Surveillance of Swine Influenza Virus

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World-wide dissemination of classical SIV, H1N1(2) since 1918
Emergence of Avian-origin SIV (H1N1) in 1979
Emergence of triple reassortant SIVs in N. America since 1998
Emergence of A(H1N1)pdm09 virus in human by a reassortant of SIVs
Human to pig transmission of A(H1N1)pdm09 virus and reassortments with epidemic SIVs

- A(H1N1)pdm09 viruses in pigs
- Reassortant virus between endemic SIVs and A(H1N1)pdm09 viruses
Human infection by H3N2v in US since 2011

Triple reassortant SIV

AO-SIV
Human infection by H3N2v in US since 2011
Human infection by H3N2v in US since 2011
Human infection by H3N2v in US since 2011
Infected: 340, Hospitalized: 17, Death: 1

Human infection by H3N2v in US since 2011
A Zoonosis
Surveillance of SIV in pig farms
Characterization of isolated SIVs
Pig to human transmission
Surveillance of SIVs

Vietnam since 2010

Thailand since 2008
**Collaboration with DLD and NIAH, Thailand by J-GRID project**

<table>
<thead>
<tr>
<th></th>
<th>2008</th>
<th>2009</th>
<th>2010</th>
<th>2011</th>
<th>2012</th>
<th>2013</th>
<th>Total</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>3*/340**</td>
<td>13/421</td>
<td>0/0</td>
<td>11/660</td>
<td>20/374</td>
<td>16/1206</td>
<td>63/3001</td>
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Subtyping

<table>
<thead>
<tr>
<th></th>
<th>H1N1</th>
<th>H3N2</th>
<th>Mix infection</th>
<th>Total characterized</th>
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<tbody>
<tr>
<td></td>
<td>28</td>
<td>15</td>
<td>11</td>
<td>54</td>
</tr>
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</table>

*: # of virus isolated
**: # of nasal swab collected
SIVs are isolated from clinically healthy piglets
**Collaboration with DAH, Vietnam since 2010**

*Northern part: NCVD
Southern part: RAHO6*

<table>
<thead>
<tr>
<th>Region</th>
<th>2010</th>
<th>2011</th>
<th>2012</th>
<th>Total</th>
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</thead>
<tbody>
<tr>
<td>Northern</td>
<td>0/377*</td>
<td>9/379</td>
<td>0/400</td>
<td>0/400</td>
</tr>
<tr>
<td>Southern</td>
<td>0/375**</td>
<td>0/375</td>
<td>1/370</td>
<td>50/399</td>
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<tr>
<td>Total</td>
<td>0/754</td>
<td>9/754</td>
<td>1/770</td>
<td>50/799</td>
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</tbody>
</table>

*  Number of virus isolated/Number of nasal swab collected.
**  Slaughter house

**Subtyping**

<table>
<thead>
<tr>
<th>Region</th>
<th>H1N1</th>
<th>H1N2</th>
<th>H3N2</th>
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<tbody>
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<td>Northern</td>
<td>9</td>
<td>9</td>
<td>32</td>
</tr>
<tr>
<td>Southern</td>
<td>19</td>
<td>34</td>
<td>30</td>
</tr>
<tr>
<td>Total</td>
<td>28</td>
<td>43</td>
<td>62</td>
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</tbody>
</table>
Genetic origin of Thai and Vietnamese SIVs

AO-SIV from Europe

Triple Reassortant SIV from N. America

Classical SIV

Thai SIVs

Vietnamese SIVs
Surveillance of SIV in pig farms
Characterization of isolated SIVs
Pig to human transmission
Future direction of study

- Longitudinal active surveillance in collaboration with DAH, Vietnam
- Characterization of isolated SIVs
- Pig to human transmission
**Future direction of study**

- Longitudinal active surveillance in collaboration with DAH, Vietnam
- Genetic characterization and experimental infection study of the isolates
- Pig to human transmission
Future direction of study

- Longitudinal active surveillance in collaboration with DAH, Vietnam
- Genetic characterization and experimental infection study of the isolates
- Human serology in collaboration with Oxford University Clinical Research Unit, Vietnam
Control of SIV in pig population reduces economic burden on pig industry and risk of emerging a novel SIV with pandemic potential.