Nine to Twelve weeks</td>
<td>36.69%</td>
<td>62</td>
<td>14.69%</td>
<td>26</td>
<td>33%</td>
</tr>
<tr>
<td>Thirteen to Twenty-Four Weeks</td>
<td>14.20%</td>
<td>24</td>
<td>23.16%</td>
<td>41</td>
<td>22%</td>
</tr>
<tr>
<td>Greater Then Twenty-Four Weeks</td>
<td>36.09%</td>
<td>61</td>
<td>26.55%</td>
<td>47</td>
<td>22%</td>
</tr>
<tr>
<td>Grand Total</td>
<td>100.00%</td>
<td>169</td>
<td>100.00%</td>
<td>177</td>
<td>100%</td>
</tr>
</tbody>
</table>
Percentage of respiratory specimens that tested positive for influenza
By influenza transmission zone

Note: The available country data were joined in larger geographical areas with similar influenza transmission patterns to be able to give an overview (www.who.int/influenza/surveillance_monitoring/updates/EN_GIP_Influenza_transmission_zones.pdf). The displayed data reflect reports of the week from the 17 April 2017 to 30 April 2017, or up to two weeks before if not sufficient data were available for that area.

The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: Global Influenza Surveillance and Response System (GISRS), FluNet (www.who.int/flu).
A(H1N1)pdm09 viruses
September 2016 – May 2017
H1N1pddm09 Genetic Groups since September 1, 2016
Based on HA Sequence Availability

<table>
<thead>
<tr>
<th>Genetic Group</th>
<th>Africa</th>
<th>Asia</th>
<th>Europe</th>
<th>North America</th>
<th>Oceania</th>
<th>Central and South America</th>
</tr>
</thead>
<tbody>
<tr>
<td>6B</td>
<td>10</td>
<td>3</td>
<td>83</td>
<td>236</td>
<td>23</td>
<td></td>
</tr>
<tr>
<td>6B.1</td>
<td>77%</td>
<td>2%</td>
<td>97%</td>
<td>100%</td>
<td>92%</td>
<td></td>
</tr>
<tr>
<td>6B.2</td>
<td></td>
<td>1%</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6C</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
# Influenza A(H1)PDM09 Viruses Characterized by HI

<table>
<thead>
<tr>
<th></th>
<th>U.S.A.</th>
<th>North America</th>
<th>Europe</th>
<th>Asia</th>
<th>Cent / So America</th>
<th>Africa</th>
<th>Oceania</th>
<th>Total (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>February 2016 - August 2016</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/CALIFORNIA/07/2009-LIKE*</td>
<td>750</td>
<td>33</td>
<td>66</td>
<td>101</td>
<td>303</td>
<td>76</td>
<td>2</td>
<td>1331 (99%)</td>
</tr>
<tr>
<td>A/CALIFORNIA/07/2009-LIKE**</td>
<td>6</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>10</td>
<td>10 (1%)</td>
</tr>
<tr>
<td>A/CALIFORNIA/07/2009-LIKE*** LOW</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>5</td>
<td>5 (0%)</td>
</tr>
<tr>
<td></td>
<td>758</td>
<td>36</td>
<td>67</td>
<td>102</td>
<td>304</td>
<td>77</td>
<td>2</td>
<td>1346</td>
</tr>
<tr>
<td><strong>September 2016 - May 2017</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/CALIFORNIA/07/2009-LIKE*</td>
<td>288</td>
<td>37</td>
<td>55</td>
<td>12</td>
<td>12</td>
<td>12</td>
<td>4</td>
<td>408 (99.3%)</td>
</tr>
<tr>
<td>A/CALIFORNIA/07/2009-LIKE**</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1 (0.2%)</td>
</tr>
<tr>
<td>A/CALIFORNIA/07/2009-LIKE*** LOW</td>
<td>2</td>
<td></td>
<td>55</td>
<td>12</td>
<td>12</td>
<td>12</td>
<td>5</td>
<td>411</td>
</tr>
<tr>
<td></td>
<td>290</td>
<td>37</td>
<td>55</td>
<td>12</td>
<td>12</td>
<td>12</td>
<td>5</td>
<td>411</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1757</td>
</tr>
</tbody>
</table>

* < 4-fold low to reference virus

** = 4-fold low to the reference virus

*** ≥ 8-fold low to the reference virus

Preliminary Data: 05/17/2017
Summary of A(H1N1)pdm09 Viruses

- From September 2016 to present, influenza A(H1N1)pdm09 activity was generally low globally
- Vast majority of viruses fell into phylogenetic HA subclades 6B.1
  - Subclade 6B.2 viruses were detected at very low level in Asia and Oceania
- The majority of recent A(H1N1)pdm09 viruses were antigenically indistinguishable from the current vaccine virus A/California/07/2009 and A/Michigan/45/2015 (vaccine virus for 2017 southern hemisphere) using post-infection ferret antisera and HI tests
A(H3N2) viruses
September 2016 – May 2017
H3N2 Genetic Groups since September 1, 2016
Based on HA Sequence Availability

<table>
<thead>
<tr>
<th>HA Genetic Group</th>
<th>Africa</th>
<th>Asia</th>
<th>Europe</th>
<th>North America</th>
<th>Oceania</th>
<th>Central and South America</th>
</tr>
</thead>
<tbody>
<tr>
<td>3C</td>
<td>6</td>
<td>7</td>
<td>36</td>
<td>118</td>
<td>141</td>
<td>16</td>
</tr>
<tr>
<td>3C.2</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>6</td>
<td>10</td>
<td>16</td>
</tr>
<tr>
<td>3C.2a</td>
<td>12</td>
<td>426</td>
<td>974</td>
<td>519</td>
<td>35</td>
<td>72</td>
</tr>
<tr>
<td>3C.2a1</td>
<td></td>
<td>394</td>
<td></td>
<td>2095</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3C.3a</td>
<td></td>
<td>1</td>
<td>31</td>
<td>67</td>
<td>10%</td>
<td>9%</td>
</tr>
</tbody>
</table>

CDC
# H3 Focus Reduction Assay (04/27/2017)

## Reference Ferret Antisera

<table>
<thead>
<tr>
<th>Reference Viruses</th>
<th>3C.2a</th>
<th>3C.2a1</th>
</tr>
</thead>
<tbody>
<tr>
<td>SIAT MI/15</td>
<td>2560</td>
<td></td>
</tr>
<tr>
<td>SIAT HK/7127</td>
<td>2560</td>
<td>320</td>
</tr>
<tr>
<td>SIAT MD/23</td>
<td>2560</td>
<td>320</td>
</tr>
<tr>
<td>SIAT PA/92</td>
<td>320</td>
<td>160</td>
</tr>
<tr>
<td>SIAT EGG HK/50</td>
<td>160</td>
<td>160</td>
</tr>
<tr>
<td>SIAT EGG NR/3806</td>
<td>160</td>
<td>160</td>
</tr>
<tr>
<td>SIAT SZ/9715293</td>
<td>3C.2a</td>
<td></td>
</tr>
</tbody>
</table>

**GROUP PASS. Date collected**
- **1** A/MICHIGAN/15/2014  2014/09/24
- **2** A/HONG KONG/7127/2014  2014/07/29
- **3** A/MARYLAND/23/2016  2016/11/26
- **4** A/ PENNSYLVANIA/92/2016  2016/10/29
- **5** A/HONG KONG/50/2016  2016/XX/XX
- **6** A/NORWAY/3806/2016  2016/XX/XX
- **7** A/SWITZERLAND/9715293/2013  2013/12/06

## Test Viruses

<table>
<thead>
<tr>
<th>Test Viruses</th>
<th>3C.2a</th>
<th>3C.2a1</th>
</tr>
</thead>
<tbody>
<tr>
<td>SIAT MI/15</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SIAT HK/7127</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SIAT MD/23</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SIAT PA/92</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SIAT EGG HK/50</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SIAT EGG NR/3806</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SIAT SZ/9715293</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**GROUP PASS. Date collected**
- **8** A/LEBANON/2469/2017  2017/02/07
- **9** A/NEW YORK/10/2017  2017/02/09
- **10** A/NEW YORK/12/2017  2017/02/21
- **11** A/TEXAS/60/2017  2017/02/27
- **12** A/ILLINOIS/17/2017  2017/02/20
- **13** A/ILLINOIS/18/2017  2017/02/21
- **14** A/ILLINOIS/19/2017  2017/02/22
- **15** A/ILLINOIS/20/2017  2017/02/24
- **16** A/INDIANA/15/2017  2017/02/17
- **17** A/TEXAS/54/2017  2017/02/16
- **18** A/OKLAHOMA/11/2017  2017/02/22
- **19** A/NEW JERSEY/17/2017  2017/02/27
- **20** A/PENNSYLVANIA/15/2017  2017/02/15
### Influenza A(H3N2) Viruses Characterized by HI/FRA

<table>
<thead>
<tr>
<th></th>
<th>U.S.A.</th>
<th>North America</th>
<th>Europe</th>
<th>Asia</th>
<th>Cent / So America</th>
<th>Africa</th>
<th>Oceania</th>
<th>Total (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>February 2016 - August 2016</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/HONG KONG/4801/2014-LIKE*</td>
<td>151</td>
<td>5</td>
<td>6</td>
<td>34</td>
<td>16</td>
<td>40</td>
<td>3</td>
<td>255 (45.9%)</td>
</tr>
<tr>
<td>A/HONG KONG/4801/2014-LIKE**</td>
<td>183</td>
<td>2</td>
<td>3</td>
<td>30</td>
<td>4</td>
<td>14</td>
<td>12</td>
<td>248 (44.6%)</td>
</tr>
<tr>
<td>A/HONG KONG/4801/2014-LIKE*** LOW</td>
<td>38</td>
<td>2</td>
<td>3</td>
<td>6</td>
<td>4</td>
<td>53</td>
<td>9.5%</td>
<td>556</td>
</tr>
<tr>
<td></td>
<td>372</td>
<td>7</td>
<td>11</td>
<td>67</td>
<td>26</td>
<td>58</td>
<td>15</td>
<td>556</td>
</tr>
<tr>
<td><strong>September 2016 - May 2017</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A/HONG KONG/4801/2014-LIKE*</td>
<td>504</td>
<td>17</td>
<td>27</td>
<td>32</td>
<td>43</td>
<td>41</td>
<td>664 (65.5%)</td>
<td></td>
</tr>
<tr>
<td>A/HONG KONG/4801/2014-LIKE**</td>
<td>233</td>
<td>10</td>
<td>24</td>
<td>21</td>
<td>14</td>
<td>3</td>
<td>4</td>
<td>309 (30.5%)</td>
</tr>
<tr>
<td>A/HONG KONG/4801/2014-LIKE*** LOW</td>
<td>36</td>
<td>2</td>
<td>2</td>
<td></td>
<td>1</td>
<td>41</td>
<td>4.0%</td>
<td>1014</td>
</tr>
<tr>
<td></td>
<td>773</td>
<td>27</td>
<td>53</td>
<td>55</td>
<td>57</td>
<td>3</td>
<td>46</td>
<td>1014</td>
</tr>
</tbody>
</table>

* < 4-fold low to reference virus
** = 4-fold low to the reference virus
*** ≥ 8-fold low to the reference virus

Preliminary Data: 05/17/2017
Summary of A(H3N2) Viruses

• High levels of influenza A(H3N2) activity was detected in many parts of the world during the 2016-2017 influenza season.

• The majority of influenza A(H3N2) viruses collected from September 2016 to present time fell into the phylogenetic clades 3C.2a and subclade 3C.2a1.

• Ferret antisera raised against reference cell-propagated 3C.2a viruses (e.g. A/Hong Kong/4801/2014-like) inhibited a majority of viruses tested in HI and FRA.
  • Including viruses in clade 3C.2a and subclade 3C.2a1 viruses.
Influenza B viruses
September 2016 – May 2017
Influenza B Genetic Groups since September 1, 2016
Based on HA Sequence Availability

<table>
<thead>
<tr>
<th>Genetic Group</th>
<th>Africa</th>
<th>Asia</th>
<th>Europe</th>
<th>North America</th>
<th>Oceania</th>
<th>Central and South America</th>
</tr>
</thead>
<tbody>
<tr>
<td>V1A</td>
<td>3</td>
<td>60</td>
<td>117</td>
<td>317</td>
<td>13</td>
<td>26</td>
</tr>
<tr>
<td>V1A Dalek K162N163</td>
<td>2</td>
<td>7</td>
<td>7</td>
<td>474</td>
<td>13</td>
<td>54</td>
</tr>
<tr>
<td>Y2</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>41</td>
<td>84</td>
<td>87</td>
</tr>
<tr>
<td>Y3</td>
<td></td>
<td></td>
<td>113</td>
<td>317</td>
<td></td>
<td>33</td>
</tr>
<tr>
<td>Y3V1A</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>13</td>
<td>68</td>
</tr>
</tbody>
</table>
B/Victoria-Lineage Viruses
Evolutionary Relationships Among Influenza B Victoria Hemagglutinin (HA) Genes, 2016-2017

Current Northern Hemisphere Vaccine Strain

- LR: Low Reactor to B/Brissbane/60/2008 (≥ 8 fold)
- #: Egg Isolate
- VNR: Virus Not Recovered
- ORG: Original Clinical Specimen

December 2016
January 2017
February 2017
March 2017

V1A.1
K162Deletion N163Deletion

V1A
### Reference Ferret Antisera

<table>
<thead>
<tr>
<th>Strain Designation</th>
<th>HA Genetic Group</th>
<th>V1A</th>
<th>V1A.1</th>
<th>MDCK</th>
<th>MDCK</th>
<th>EGG</th>
<th>MDCK</th>
<th>WHO B Yam</th>
<th>WHO B Vic</th>
<th>Passag E</th>
<th>Date Collected</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 B/BRISBANE/60/2008</td>
<td>V1A</td>
<td>640</td>
<td>640</td>
<td>320</td>
<td>640</td>
<td>20</td>
<td>640</td>
<td>20</td>
<td>640</td>
<td>E4/E4</td>
<td>8/4/2008</td>
</tr>
<tr>
<td>3 B/TX/02/2013</td>
<td>V1A</td>
<td>160</td>
<td>320</td>
<td>160</td>
<td>20</td>
<td>40</td>
<td>10</td>
<td>1280</td>
<td>M1/C2</td>
<td></td>
<td>1/9/2013</td>
</tr>
<tr>
<td>5 B/MARYLAND/15/2016</td>
<td>V1A.1</td>
<td>80</td>
<td>40</td>
<td>20</td>
<td>160</td>
<td>320</td>
<td>&lt;10</td>
<td>10</td>
<td></td>
<td></td>
<td>12/27/2016</td>
</tr>
</tbody>
</table>

### Test Viruses

<table>
<thead>
<tr>
<th>Strain Designation</th>
<th>HA Genetic Group</th>
<th>V1A</th>
<th>V1A</th>
<th>MDCK</th>
<th>MDCK</th>
<th>EGG</th>
<th>MDCK</th>
<th>WHO B Yam</th>
<th>WHO B Vic</th>
<th>Passag E</th>
<th>Date Collected</th>
</tr>
</thead>
<tbody>
<tr>
<td>6 B/ARIZONA/06/2017</td>
<td>V1A</td>
<td>160</td>
<td>320</td>
<td>160</td>
<td>20</td>
<td>40</td>
<td>10</td>
<td>640</td>
<td>C1</td>
<td>2/14/2017</td>
<td></td>
</tr>
<tr>
<td>7 B/ARIZONA/07/2017</td>
<td>V1A</td>
<td>160</td>
<td>320</td>
<td>160</td>
<td>20</td>
<td>20</td>
<td>10</td>
<td>640</td>
<td>C1</td>
<td>2/16/2017</td>
<td></td>
</tr>
<tr>
<td>8 B/ILLINOIS/14/2017</td>
<td>V1A</td>
<td>160</td>
<td>320</td>
<td>160</td>
<td>10</td>
<td>40</td>
<td>10</td>
<td>640</td>
<td>C1</td>
<td>3/4/2017</td>
<td></td>
</tr>
<tr>
<td>9 B/MINNESOTA/11/2017</td>
<td>V1A</td>
<td>160</td>
<td>320</td>
<td>160</td>
<td>20</td>
<td>40</td>
<td>10</td>
<td>640</td>
<td>C1</td>
<td>3/5/2017</td>
<td></td>
</tr>
<tr>
<td>10 B/TX/32/2017</td>
<td>V1A</td>
<td>160</td>
<td>320</td>
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<td>320</td>
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<td>C1</td>
<td>3/6/2017</td>
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</tbody>
</table>
Summary of B/Victoria $\Delta K_{162} N_{163}$ Mutants

- Detected in 19 States, 1 in Canada and 2 case in Norway
- All $\Delta K_{162} N_{163}$ deletion mutants were antigenically low to recent B/Victoria lineage reference viruses
## Influenza B/Victoria Lineage Viruses Characterized by HI

<table>
<thead>
<tr>
<th></th>
<th>U.S.A.</th>
<th>North America</th>
<th>Europe</th>
<th>Asia</th>
<th>Cent / So America</th>
<th>Africa</th>
<th>Oceania</th>
<th>Total (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>February 2016 - August 2016</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B/BRISBANE/60/2008-LIKE*</td>
<td>125</td>
<td>9</td>
<td>6</td>
<td>44</td>
<td>32</td>
<td>29</td>
<td>3</td>
<td>248 (32%)</td>
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<tr>
<td>B/BRISBANE/60/2008-LIKE**</td>
<td>325</td>
<td>7</td>
<td>17</td>
<td>91</td>
<td>41</td>
<td>36</td>
<td></td>
<td>517 (67%)</td>
</tr>
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<td>5</td>
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<td>3</td>
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<td></td>
<td>10</td>
<td>10 (1%)</td>
</tr>
<tr>
<td></td>
<td>455</td>
<td>17</td>
<td>26</td>
<td>135</td>
<td>73</td>
<td>66</td>
<td>3</td>
<td>775</td>
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<tr>
<td><strong>September 2016 - May 2017</strong></td>
<td></td>
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<td></td>
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<tr>
<td>B/BRISBANE/60/2008-LIKE*</td>
<td>74</td>
<td>5</td>
<td>4</td>
<td>40</td>
<td>25</td>
<td>6</td>
<td>1</td>
<td>155 (32%)</td>
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<tr>
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<td>18</td>
<td>24</td>
<td>15</td>
<td>4</td>
<td>3</td>
<td>284 (59%)</td>
</tr>
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<td>42</td>
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<td>42 (9%)</td>
</tr>
<tr>
<td></td>
<td>335</td>
<td>6</td>
<td>22</td>
<td>64</td>
<td>40</td>
<td>10</td>
<td>4</td>
<td>481</td>
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<tr>
<td><strong>Total</strong></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1256</td>
</tr>
</tbody>
</table>

* < 4-fold low to reference virus

** = 4-fold low to the reference virus

*** ≥ 8-fold low to the reference virus

Preliminary Data: 05/17/2017
Influenza B/Yamagata Lineage Viruses Characterized by HI

<table>
<thead>
<tr>
<th></th>
<th>U.S.A.</th>
<th>North America</th>
<th>Europe</th>
<th>Asia</th>
<th>Cent / So America</th>
<th>Africa</th>
<th>Oceania</th>
<th>Total (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>February 2016 - August 2016</strong></td>
<td></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
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</tr>
<tr>
<td>B/PHUKET/3073/2013-LIKE*</td>
<td>472</td>
<td>16</td>
<td>95</td>
<td>34</td>
<td>34</td>
<td>651</td>
<td>651 (97%)</td>
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</tr>
<tr>
<td>B/PHUKET/3073/2013-LIKE**</td>
<td>19</td>
<td>1</td>
<td>1</td>
<td></td>
<td></td>
<td>20</td>
<td>20 (3%)</td>
<td></td>
</tr>
<tr>
<td>B/PHUKET/3073/2013-LIKE*** LOW</td>
<td>491</td>
<td>16</td>
<td>96</td>
<td>34</td>
<td>34</td>
<td>671</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>September 2016 - May 2017</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B/PHUKET/3073/2013-LIKE*</td>
<td>357</td>
<td>14</td>
<td>19</td>
<td>12</td>
<td>1</td>
<td>56</td>
<td>459 (95%)</td>
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<tr>
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<td>1</td>
<td></td>
<td></td>
<td>22</td>
<td>22 (5%)</td>
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<tr>
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<td>1</td>
<td>56</td>
<td>481</td>
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<tr>
<td><strong>Total</strong></td>
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</tr>
</tbody>
</table>

* < 4-fold low to reference virus
** = 4-fold low to the reference virus
*** ≥ 8-fold low to the reference virus

Preliminary Data: 05/17/2017
Summary of Influenza B Viruses

• B/Victoria and B/Yamagata lineage viruses are co-circulating in the Americas at different levels. In North Americas, the proportion of B/Yamagata lineage viruses is increasing.

• B/Victoria lineage viruses
  • All HA genes belonged to genetic clade 1A.
  • The Majority of recently circulating viruses were well inhibited by ferret antisera raised against cell culture-propagated B/Brisbane/60/2008 or B/Texas/2/2013 viruses.
  • A group of deletion mutants, which were initially detected in Dominica Rep., were identified in the U.S., Canada and Norway.
  • All ΔK162N163 deletion mutants were antigenically low to recent B/Victoria lineage reference viruses

• B/Yamagata lineage viruses
  • All HA genes belonged to genetic clade 3.
  • Recently circulating viruses were well inhibited by ferret antisera raised against cell culture- and egg-propagated B/Phuket/3073/2013 viruses.
Acknowledgements

• WHO Collaborating Centers in Beijing, Melbourne, London and Tokyo and WHO Geneva staff

  • GISRS; National Influenza Centers
  • University of Cambridge partners

• Essential Regulatory Laboratories

• US partners:
  • Association of Public Health Laboratories