

## Follow-up report No.1 (Final report)

Report reference: DLF/2014-001, Reference OIE : 15217, Report Date : 07/05/2014, Country : Laos

### Report Summary

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		<b>Date submitted to OIE</b>	07/05/2014

<b>Animal type</b>	Terrestrial	<b>Date of report</b>	07/05/2014
<b>Disease</b>	Highly pathogenic avian influenza	<b>Date of start of the event</b>	13/03/2014
<b>Causal Agent</b>	Highly pathogenic avian influenza virus	<b>Date of pre-confirmation of the event</b>	18/03/2014
<b>Serotype(s)</b>	H5N6	<b>Date of last occurrence</b>	12/2008
<b>Reason</b>	Reoccurrence of a listed disease	<b>Diagnosis</b>	Laboratory (advanced)
<b>Country or zone</b>	a zone or compartment	<b>Clinical signs</b>	Yes
<b>Number of reported outbreaks</b>	submitted= 1, Draft= 0		

### Outbreak details

Province	Number of outbreaks	District	Sub-district	Unit Type	Location	Latitude	Longitude	Start Date	End Date:
XAYABURY-other report - submitted	-	Xayabury		Village	Nator Ngai	19.22979	101.7135	13/03/2014	31/03/2014
Species	Measuring units	Susceptible	Cases	Deaths	Destroyed	Slaughtered			
Birds	Animals	5142	457	457	543	0			
Affected Population	The affected birds were newly introduced into the village one week before the outbreak occurred.								

### Outbreak summary: Total outbreaks = 1 (Submitted)

Species	Susceptible	Cases	Deaths	Destroyed	Slaughtered
Birds	5142	457	457	543	0

### Epidemiology

#### Epidemiological comments

Samples from this outbreak have now been tested at the Australian Animal Health Laboratory. Sequencing analysis of original samples (post-mortem tissues) from both chickens and ducks shows that these are H5N6 highly pathogenic avian influenza viruses, with the highly pathogenic HA cleavage site sequence motif, PLRERRRRK\*GLF. Phylogenetic analysis of the HA gene sequence indicates that the HA is derived from the Asian H5N1 clade 2.3.4 HA lineage; however, they clustered with 'variant' (reassortant) clade 2.3.4 H5 HPAI viruses from China of various NA subtypes. Follow-up sequencing of virus isolates from these samples confirms these findings. Full genome sequencing has been completed.

#### Source of the outbreak(s) or origin of infection

- Introduction of new live animals

### Measures applied

Applied	To be applied
<ul style="list-style-type: none"> <li>• quarantine</li> <li>• movement control inside the country</li> <li>• screening</li> <li>• disinfection of infected premises/establishment(s)</li> <li>• modified stamping out</li> </ul>	<ul style="list-style-type: none"> <li>• no planned control measures</li> </ul>
Animals treated	Vaccination Prohibited
No	Yes

### Future Reporting

The report and all its outbreaks have been resolved.

## Outbreak maps

