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\textsuperscript{3}Centre for Veterinary Diagnostics, Ho Chi Minh City, Vietnam

*In memory of our friend and colleague
### Spatial distribution of FMD outbreaks 2015–2016

<table>
<thead>
<tr>
<th></th>
<th>2015</th>
<th>2016</th>
<th>2017*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cambodia</td>
<td>43</td>
<td>71</td>
<td>49</td>
</tr>
<tr>
<td>Lao PDR</td>
<td>10</td>
<td>45</td>
<td>17</td>
</tr>
<tr>
<td>Malaysia</td>
<td>10</td>
<td>71</td>
<td>17</td>
</tr>
<tr>
<td>Myanmar</td>
<td>39</td>
<td>27</td>
<td>53</td>
</tr>
<tr>
<td>Thailand</td>
<td>183</td>
<td>262</td>
<td>31</td>
</tr>
<tr>
<td>Viet Nam</td>
<td>60</td>
<td>37</td>
<td>3</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>345</td>
<td>513</td>
<td>170</td>
</tr>
</tbody>
</table>

*Up to July

Source: Yu Qiu, OIE SRR-SEA, Bangkok
Summary of events 2015–2017

Eastward movement from Pool 2
2015 - O/Ind/2001d
2016 – O/Ind/2001d
2017 – Asia1/G-VIII
Antigen matching studies by LP-ELISA – Serotype O

• Bovine vaccinate serum
  • O₁ Manisa
  • O-3039

• Homologous reagents

• Field isolates from Thailand, Lao PDR, Vietnam, Cambodia & Myanmar

• 58 isolates studied
  • 41 from OIE RRL, Pakchong, Thailand
  • 17 from RAHO6, Ho Chi Minh City, Vietnam
Antigen matching studies by LP-ELISA – Serotype A

• Bovine vaccinate serum
  • A/MAY/97
• Homologous reagents
• Field isolates from Thailand, Vietnam & Cambodia
• 75 isolates studied
  • 49 from OIE RRL, Pakchong, Thailand
  • 26 from RAHO6, Ho Chi Minh City, Vietnam
Relative homology with the reference vaccine strains (based on r1 values by LPELISA)

<table>
<thead>
<tr>
<th></th>
<th>O1 Manisa</th>
<th>O-3039</th>
<th>A Malaysia 97</th>
</tr>
</thead>
<tbody>
<tr>
<td>Homologous (%)</td>
<td>25.9</td>
<td>81.0</td>
<td>93.3</td>
</tr>
<tr>
<td>Intermediary (%)</td>
<td>10.3</td>
<td>6.9</td>
<td>4.0</td>
</tr>
<tr>
<td>Heterologous (%)</td>
<td>22.4</td>
<td>3.5</td>
<td>2.7</td>
</tr>
<tr>
<td>Not binding (%)</td>
<td>41.4</td>
<td>8.6</td>
<td>0.0</td>
</tr>
<tr>
<td>Total samples</td>
<td>58</td>
<td>58</td>
<td>75</td>
</tr>
</tbody>
</table>

• Genotypes/lineages 2015–2017
  • O/SEA genotype variants
  • O Cathay topotype variants
  • O/SEA/Mya-98 lineage
  • O/ME-SA/Ind 2001d variants

• Two separate incursions of O/ME-SA/Ind2001d sub-lineage
  • Lao PDR and Vietnam (2015)
  • Myanmar and Thailand (2016-2017)

• Three sub-lineages of O/SEA/Mya-98 were recorded (2009-2013; 2015-2016 and 2016-2017)

• RRL: Mya-98 – 12; Ind2001d – 13; Others could not be characterised due to lack of sequences

• RAHO6: Mya-98 – 7; Ind2001d – 5, Cathay – 6 & PanAsia – 1; Others could not be characterised due to lack of sequences

Sequences generated by OIE RRL, Pakchong

  - A/Asia/SEA-97 – still dominant
  - In 2011–2012 a new lineage, TAI 2012, was detected and has become dominant since 2015–2017
  - Within this new lineage, new variants have been detected from Cambodia since 2015
- RRL isolates – 20 belonged to SEA-97 variants while 22 belonged to TAI 2012 sublineage
- RAHO6 isolates – 16 belonged to SEA-97 variants; others could not be characterised (sequences not available)
## Antigen Matching vs Phylogeny

<table>
<thead>
<tr>
<th>Serotype</th>
<th>Genotype/Lineage</th>
<th>Homologous</th>
<th>Intermediary</th>
<th>Heterologous</th>
<th>Not Binding</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>O1 Manisa</strong></td>
<td>O/ME-SA/Panasia</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>O/ME-SA/Ind2001d</td>
<td>8</td>
<td>2</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>O/SEA/Mya-98</td>
<td>6</td>
<td>3</td>
<td>6</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>O/Cathay</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>Uncharacterised</td>
<td>1</td>
<td>0</td>
<td>3</td>
<td>10 *</td>
</tr>
<tr>
<td><strong>O-3039</strong></td>
<td>O/ME-SA/Panasia</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>O/ME-SA/Ind2001d</td>
<td>16</td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>O/SEA/Mya-98</td>
<td>15</td>
<td>2</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>O/Cathay</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td></td>
<td>Uncharacterised</td>
<td>14</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

*At least 6 could be Cathay*
## Antigen Matching vs Phylogeny

<table>
<thead>
<tr>
<th>Serotype</th>
<th>Genotype/Lineage</th>
<th>Homologous</th>
<th>Intermediary</th>
<th>Heterologous</th>
<th>Not Binding</th>
</tr>
</thead>
<tbody>
<tr>
<td>A/MAY/97</td>
<td>ASIA/SEA-97</td>
<td>35</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>ASIA/SEA-97 (TAI 2012)</td>
<td>18</td>
<td>2</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>Uncharacterised</td>
<td>17</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
Conclusions

• Appearance of new lineages of viruses within Pool 1 (SEA)
  • Indicates a dynamic endemic situation
  • New variants emerging due to poor vaccines or less coverage

• ‘Trans-pool’ migration is of major concern - Pool 2 (ME-SA)
  • Indicating possible changes in animal movement patterns
  • Bigger potential risk for vaccine failures
  • More pronounced outbreaks due to naïve population
Conclusions

• Suitable commercial vaccine strains for the current situation
  • Serotype A: A Malaysia 97
  • Serotype O: O-3039

• Continued, real-time monitoring for the emergence of variant strains in SEA by both vaccine matching studies and phylogenetic analysis is required for effective control of the disease in this region

• Australia is committed to working closely with the countries in the region for management and control of the disease
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Thank you

Transboundary Animal Disease Mitigation Team

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