

Integrated epidemiological and phylogeographical analysis of a H3N1 low pathogenic avian influenza outbreak with atypical pathogenicity, Belgium, 2019

S. Van Borm^{1*†}, G. Boseret^{2*}, S. Dellicour^{3*}, M. Steensels¹, V. Roupie¹, F. Vandebussche¹, E. Matthijs¹, A. Vilain², M. Driesen², M. Dispas², M. Gilbert³, B. Lambrecht¹, T. van den Berg¹

¹Animal Infectious Diseases, Sciensano, Brussels, Belgium

²Veterinary Epidemiology, Sciensano, Brussels, Belgium

³Spatial epidemiology Lab, Université Libre de Bruxelles, Brussels, Belgium

*equal contribution

†presenting author

Corresponding Author: steven.vanborm@sciensano.be

Abstract

In 2019, Belgium was hit by an outbreak of LPAI of subtype H3N1 with atypical high mortality (up to 60% in breeder and layer hens). The epidemic spread to 82 farms in Belgium and 3 epidemiologically linked farms in France. Although non-notifiable under international legislation, containment measures were implemented, and the outbreak resulted in a serious economic cost. Intravenous inoculation of young chickens confirmed a low pathogenic pathotype. However, both field observations and experimental inoculation of adult layer hens confirmed systemic spread of the virus and high viral loads in the oviduct. Further studies confirmed systemic disease and high mortality in laying hens. The systemic replication including neurotropism and endotheliotropism of the virus was demonstrated to be linked to neuraminidase associated plasminogen recruitment as a mechanism allowing furin-independent endoproteolytic viral hemagglutinin (HA) protein activation.

The present study integrated epidemiological data with high resolution full genome spatially explicit phylogeographical analysis to investigate the dynamics of the 2019 H3N1 LPAI outbreak in Belgium. In addition, the spatially explicit genetic outbreak reconstruction was used to interrogate specific epidemiological hypotheses to assess the overall importance of antropogenic, metereological, and geographical factors in the spread of the H3N1 LPAI virus during the studied outbreak. To this purpose, the complete or near-complete genome sequence of 104 clinical samples representing 85% of the 82 affected farms was determined. The full genome spatiotemporal reconstruction of the epidemic highlighted that the dominating dispersal direction was from northeast to southwest with sporadic dispersal in other directions, including a long distance NW->SE dispersal event to the province of Luxemburg. Integration with detailed metereological data in the outbreak area identified a moderate contribution of wind-based dispersal during part of the epidemic. Multivariate analysis only showed a strong effect of geographical proximity, but failed to identify an overall role of transportation or social contact variables on the observed phylogeographical reconstruction. However, case-specific and local correlations between epidemiologically predicted clusters (based on transport data and human movements) were evident throughout the outbreak, illustrating the potential contribution of these epidemiological factors in local cases.

Our analysis highlighted the complex multifactorial nature of a viral epidemic, and the value of integrating genetic, metereological and epidemiological data in tracing efforts.