Molecular Epidemiology of Foot-and-Mouth Disease Virus in Tanzania

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Foot-and-mouth disease (FMD) is endemic in Tanzania

First FMD outbreak reports ~ 1954

Animal affected: Cattle, Pigs, small ruminants, wild animals

Outbreaks occur in different geographic regions

Factors associated with outbreaks are not clearly known
FMD virus (FMDV)

- **Aphthovirus** of the family **picornaviridae**
- Non-enveloped, icosahedral virus, 26 nm in diameter
- +ve sense ss RNA virus
- Seven serotypes exist: A, O, C, Asia 1 and SAT1-3)
- Displays high genetic and antigenic variation
FMDV genome orientation

L2A 3C Primary cleavages
Poly(C)

L1A 1B 1C 1D 2A 2B 2C 3A 3B 3C 3D Secondary cleavages

1B/RNA? 3C 3C 3C 3C 3C 3C

Kilobases

Protease Carboxy-terminal self-cleaving Protease Capsid NTP binding* Polymerase Genome-linked (VPg) Membrane-binding (VP4) Protease Polymerase

Membrane-binding VP4 VP2 VP3 VP1

VPG 5'UTR AAA (n)

3'UTR

variable VP1 region sequences used for isolate characterisation
231 samples (epithelial tissues, probang samples, and whole blood) were submitted to the WRLFMD from 1967 to 2009 for analysis

Lab analysis for FMDV was conducted by VI, CF, Antigen ELISA, RT-PCR and sequencing of the VP1 gene

Phylogenies of VP1 sequences were determined by neighbor-joining method
Detection rate of FMDV

<table>
<thead>
<tr>
<th>Years</th>
<th>FMDV detection</th>
<th>Sample collected</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1968-1977</td>
<td>16</td>
<td>37</td>
<td>53</td>
</tr>
<tr>
<td>1978-1987</td>
<td>11</td>
<td>12</td>
<td>23</td>
</tr>
<tr>
<td>1988-1997</td>
<td>5</td>
<td>5</td>
<td>10</td>
</tr>
<tr>
<td>1998-2007</td>
<td>58</td>
<td>95</td>
<td>153</td>
</tr>
<tr>
<td>2008-2010</td>
<td>14</td>
<td>82</td>
<td>96</td>
</tr>
<tr>
<td>Total</td>
<td>104</td>
<td>231</td>
<td>335</td>
</tr>
</tbody>
</table>

- Detection rate varied with time and geographic location
- Are the correct samples being collected?
- Preservation of the samples?
Detection frequency of FMDV serotypes

- Type O: 26.4% (27 cases)
- Type A: 14.1% (15 cases)
- Type SAT1: 46.2% (49 cases)
- Type SAT2: 11.3% (13 cases)
Phylogenetic tree: serotype “A”

Coloured blue: Tanzania strains, which belong to the Africa G-I
Phylogenetic tree: serotype “O”

Coloured red: Tanzania strains, which belong to the EA-2 topotype
Phylogenetic tree: serotype “SAT1”

Coloured red: Tanzania strains, which belong to the NWZ and other topotype
Recommendations

• FMD outbreak investigation:
  – More sample collection and appropriate diagnosis is needed

• Research to describe the complex epidemiology and endemicity of FMD in Tanzania and other parts of Africa is needed

• Molecular characterisation and analysis of many FMD samples is needed to elucidate the phylodynamics and evolutionary nature of FMDV

• Cross-protection and vaccine-matching of the field isolates to available vaccines is required
Coloured blue: Tanzania strains, which belong to the IV topotype
Phylogenetic tree: serotype “SAT2” (ii)

Note:
The tree include viruses isolated in 2010-2011

Coloured blue: Tanzania strains, which belong to the IV topotype
Discussion and conclusion

- Serotypes A, O, SAT1 and SAT2 are the main cause of FMD outbreaks in Tanzania
- FMDV isolates so far detected in Tanzania are genetically related to lineages and topotypes from West and East Africa
- Presence of multiple serotypes and topotypes complicates FMD control in the region
- Understanding the spatio-temporal distribution, epidemiology, genetic and antigenic characteristics of circulating FMDV is a prerequisite for control of FMD in Tanzania and other parts of Africa
Acknowledgement

wellcome trust

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