

Transmission characteristics of Highly Pathogenic Avian Influenza (H5N8) virus during outbreaks in the Netherlands in 2014

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Purpose

Outbreaks of Highly Pathogenic Avian Influenza (HPAI) occurred in November 2014 on three layer, one broiler-breeder and one duck farm distributed over four different regions in the Netherlands. The HPAI virus was of subtype H5N8, that before it entered Europe had been found in South Korea, China, Japan and Russia and was subsequently detected in North America. Here we quantify virus transmission during the episode of outbreaks.

Methods

Sharply increasing mortality was most striking in the broiler-breeder and layer flocks, which is in line with reports from other countries. Within-flock transmission was quantified using mortality data assuming that the number of infected birds at day t after virus introduction equals $I_0 \cdot \exp(rt)$, with I_0 number of infected birds at the start (assumed as 1) and r the exponential growth rate parameter. Using a GLM with poisson error distribution and a log-link function with the number of dead birds as dependent variable and farm as independent variable r was calculated. The duck farm was excluded, because mortality was low and did not fulfill the assumption of exponential growth.

Results

The above model showed $r = 1.02$ (95% CI :0.98-1.06). Next, using a generation interval T of 2.25 days (95% CI: 1.87-2.63), derived from experimental data, the average number of secondary infections caused by one infectious chicken, was estimated by $R_0 = \exp(rT)$ at 9.9 (95% CI 6.7-14.6). In addition, on all farms infection was only detectable in one poultry house, indicating absence of transmission between poultry houses at the time of detection. Moreover, genome sequences of the isolates point to separate virus introductions in the four different regions and a single event of between farm transmission in one of the regions. The introductions were most likely caused by contact with wild (water)birds.

Conclusions

The transmissibility of HPAI H5N8 virus among chickens in direct contact is high. However, no indirect transmission to chickens in other houses and only one event of between farm transmission was observed indicating both early detection and effective control of spread.

Relevance

Quantified transmission parameters are useful to improve surveillance and control programs.