Influenza A(H6N1) Virus in Dogs, Taiwan

Hui-Ting Lin,¹ Ching-Ho Wang,¹ Ling-Ling Chueh, Bi-Ling Su, Lih-Chiann Wang

We determined the prevalence of influenza A virus in dogs in Taiwan and isolated A/canine/Taiwan/E01/2014. Molecular analysis indicated that this isolate was closely related to influenza A(H6N1) viruses circulating in Taiwan and harbored the E627K substitution in the polymerase basic 2 protein, which indicated its ability to replicate in mammalian species.

Infections with influenza viruses are rare in dogs. However, interspecies transmission of an equine influenza A(H3N8) virus to dogs was identified during a respiratory disease outbreak in Florida, USA, in 2004 (1). Influenza A(H6N1) virus is the most common naturally occurring avian influenza virus in Taiwan (2). Therefore, to determine to the prevalence of influenza A virus infection in dogs in Taiwan, we performed serologic analysis, 1-step reverse transcription PCR (RT-PCR) screening, and virus isolation.

The Study
A total 474 serum specimens were collected in Taiwan during October 2012–October 2013. Two hundred eighty-one specimens were collected from household (owned) dogs at the National Taiwan University Veterinary Hospital in Taipei. The remaining 193 serum specimens were obtained from free-roaming dogs in rural areas.

All serum specimens were tested for antibodies against influenza A virus by using a species-independent blocking ELISA (Influenza A Virus Antibody Test Kit; Idexx, Westbrook, ME, USA). All antibody-positive serum specimens were further tested by using a hemagglutination inhibition (HI) assay. HI was determined according to procedures recommended by the World Organisation for Animal Health.

Chicken erythrocytes (1%) were used. Serum samples were treated with receptor-destroying enzyme (Denka Seiken, Tokyo, Japan) before conducting the assay to destroy nonspecific inhibitors (3). A/chicken/Taiwan/2838V/2000 (H6N1) and A/chicken/Taiwan/1209/03 (H5N2) viruses were used as antigens.

Nasal swab specimens were collected from dogs with respiratory signs, such as nasal discharge, sneezing, coughing, at the National Taiwan University Veterinary Hospital during November 2012–February 2014. Specimens were suspended in viral transportation medium (Creative, Taipei, Taiwan), and RNA was extracted by using a commercial kit (Viral RNA Mini Kit; QIAGEN, Hilden, Germany)

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Polymerase basic 2 (PB2), PB1, nucleoprotein (NP), and nonstructural protein (NS) genes were closely related to those of H6N1 subtype virus isolates from chickens in Taiwan (similarity range 97%–99%). Polymerase acidic (PA) and M genes had the highest nucleotide sequence similarity (99%) to A/chicken/Taiwan/2593/2012 (H5N2). On the basis of HA and NA sequence analysis results, A/canine/Taiwan/E01/2014 was designated an H6N1 subtype influenza virus.

Only 1 basic amino acid (PQIATR*G) was found at the HA cleavage site of A/canine/Taiwan/E01/2014. G228S substitution (H3 numbering) on the receptor binding site for HA was also observed for this virus, which indicated increased virus binding ability for the α2–6 sialic acid receptor (6,7). In NA, a 14-aa deletion in the NA stalk region was observed at aa positions 42–53 and 68–69, which is associated with virus circulation in domestic poultry. The amino acid H275Y substitution (oseltamivir resistance marker) in NA was not found in this virus. In the M2 protein, A/canine/Taiwan/E01/2014 had an S31N substitution, which suggested resistance to adamantanes (8,9).

Other major signatures associated with replication ability in a mammalian host or pathogenicity were also observed, including E627K in the PB2 and the PDZ ligand domain at the C-terminal region of NS1 of this virus. Additional molecular comparisons with H6N1 subtype virus (A/Taiwan/2/2013) isolated from humans (7,10,11) and from dogs experimentally infected H6N1 subtype virus (A/mallard/San-Jiang/275/2007) (12) were made (Table 2).

Phylogenetic analysis of HA and NA gene segments indicated that A/canine/Taiwan/E01/2014 belongs to the H6N1 lineage that has been circulating in chickens in Taiwan since 1997 (Figure, panels A, B). Although the lineage of internal gene segments (PB2, PB1, PA, NP, M, and NS) is composed mainly of H6N1 subtype viruses isolated in Taiwan, some H5N2 subtype isolates in the H6N1 lineage were observed.

### Table 1. Homology of nucleotide sequences of A/canine/Taiwan/E01/2014 (H6N1) influenza virus isolated from dogs in Taiwan compared with related sequences from the Global Initiative on Sharing All Influenza Data*

<table>
<thead>
<tr>
<th>Gene segment</th>
<th>Virus with highest identity</th>
<th>% Identity</th>
<th>Accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td>PB2</td>
<td>A/chicken/Taiwan/1843/2012 (H6N1)</td>
<td>98</td>
<td>EPI510830</td>
</tr>
<tr>
<td>PB1</td>
<td>A/chicken/Taiwan/A2837/2013 (H6N1)</td>
<td>97</td>
<td>EPI459872</td>
</tr>
<tr>
<td>PA</td>
<td>A/chicken/Taiwan/2593/2012 (H5N2)</td>
<td>99</td>
<td>EPI510622</td>
</tr>
<tr>
<td>HA</td>
<td>A/chicken/Taiwan/1843/2012 (H6N1)</td>
<td>99</td>
<td>EPI519832</td>
</tr>
<tr>
<td>NP</td>
<td>A/chicken/Taiwan/67/2013 (H6N1)</td>
<td>98</td>
<td>EPI510875</td>
</tr>
<tr>
<td>NA</td>
<td>A/chicken/Taiwan/2084/2012 (H6N1)</td>
<td>99</td>
<td>EPI510837</td>
</tr>
<tr>
<td>M</td>
<td>A/chicken/Taiwan/2593/2012 (H5N2)</td>
<td>99</td>
<td>EPI510660</td>
</tr>
<tr>
<td>NS</td>
<td>A/chicken/Taiwan/67/2013 (H6N1)</td>
<td>97</td>
<td>EPI510878</td>
</tr>
</tbody>
</table>

*All viruses were from avian sources. PB, polymerase basic; PA, polymerase acidic; HA, hemagglutinin; NP, nucleoprotein; NA, neuraminidase; M, matrix; NS, nonstructural protein.

### Table 2. Molecular characterization of A/canine/Taiwan/E01/2014 (H6N1) influenza virus and 2 other influenza viruses, Taiwan*

<table>
<thead>
<tr>
<th>Gene, amino acid substitution</th>
<th>Virus</th>
<th>Function</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A/canine/Taiwan/E01/2014</td>
<td>A/Taiwan/2/2013</td>
</tr>
<tr>
<td>PB2 E627K</td>
<td>K</td>
<td>E</td>
</tr>
<tr>
<td>D701Q</td>
<td>D</td>
<td>D</td>
</tr>
<tr>
<td>PB1-F2 N68S</td>
<td>N</td>
<td>Truncated form</td>
</tr>
<tr>
<td>HA Cleavage site</td>
<td>Single basic amino acid (PQIATR*G)</td>
<td>Single basic amino acid (PQIATR*G)</td>
</tr>
<tr>
<td>Q226L</td>
<td>Q</td>
<td>Q</td>
</tr>
<tr>
<td>G228S</td>
<td>S</td>
<td>S</td>
</tr>
<tr>
<td>NA H275Y 41–52 and 68–69 deletions</td>
<td>H</td>
<td>H</td>
</tr>
<tr>
<td>M S31N</td>
<td>N</td>
<td>N</td>
</tr>
<tr>
<td>NS1 D92E EPEV sequence (C-terminus)</td>
<td>D</td>
<td>D</td>
</tr>
<tr>
<td>M EPEV</td>
<td>EPEV</td>
<td>EPEV</td>
</tr>
</tbody>
</table>

*PB, polymerase basic; HA, hemagglutinin; NA, neuraminidase; M, matrix; NS, nonstructural protein.
†HA cleavage site.
Conclusions
Avian influenza A(H6N1) viruses have been widespread in chickens in Taiwan since 1972 (13–15). These viruses are clustered in a unique lineage that differs from viruses circulating in Hong Kong and southeastern China since 1997 (13). Unlike avian species, H6 subtype virus infections are rare in mammals.

In this study, 9 of 474 dog serum specimens were positive for influenza A virus by ELISA, and 4/185 (2.1%) dogs had RT-PCR–positive results for this virus. A/canine/Taiwan/E01/2014 was isolated from 1 dog that was co-infected with canine distemper virus. On the basis of molecular analysis of A/canine/Taiwan/E01/2014, HA,
NA, PB1, PB2, NP, and NS genes showed high homology (>97% nucleotide identity) with avian H6N1 subtype virus isolates that are currently prevalent in Taiwan. PA and M genes of A/canine/Taiwan/E01/2014 showed 99% nucleotide identity with A/chicken/Taiwan/2593/2013 (H5N2).

Phylogenetic analysis showed that 8 eight virus genes were derived from H6N1 subtype viruses isolated in Taiwan. All 8 influenza virus genes found in the dog probably originated from avian sources. We speculate that a complete avian influenza virus had infected this dog. However, additional analysis is required to verify this hypothesis.

Acknowledgments
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Dr Lin is a postgraduate scientist at the National Taiwan University Veterinary Hospital, Taipei, Taiwan. Her research interests are veterinary virology and internal medicine in companion animals.

References

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Technical Appendix

Technical Appendix Figure. Phylogenetic relationship between influenza A(H6N1) virus A/canine/Taiwan/E01/2014 isolated from dogs in Taiwan and other influenza A virus lineages. Boxes indicate strain isolated in this study. Maximum-likelihood with bootstrap analysis was conducted with 1,000 replications. Only branches with bootstrap values >75% are indicated on phylogenetic trees. A) Polymerase acidic, B) nucleoprotein, C) matrix, D) nonstructural protein, and E) polymerase basic 1 genes of A/canine/Taiwan/E01/2014 are clustered with H6N1 subtype trains isolated in Taiwan during 2012–2013 in Taiwan. Scale bars indicate nucleotide substitutions per site.