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Irrespective of the fair of origin, the genomic sequences of all 11 human-like H3N2 virus isolates from swine were >99.89% identical to each other, demonstrating clonal expansion of 1 virus across 2 states. This pattern of virus dissemination within the exhibition swine population was a hallmark of the 2012 fair season, when 306 H3N2v human cases were reported (6).

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### Conclusions

Variant influenza infections in humans continue to occur through contact with exhibition swine; often, the cases are in swine exhibitors with close and prolonged swine exposure. The concurrent detection of genetically identical influenza A viruses from exhibition swine across 2 states illustrates the rapidity with which this virus, and potentially other pathogens, can move within the highly mobile exhibition swine population. In addition to the zoonotic risks of influenza A virus, this pattern serves as a warning of possible dissemination of other emerging or high-consequence diseases in swine. Management practices common in the exhibition swine industry (i.e., frequent exhibition and relaxed biosecurity) facilitate the rapid dissemination of influenza virus across a large geographic landscape (14). Collaboration between animal and public health officials facilitated this investigation. Methods to control intraspecies and interspecies influenza virus transmission during swine shows have been outlined by the National Association of State Public Health Veterinarians (http://nasphv.org/Documents/Influenza_Transmission_at_Swine_Exhibitions_2016.pdf).

The recovery of human-like H3 influenza A viruses from exhibition swine supports previous studies demonstrating that the US commercial swine herd can serve as an influenza A reservoir for the much smaller exhibition swine population, which is more accessible to humans. Within the US commercial herd, the proportion of H3 isolates containing human-like H3 nearly doubled to 46% in spring and summer 2016 (data not shown). Whereas human-like H3s have been circulating, reassorting, and becoming more prevalent in the commercial swine population since 2012, introduction and expansion of the human-like H3 reassortant influenza A viruses in exhibition swine facilitated documented zoonoses from this genotype. The path traversed by this human-like H3, from initial introduction from humans to swine until the zoonotic transmission events of 2016, demonstrates how novel viruses can be generated and maintained in animal populations and, subsequently, can infect humans through specific eco-logic niches like swine exhibitions or live-animal markets (15). Therefore, continued surveillance in swine populations is imperative for detecting novel influenza A viruses that threaten swine and human health.

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<th>No. swine sampled</th>
<th>No. (%) positive rRT-PCR</th>
<th>Isolation</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>Yes</td>
<td>20</td>
<td>20 (100)</td>
<td>18 (90)</td>
</tr>
<tr>
<td>B</td>
<td>No</td>
<td>20</td>
<td>17 (85)</td>
<td>17 (85)</td>
</tr>
<tr>
<td>C</td>
<td>No</td>
<td>20</td>
<td>20 (100)</td>
<td>18 (90)</td>
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<tr>
<td>D</td>
<td>No</td>
<td>20</td>
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<td>14 (70)</td>
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<tr>
<td>E</td>
<td>Yes</td>
<td>20</td>
<td>20 (100)</td>
<td>18 (90)</td>
</tr>
<tr>
<td>F</td>
<td>No</td>
<td>20</td>
<td>15 (75)</td>
<td>12 (60)</td>
</tr>
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* Nasal swab or nasal wipe samples were collected from swine at the end of the fair. ILI, influenza-like illness; rRT-PCR, real-time reverse transcription PCR.
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<th>PB2</th>
<th>PB1</th>
<th>PA</th>
<th>HA</th>
<th>NP</th>
<th>NA</th>
<th>M</th>
<th>NS</th>
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<tr>
<td>H3 genotype 1, n = 2</td>
<td>trig</td>
<td>trig</td>
<td>trig</td>
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<td>pdm</td>
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</tr>
<tr>
<td>Human-like H3, n = 11</td>
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