

H3N1 AI in poultry: spreading to France...

*Anses / Ploufragan-Plouzané-Niort laboratory
NRL for avian influenza and ND*

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The cases

■ Farm A:

clinical suspicion declared 20/05/19

breeding flock for broiler production (2 barns, 48 wks old)

Nord department (59), 5 km from Belgian border

symptoms began 17/05:

↘ feed intake, egg drop (discolored shells), ↗ mortality

21/05: rtRT-PCR screening by official local lab / tr. + cl. swabs

M + / H5 - / H7 -

22/05: partial HA / NA sequencing (NRL)

→ H3N1 confirmed

27/05: culling of the flock

Observed mortality

	Barn 1 (n ≈ 8200 birds)	Barn 2 (n ≈ 9000 birds)
17/5	75	
18/5	127	
19/5	450	
20/5	unrecorded	
21/5		25
estimated cumulated % mortality → 27/5	≈ 25 %	
	≈ 15-20 %	

The cases (2)

■ Farm B:

within 3-km temporary control zone around farm A

retrospective investigation on a suspect clinical case:

81-wk old breeding flock for broiler production, culled on 02/5

mild respiratory symptoms + 1 wk later: 5% egg drop, 1.5% mortality over 2 days

environmental samples from the barn (C & D in progress)

detected in M-gene + H3-specific real-time RT-PCR (Ferreira et al. 2015)

no HA/NA sequences available

The cases (3)

■ Farm C:

clinical suspicion declared on 12/6

≈ 20 km south of farm A, close to Belgian border

➤ mortality in a moulting breeding flock for broiler production:

cumulated 2% over 2 days before culling decided by owner, on 12/6

tracheal + cloacal swabs (sampled after culling)

detected in H3-specific real-time RT-PCR + N1-specific rtRT-PCR

(Payungporn et al. 2006)

Linking the cases

- all 3 confirmed farms depend on the same integrating coupled hatchery (BE + FR)
- close proximity btw farm A and farm B
+ same egg collection circuit
- multiple Belgium / France connections
through hatchery's network

movements of animals + hatching eggs

common veterinarian + vaccination team + transport team

common feed supply

The virus

- Full genome sequence obtained from farm A:

99.6% - 100% identity with A/Gallus gallus/Belgium/3497_0001/2019

N1 stalk truncation conserved

distinctive feature: 30-nt deletion in NS1 inter-domain

- Virus isolated → amplification in progress for future infection/transmission studies

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