## Event summary: Foot and mouth disease, Tunisia

<table>
<thead>
<tr>
<th>Event Details</th>
<th>Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>Start of event</td>
<td>25/04/2014</td>
</tr>
<tr>
<td>Confirmation</td>
<td>26/04/2014</td>
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<tr>
<td>Report date</td>
<td>29/04/2014</td>
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<tr>
<td>Submission date</td>
<td>29/04/2014</td>
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<td>Reason</td>
<td>Reoccurrence</td>
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<tr>
<td>This event pertains to</td>
<td>the whole country</td>
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<tr>
<td>Number of outbreaks</td>
<td>134</td>
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<tr>
<td>Date resolved</td>
<td>Continuing</td>
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### Tunisia has submitted the following immediate notification and follow-up report(s) to OIE.

<table>
<thead>
<tr>
<th>View</th>
<th>Report Date</th>
<th>Date submitted to OIE</th>
<th>Report Type</th>
<th>Sequences</th>
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<tbody>
<tr>
<td>Full</td>
<td>29/04/2014</td>
<td>29/04/2014</td>
<td>Immediate notification</td>
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<td>Full</td>
<td>09/05/2014</td>
<td>08/05/2014</td>
<td>Follow-up Report 1</td>
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<tr>
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<td>13/05/2014</td>
<td>13/05/2014</td>
<td>Follow-up Report 2</td>
<td>genomic sequences</td>
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</tbody>
</table>
OIE platform for pathogen genomics - Objectives

The platform will:
- Gather genomic sequences from the OIE reference laboratories
- Provide a service for data storage
- Provide sequencing information within and outside the OIE reference laboratories network
- Provide assistance and expertise for sequence assembly and data analyses within and outside the OIE reference laboratories and collaborating centers network
- Facilitate the participation of non-OIE reference laboratories to the platform and upload their own sequences
- Develop consensus to define reference genomes
- To define property rights, accessibility and proper use of data

Last Sequences

15/06/2014 Tunisia - Foot and mouth disease Serotype O
20/04/2014 Tunisia - Foot and mouth disease Serotype O
18/09/2013 Italy - Bluetongue serotype 2
10/05/2013 Italy - Listeria
<table>
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<tr>
<th>Sequence ID</th>
<th>Collection Date</th>
<th>Country</th>
<th>Disease</th>
<th>Serotype</th>
<th>OIE code</th>
<th>Animal</th>
<th>Detail</th>
<th>Raw Seq</th>
<th>Analysis</th>
<th>WAHID rep</th>
<th>BioBank</th>
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<td>Tunisia</td>
<td>FMD</td>
<td>O</td>
<td>available</td>
<td>cattle</td>
<td>NA</td>
<td>NA</td>
<td>immediate</td>
<td>follow up</td>
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<tr>
<td>seq 2</td>
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<td>O</td>
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<td>NA</td>
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<td></td>
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<tr>
<td>seq 3</td>
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<td>Italy</td>
<td>Bluetongue</td>
<td>2</td>
<td>available</td>
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<td>pigs</td>
<td>NA</td>
<td>NA</td>
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</table>

**User Feedback** Email the support team if you have a comment on this system.

World Animal Health Information System (WAHIS) - Version: 2
Copyright (c) World Organisation for Animal Health (OIE) 2012
Release date: 30 December 2013 2013
Foot and mouth disease virus serotype O, VP1

PATHOGEN GENOMIC DETAILS

Sequence

>XX5554X | Foot and mouth disease virus serotype O
GTTAAAACAGGATCGCGATGGATGACGTTCGCGCATTCAATTATATGGACGTAATACCCAGAGCATTTATT
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GATGACGCTAAATACCTGAGATGCTGGGGAATATTAGATGGTGAGTGGATAGGAAATGAGAATTTAA

User Feedback
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Release date: 30 December 2013 2013
Foot and mouth disease virus serotype O, VP1

PATHOGEN GENOMIC DETAILS

**Epidemiological details**
Date of report: 29/04/2014

Country: Tunisia
County: Somaa
Coordinate system: WGS84
Projection: UTM zone 32
Latitude: 36.544
Longitude: 10.782

Disease: Foot and mouth disease
Causal agent: ssRNA virus, Picornaviridae
Serotype: O
Animal category: Domestic
Species: Cattle

Number of animals
Susceptible: 17
Cases: 2
Death: 0
Destroyed: 0
Slaughtered: 2

**Sequence details**
Sequence number: XX5545X

Submitter: John Smith
Laboratory: IZSLER
Number of sequences: 1
Sequence: gene VP1
Method: Sanger
Sequencing platform: 3500xL Genetic Analyzer ABI
Sequence length: 639bp

Bibliographic reference: NA
Foot and mouth disease virus serotype O, VP1

PATHOGEN GENOMIC DETAILS

User Feedback Email the support team if you have a comment on this system.

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Copyright (c) World Organisation for Animal Health (OIE) 2012
Release date: 30 December 2013 2013
Bluetongue virus 2 strain 2/HIT, VP1

PATHOGEN GENOMIC DETAILS

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<th>Sequence</th>
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Bluetongue virus 2 strain 2/HIT, VP1

PATHOGEN GENOMIC DETAILS

**Sequence Details**
- Sequence number: XX1231X
- Sumbitter: Marco Caporale
- Laboratory: IZSAM
- Number of sequences: 1
- Sequence: VP1, complete sequence
- Method: NGS
- Sequencing platform: Illumina MiSeq
- Sequence length: 4030bp

**Bibliographic reference:** NA

**Epidemiological details**
- Date of report: 11/04/2014
- Country: Italy
- County: Sardinia
- Coordinate system: WGS84
- Projection: UTM zone 2
- Latitude: 42.00
- Longitude: 27.68

**Disease:** Bluetongue
**Causal agent:** dsRNA virus, Orbivirus
**Serotype:** 2
**Animal category:** Domestic
**Species:** Sheep

**Number of animals**
- Susceptible: 250
- Cases: 26
- Death: 10
- Destroyed: 0
- Slaughtered: 2
Bluetongue virus 2 strain 2/HIT, VP1

PATHOGEN GENOMIC DETAILS

Sequence Information Quality
Bluetongue virus 2 strain 2/HIT, VP1

PATHOGEN GENOMIC DETAILS

Sequence Information Quality

>XX1231X Bluetongue virus 2 strain 2/HIT | VP1
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TACCTAGAGAGAGGCAATCTCGTGTAACTCTTCTCGTGTAGTATGTTAGGAGTTAGA

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Release date: 30 December 2013
**Bluetongue virus 2 strain 2/HIT, VP1**

### PATHOGEN GENOMIC DETAILS

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<td>Serotype: 2</td>
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<td>Animal category: Domestic</td>
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<tr>
<td>Species: Sheep</td>
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Number of animals

- Susceptible: 250
- Cases: 26
- Death: 10
- Destroyed: 0
- Slaughtered: 2

User Feedback: Email the support team if you have a comment on this system.
Bluetongue virus 2 strain 2/HIT, VP1

**PATHOGEN GENOMIC DETAILS**

- Sequence
- Information
- Quality

**Quality scores across all bases (Sanger / Illumina 1.9 encoding)**

**Sequence content across all bases**

*User Feedback* Email the support team if you have a comment on this system.

World Animal Health Information System (WAHIS) - Version: 2
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Release date: 30 December 2013 2013
Epidemiological Data

Date: dd/MM/yyyy
Disease: Select disease
- bluetongue
- foot and mouth disease

Casual Agent:
Serotype:

County: first administrative division
Latitude e Longitude:

Animal Category:
- Domestic
  Species
- Wild
  Latin Name:

Number of Animal:
Susceptible:
Deaths:
Cases:
Slaughtered:

NEXT ->
**Sequence file:**

- Mandatory: FASTQ, FASTA or other generated by NGS system or output of a pipeline

**Sequencing platform:**

- Mandatory: e.g.: 3500xL Genetic Analyzer ABI, Ion torrent, Illumina, etc.

**Quality parameters:**

- Mandatory: sequence depth and coverage used to produce the sequence
  - N50
  - % reads Q20, Q30 and Q40
  - Average reads length
  - Quality Graphic Output ex. Fast QC only coverage

**Assembly pipeline:**

- Optional: the software used to assemble sequences
  - e.g. Software (Mira, Velvet, BWA, Workbench, DNASTar.....)
Whole genome shotgun sequencing of Listeria monocytogenes str. 03445X

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<th>N° of spots</th>
<th>N° of bases</th>
<th>GC content</th>
<th>Size</th>
<th>Publication</th>
<th>Access</th>
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<td>927,964</td>
<td>400.9 Mbp</td>
<td>33.40%</td>
<td>293.7 M</td>
<td>10 Oct 2014</td>
<td>Public</td>
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</table>

Phred quality score

- Experiment Name: TKK00XX12  Listeria monocytogenes str. 03445X
- Platform: Illumina MiSeq
- Sample description: Soft cheese

User Feedback: Email the support team if you have a comment on this system.
Whole genome shotgun sequencing of listeria monocytogenes str. 03445X

>1 - PFY178909

```
ATCCCCCAACGGGTTTTCCCTTCTTTG
CACCAACCCCACTTTGCTTTCTCTCT
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GCGTTTGGTTCCTTGCGCTTCTTCT
TGCTTGTGGCACGCTGATGTCTTTT
ACTTTGCTTCGGGTGATGTGCTTTT
GCCTTGCTCCAGCTGATGTGCTTTT
```

User Feedback
Email the support team if you have a comment on this system.
World Animal Health Information System (WAHIS) - Version: 2
Copyright (c) World Organisation for Animal Health (OIE) 2012
Release date: 30 December 2013 2013
Whole genome shotgun sequencing of Listeria monocytogenes str. 03445X

Run     PFY178909
Size    293.7 Mb  [HTTP]  [FTP]

User Feedback Email the support team if you have a comment on this system.

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Release date: 30 December 2013
 CHAPTER 2.1.5.

FOOT AND MOUTH DISEASE

SUMMARY

Foot and mouth disease (FMD) is the most contagious disease of mammals and has a great potential for causing severe economic loss in susceptible cloven-hoofed animals. There are seven serotypes of FMD virus (FMDV), namely, O, A, C, SAT 1, SAT 2, SAT 3 and Asia 1. Infection with one serotype does not confer immunity against another. FMD cannot be differentiated clinically from other vesicular diseases, such as swine vesicular disease, vesicular stomatitis and vesicular exanthema. Laboratory diagnosis of any suspected FMD case is therefore a matter of urgency.

Typical cases of FMD are characterised by a vesicular condition of the feet, buccal mucosa and, in females, the mammary glands. Clinical signs can vary from mild to severe, and fatalities may occur, especially in young animals. In some species the infection may be subclinical, e.g. African buffalo (Syncerus caffer). The preferred tissue for diagnosis is epithelium from unruptured or freshly
CHAPTER 2.1.3.

BLUETONGUE

SUMMARY

Bluetongue (BT) is an infectious, non-contagious, vector-borne viral disease that affects wild and domestic ruminants such as sheep, goats, cattle, buffaloes, deer, most species of African antelope and various other Artiodactyla as vertebrate hosts. Infection with bluetongue virus (BTV) is inapparent in the vast majority of animals but can cause fatal disease in a proportion of infected sheep, deer and wild ruminants. Infection of cattle with BTV does not usually result in clinical signs, with the exception of BTV8 infection in Europe. Cattle are particularly significant in the epidemiology of the disease due to the prolonged viraemia in the absence of clinical disease. Clinical signs of BT are mainly attributable to vascular permeability and include fever, hyperaemia and congestion, facial oedema and haemorrhages, and erosion of the mucous membranes. However in mild cases of the disease, a transitory hyperaemia and slight ocular and nasal discharge may be observed.
NB: Version adopted by the World Assembly of Delegates of the OIE in May 2014

CHAPTER 2.9.7.

LISTERIA MONOCYTOGENES

SUMMARY

A wide variety of animal species can be infected with Listeria monocytogenes, but clinical listeriosis is mainly a ruminant disease, with occasional sporadic cases in other species. The main clinical manifestations of animal listeriosis are encephalitis, septicaemia and abortion, and the disease is often associated with stored forages, usually silage. Post-mortem findings and histopathology depend on the clinical presentation.

Listeriosis is one of the most important food-borne diseases of humans. The disease manifestations include septicaemia, meningitis (or meningoencephalitis) and encephalitis. In pregnant women, intrauterine or cervical infections may result in spontaneous abortion or stillbirths, and may be preceded by influenza-like signs, including fever. Listeria monocytogenes has also been associated with gastroenteric manifestations with fever. Although the morbidity of listeriosis is relatively low, the
Analyse sequence

**Sequence**
- Whole genome
  - gene 1
  - gene 2
  - gene 3

**Compare with**
- Reference sequence
  - OIE sequences
  - genBank sequences
  - ...

[Paste your sequence here]

Search for alignment

User Feedback: Email the support team if you have a comment on this system.

World Animal Health Information System (WAHIS) - Version 2
Copyright (c) World Organisation for Animal Health (OIE) 2012
Release date: 30 December 2013 2013
# Bluetongue virus 2 strain 2/HIT

## Sequence
- Whole genome
- gene 1
- gene 2
- gene 3

## Compare with
- Reference sequence
- OIE sequences
- genBank sequences

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GAGAGAAATAGATATTGAGCACAAATTGCAAAAAGAGGATAGAGAGTGGTTTGGTGCGTA
```

[Search for alignment]
Sequence alignment

**Bluetongue virus 2 strain 2/HIT**

Select sequences to analyse in the grid below:

<table>
<thead>
<tr>
<th>Description</th>
<th>Max score</th>
<th>Total score</th>
<th>Cover</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bluetongue virus 2 isolate/sheep/08/ND</td>
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<td>8003</td>
<td>100%</td>
</tr>
<tr>
<td>Bluetongue virus 2 isolate sheep/08/ABT</td>
<td>8003</td>
<td>8003</td>
<td>100%</td>
</tr>
<tr>
<td>Bluetongue virus serotype 1</td>
<td>7994</td>
<td>7980</td>
<td>99%</td>
</tr>
<tr>
<td>Bluetongue virus serotype 1</td>
<td>7992</td>
<td>7980</td>
<td>99%</td>
</tr>
<tr>
<td>Bluetongue virus 2 isolate IND-IT5</td>
<td>7965</td>
<td>7904</td>
<td>98%</td>
</tr>
<tr>
<td>Bluetongue virus 4 strain IND-IT5</td>
<td>7960</td>
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</tr>
<tr>
<td>Bluetongue virus serotype 3</td>
<td>7450</td>
<td>7200</td>
<td>97%</td>
</tr>
<tr>
<td>Bluetongue virus serotype 3</td>
<td>7450</td>
<td>7122</td>
<td>96%</td>
</tr>
<tr>
<td>Bluetongue virus 2 isolate 7293</td>
<td>7450</td>
<td>7200</td>
<td>97%</td>
</tr>
<tr>
<td>Bluetongue virus serotype 3</td>
<td>7450</td>
<td>7120</td>
<td>96%</td>
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<td>Bluetongue virus 2 strain 2-IL3</td>
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</tr>
</tbody>
</table>

*Selected sequences are displayed in the map*

**Analysis**
- Phylogenetic reconstruction
- Mutation frequencies

**Start analysis**

*User Feedback* Email the support team if you have a comment on this system.

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Release date: 30 December 2013
### Bluetongue virus 2 strain 2/HIT

#### Genomic Sequence

![Genomic Sequence Chart](chart.png)

#### Tools

- **REF**
- **2/HIT**
- **2 sheep/08/ND**
- **2 sheep/08/ABT**
- **2 IND-IT5**
- **2 27293**
- **2 2 lD09**
- **2 y863**

#### Preferences

- Email the support team if you have a comment on this system.

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CHAPTER 8.7.

FOOT AND MOUTH DISEASE

Article 8.7.1.

Introduction

For the purposes of the Terrestrial Code, the incubation period for foot and mouth disease (FMD) shall be 14 days.

For the purposes of this chapter, ruminants include animals of the family of Camelidae (except Camelus dromedarius).

For the purposes of this chapter, a case is an animal infected with FMD virus (FMDV).

The chapter deals not only with the occurrence of clinical signs caused by FMDV, but also with the presence of infection with FMDV in the absence of clinical signs.

The following defines the occurrence of FMDV infection:

1) FMDV has been isolated and identified as such from an animal or a product derived from that animal; or
2) viral antigen or viral ribonucleic acid (RNA) specific to one or more of the serotypes of FMDV has been identified in samples from one or more animals, whether showing clinical signs consistent with FMD or not, or epidemiologically linked to a confirmed or suspected outbreak of FMD, or giving cause for suspicion of previous association or contact with FMDV; or
3) antibodies to structural or nonstructural proteins of FMDV that are not a consequence of vaccination, have been identified in one or more animals showing clinical signs consistent with FMD, or epidemiologically linked to a confirmed or suspected outbreak of FMD, or giving cause for suspicion of previous association or contact with FMDV.

Standards for diagnostic tests and vaccines are described in the Terrestrial Manual.
CHAPTER 8.3.

BLUETONGUE

Article 8.2.1.

General provisions

For the purposes of the Terrestrial Code, the infective period for bluetongue virus (BTV) shall be 60 days.

Historically, the global BTV distribution has been confined between the latitudes of approximately 53°N and north of 34°S with a recent extension in Northern Europe.

In the absence of clinical disease in a country or zone, its BTV status should be determined by an ongoing surveillance programme (in accordance with Articles 8.3.16. to 8.3.21.). The programme may need to be adapted to target parts of the country or zone at a higher risk due to historical, geographical and climatic factors, ruminant population data and Culicoides ecology, or proximity to enzootic or incursion zones as described in Articles 8.3.16. to 8.3.21.

All countries or zones adjacent to a country or zone not having free status should be subjected to similar surveillance. The surveillance should be carried out over a distance of at least 100 kilometres from the border with that country or zone, but a lesser distance could be acceptable if there are relevant ecological or geographical features likely to interrupt the transmission of BTV or a bluetongue surveillance programme (in accordance with Articles 8.3.16. to 8.3.21.) in the country or zone not having free status supports a lesser distance.

When authorising import or transit of the commodities covered in the chapter, with the exception of those listed in Article 8.3.2., Veterinary Authorities should require the conditions prescribed in this chapter relevant to the BTV status of the ruminant population of the exporting country or zone.

Standards for diagnostic tests and vaccines are described in the Terrestrial Manual.