**Enhanced genetic characterization of influenza A(H3N2) viruses and vaccine effectiveness by genetic group, 2014–2015**

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**Supplementary Online Content**

Table 1. Characteristics for influenza A(H3N2)-test positive patients comparing those with genetically characterized H3N2 viruses with patients whose H3N2 viruses were not genetically characterized

Table 2. Genetic and antigenic characterization of influenza A(H3N2) viruses collected by U.S. public health laboratories from March 1, 2014 through April 10, 2015 and submitted to CDC.

**Supplementary Table 1. Characteristics for influenza A(H3N2)-test positive patients comparing those with genetically characterized H3N2 viruses with patients whose H3N2 viruses were not genetically characterized**

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| --- | --- | --- | --- |
|   | **Genetically characterized influenza A(H3N2) cases** **(N=1397)** | **Influenza A(H3N2) cases not genetically characterized** **(N=471)a** | **P-value** |
|   | n (col %) | n (col %) |   |
| **Study site** |  |  | <.0001 |
| Michigan | 201 (14.4) | 117 (24.8) |   |
| Pennsylvania | 382 (27.3) | 52 (11.0) |   |
| Texas | 191 (13.7) | 93 (19.8) |   |
| Washington | 317 (22.7) | 108 (22.9) |   |
| Wisconsin | 306 (21.9) | 101 (21.4) |   |
| **Age category** |  |  | 0.03 |
| 6 months – 8 years | 327 (23.4) | 100 (21.2) |   |
| 9–17 years | 229 (16.4) | 86 (18.3) |   |
| 18–49 years | 389 (27.9) | 147 (31.2) |   |
| 50–64 years | 205 (14.7) | 81 (17.2) |   |
| > 65 years | 247 (17.7) | 57 (12.1) |   |
| **Male** | 601 (43.0) | 192 (40.8) | 0.39 |
| **Race/ethnicityb** |  |  | 0.13 |
| White, non-Hispanic | 1081 (77.7) | 347 (74.7) |   |
| Black, non-Hispanic | 108 (7.8) | 35 (7.4) |   |
| Hispanic | 82 (5.9) | 40 (8.5) |   |
| Other, non-Hispanic | 120 (8.6) | 49 (10.4) |   |
| **Any high-risk condition** | 521 (37.3) | 165 (35.0) | 0.38 |
| **Interval from onset to specimen collection** |  | <.0001 |
| 0–2 days | 698 (50.0) | 166 (35.2) |   |
| 3–4 days | 488 (35.0) | 165 (35.0) |   |
| 5–7 days | 211 (15.1) | 140 (29.7) |   |
| **Reported general health status**b |  | 0.20 |
| Excellent/very good | 1026 (76.1) | 357 (76.1) |   |
| Good | 282 (20.3) | 94 (20.0) |   |
| Fair/poor | 83 (6.0) | 18 (3.8) |   |
| **Self/household exposure to smoke**b | 176 (12.6) | 60 (12.8) | 0.93 |
| **≥1 child <12 years of age in household**b | 522(37.6) | 213 (45.2) | 0.004 |
| **Reported fever** | 1132 (81.2) | 370 (78.7) | 0.25 |
| **Reported current health assessment, median (IQR)b** | 0.05 |
| Scale 1 (worst) – 100 (best) | 50 (40-70) | 52 (40-70) |   |
| **Vaccination status 2014–2015**c |  | 0.56 |
| ≥1 doses | 749 (53.6) | 241 (51.2) |   |
| 0 doses | 648 (46.4) | 230 (48.8) |   |

Abbreviation: IQR, interquartile range.

a Specimens from 67 enrollees were submitted for genetic characterization but failed to be characterized.

b Race/Hispanic ethnicity was unknown for 6 enrollees, reported general health status was missing for 8 enrollees, self/household exposure to tobacco smoke was missing for 3 enrollees, living in household with ≥1 child <12 years of age missing for 8 enrollees, and current health assessment missing for 5 enrollees.

c Includes patients aged 6 months to 8 years with partial vaccination and those vaccinated 0–13 days prior to illness onset.

**Supplementary Table 2. Genetic and antigenic characterization of influenza A(H3N2) viruses collected by U.S. public health laboratories from March 1, 2014 through April 10, 2015 and submitted to CDC.**

|  |  |  |  |
| --- | --- | --- | --- |
| HA genetic group | No. of specimens | No. (%) characterized by HI assay | Antigenic characterization by HI assay |
| A/Texas/50/2012-like | A/Texas/50/2012-low |
| Number (% characterized by HI) |
| 3C.2 | 15 | 14 (93%) | 14 (100%) | 0 – |
| 3C.2a | 1676 | 773 (46%) | 120 (16%) | 653 (84%) |
| 3C.2b | 20 | 19 (95%) | 11 (58%) | 8 (42%) |
| 3C.3 | 332 | 318 (96%) | 276 (87%) | 42 (13%) |
| 3C.3a | 126 | 126 (100%) | 23 (18%) | 103 (82%) |
| 3C.3b | 80 | 75 (94%) | 49 (65%) | 26 (35%) |
| Total | 2249 | 1325 (59%) | 493 (37%) | 832 (63%) |

Note: Participating U.S. public health laboratories collected and submitted 2,911 influenza A(H3N2)-positive respiratory specimens to CDC for further virus characterization; HA genetic group was not determined for 662 influenza A(H3N2)-positive specimens. Influenza A(H3N2) viruses were propagated in Madin-Darby Canine Kidney (MDCK) cells expressing alpha-2,6-sialyltransferase (SIAT1)[1](#_ENREF_1) and antigenically characterized by hemagglutination inhibition (HI) assay with guinea pig red blood cells in the presence of oseltamivir. Hemagglutination inhibition (HAI) assays provide data to identify current circulating viruses compared to the A/Texas/50/2012 vaccine reference strain as “A/Texas/50/2012-like” (≤4-fold difference in HI titer compared to A/Texas/50/2012) or “A/Texas/50/2012-low” (≥8-fold difference in HI titer compared to A/Texas/50/2012).

**Reference**

**1.** Matrosovich M, Matrosovich T, Carr J, Roberts NA, Klenk HD. Overexpression of the alpha-2,6-sialyltransferase in MDCK cells increases influenza virus sensitivity to neuraminidase inhibitors. *Journal of virology.* Aug 2003;77(15):8418-8425.