Outbreak summary: Total outbreaks = 1 (Submitted)

<table>
<thead>
<tr>
<th>Species</th>
<th>Measuring units</th>
<th>Susceptible</th>
<th>Cases</th>
<th>Deaths</th>
<th>Destroyed</th>
<th>Slaughtered</th>
</tr>
</thead>
<tbody>
<tr>
<td>Common Coot</td>
<td>Animals</td>
<td>17</td>
<td>17</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>Eurasian Wigeon (Anas penelope)</td>
<td>Animals</td>
<td>13</td>
<td>13</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

Epidemiology

Epidemiological comments:
- The H5 sequence fragment was sent to the Reference Laboratory in Padova to identify the neuraminidase (N). The Reference Laboratory confirmed that the H5 sequence fragment is directly related to highly pathogenic H5 virus sequences clade 2.3.4.4 (including the H5N8 viruses currently circulating in Russia and Europe).
- A phylogenetic analysis is on-going at the Experimental Zooprophylactic Institute (IZS), Venice (OIE Reference Laboratory). - The situation is stable (nothing to highlight).

Source of the outbreak(s) or origin of infection
- Unknown or inconclusive

Measures applied

Applied
- control of wildlife reservoirs
- surveillance outside containment and/or protection zone
- official disposal of carcasses, by-products and waste
- surveillance within containment and/or protection zone

Animals treated
Vaccination Prohibited

Future Reporting
The event is continuing. Weekly follow-up reports will be submitted.
Outbreak maps