

# COMBINING VIRUS GENOMES AND EPIDEMIOLOGICAL TRACING TO UNDERSTAND AN UNEXPECTEDLY SEVERE OUTBREAK OF AVIAN INFLUENZA IN POULTRY

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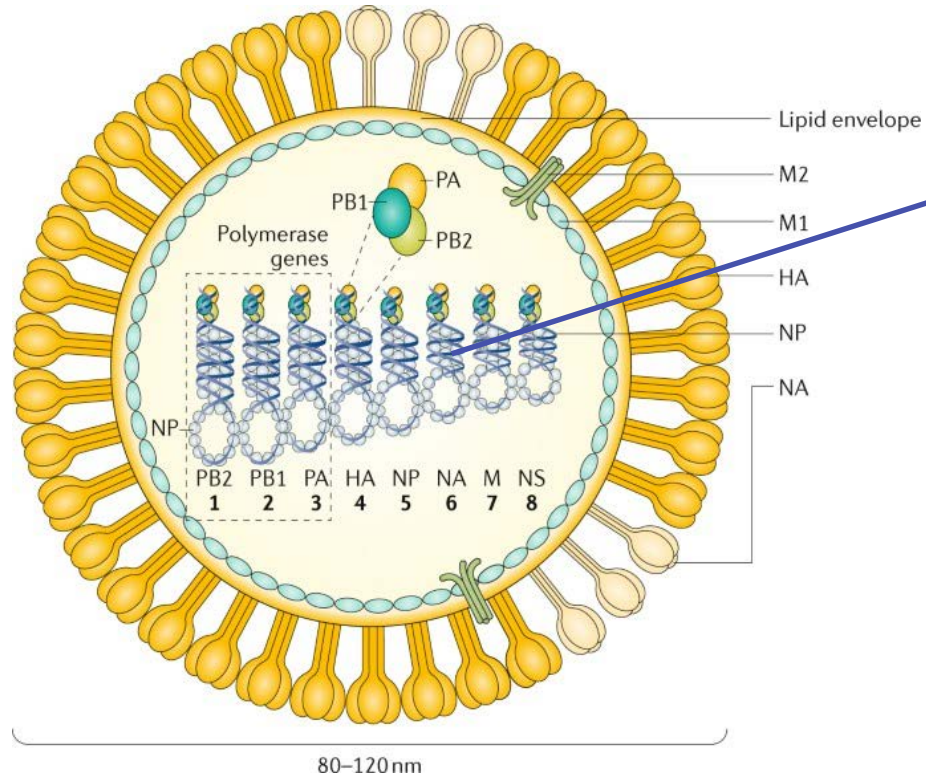
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# Combining virus genomes and epidemiological tracing to understand an unexpectedly severe outbreak of avian influenza in poultry

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# Influenza A



## Genome:

8 RNA strands, total 15 000 nt  
copying without proofreading:  
variation!

Subtypes: surface glycoproteins

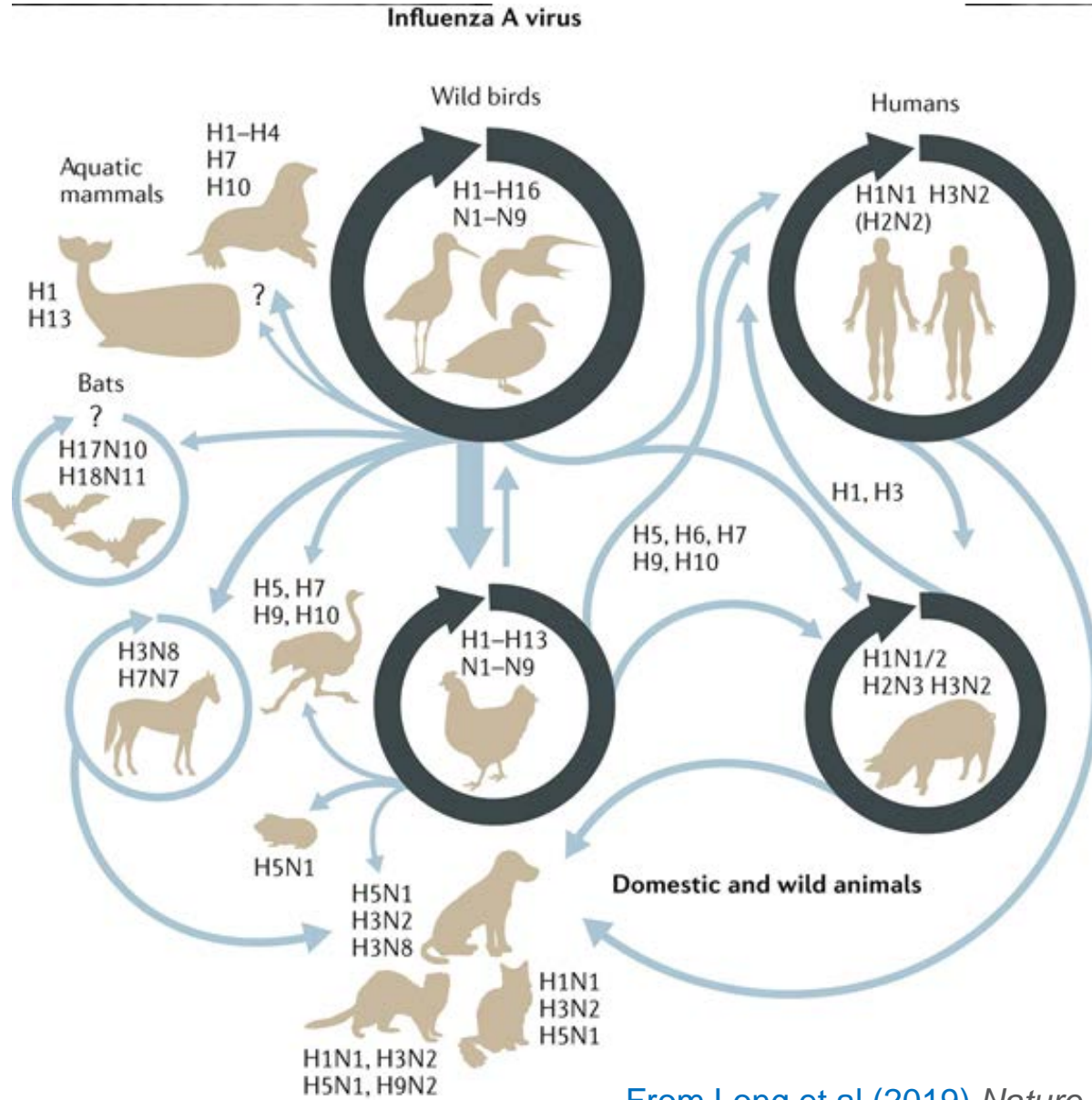
**H1-H18**

**N1-N11**

e.g. H5N1



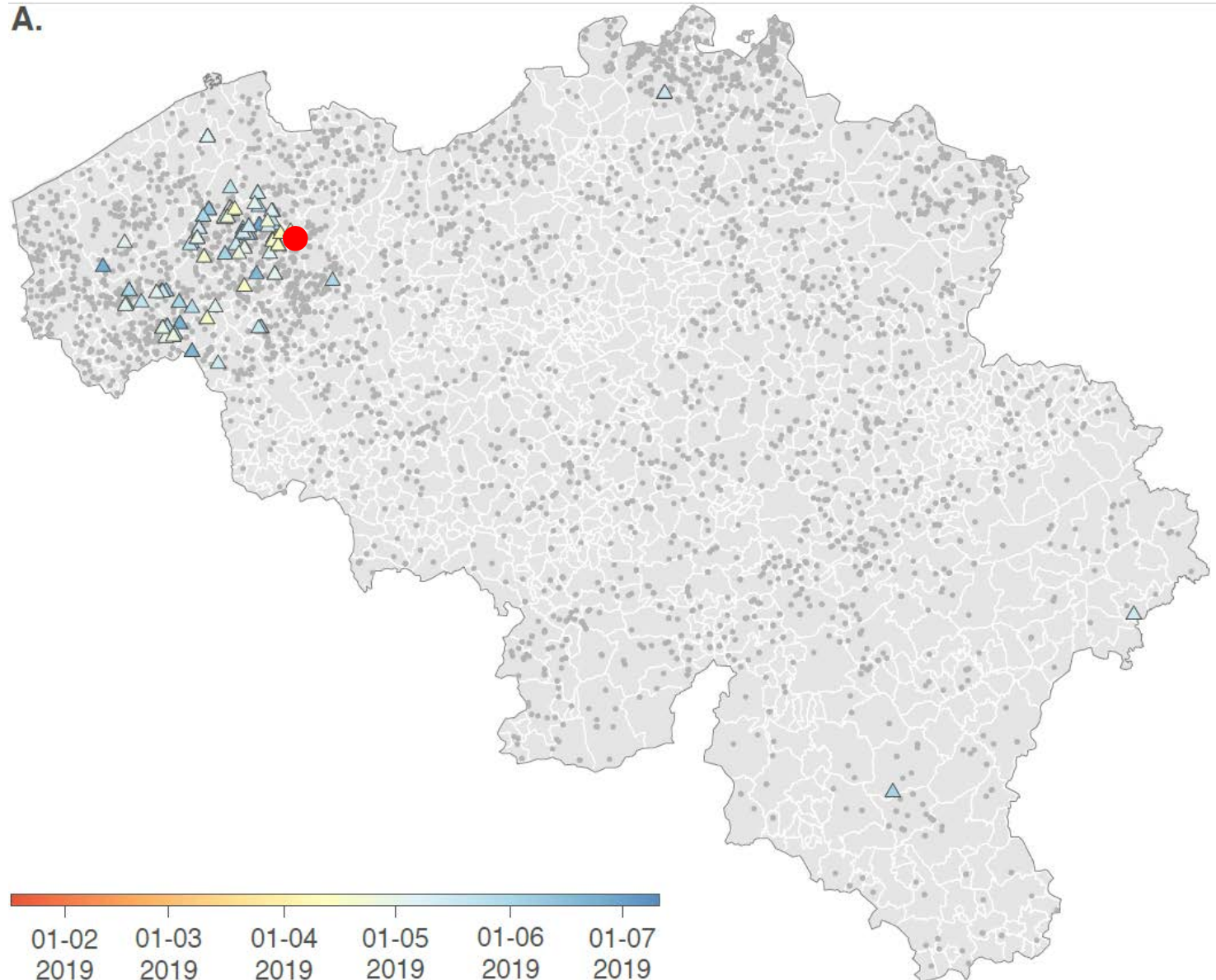
# Influenza A: a OneHealth issue



Courtesy of the National Museum of Health and Medicine, Armed Forces Institute of Pathology, Washington, D.C

# 2019: atypically severe LPAI outbreak, BE

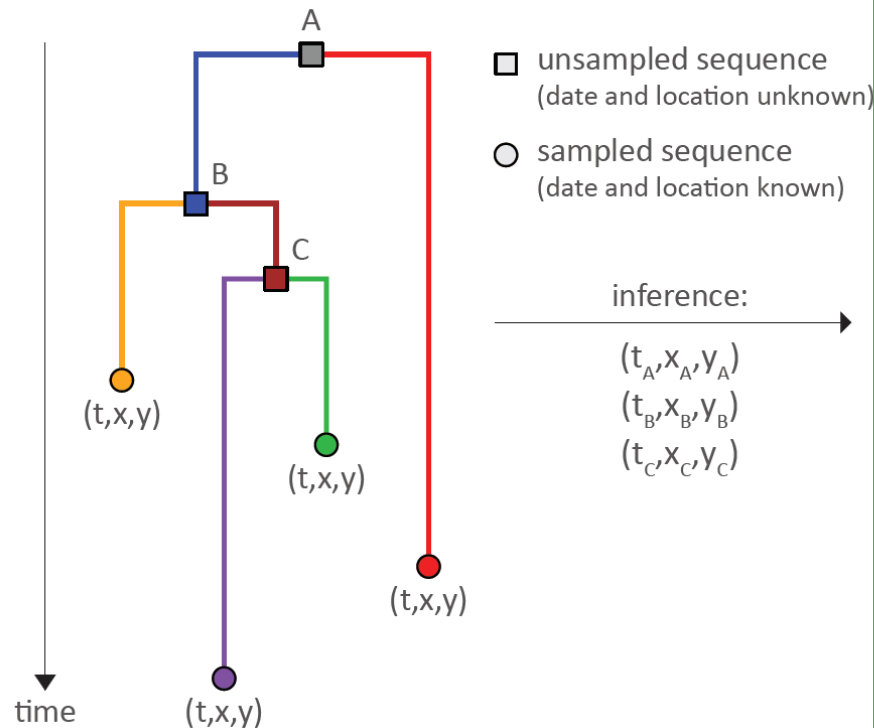
- **Farm 1:** January + re-emerge April
- H3N1, LPAI
- Fast spread in area of dense poultry farming
- Increased pathogenicity, alternative molecular mechanism
- 81 farms + 3 in France
- ↔ non-notifiable subtype, LP



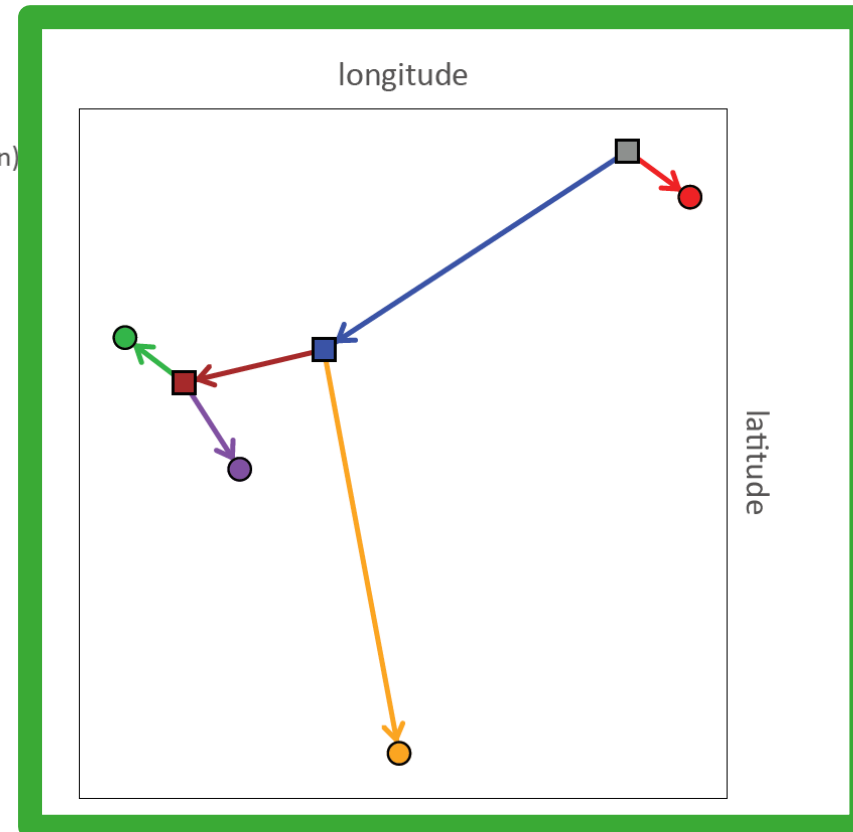
# Using RNA virus genomes to investigate virus evolution and spread dynamics

- Targeted **IAV full genome sequences** (n=104) + sample date  
→ **time**-calibrated phylogenetic reconstruction
- Sample **geographical** coordinates

**Spatially explicit outbreak reconstruction**



Maximum Clade Credibility tree



(Lemey et al. 2010, *Mol Biol Evol*)

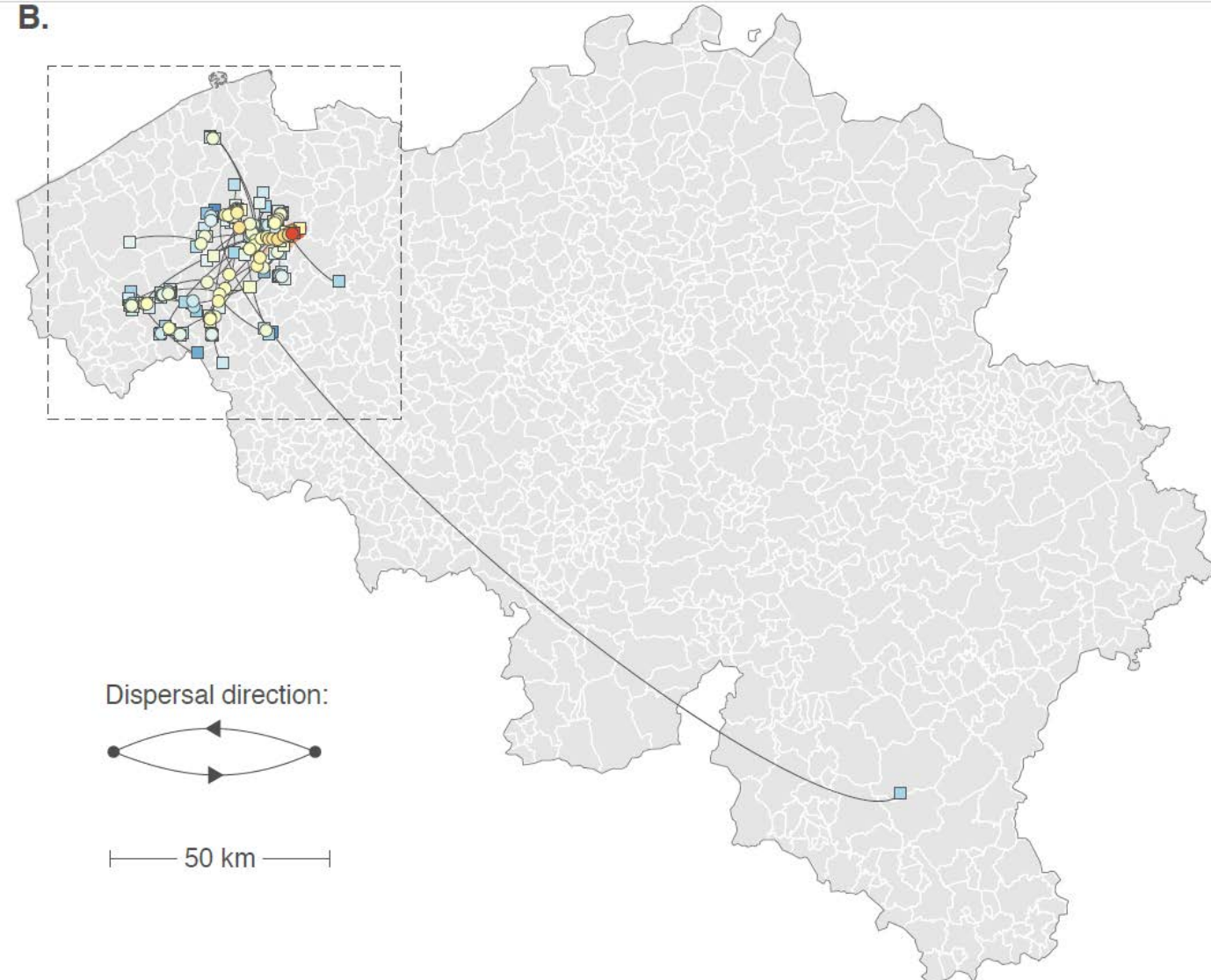
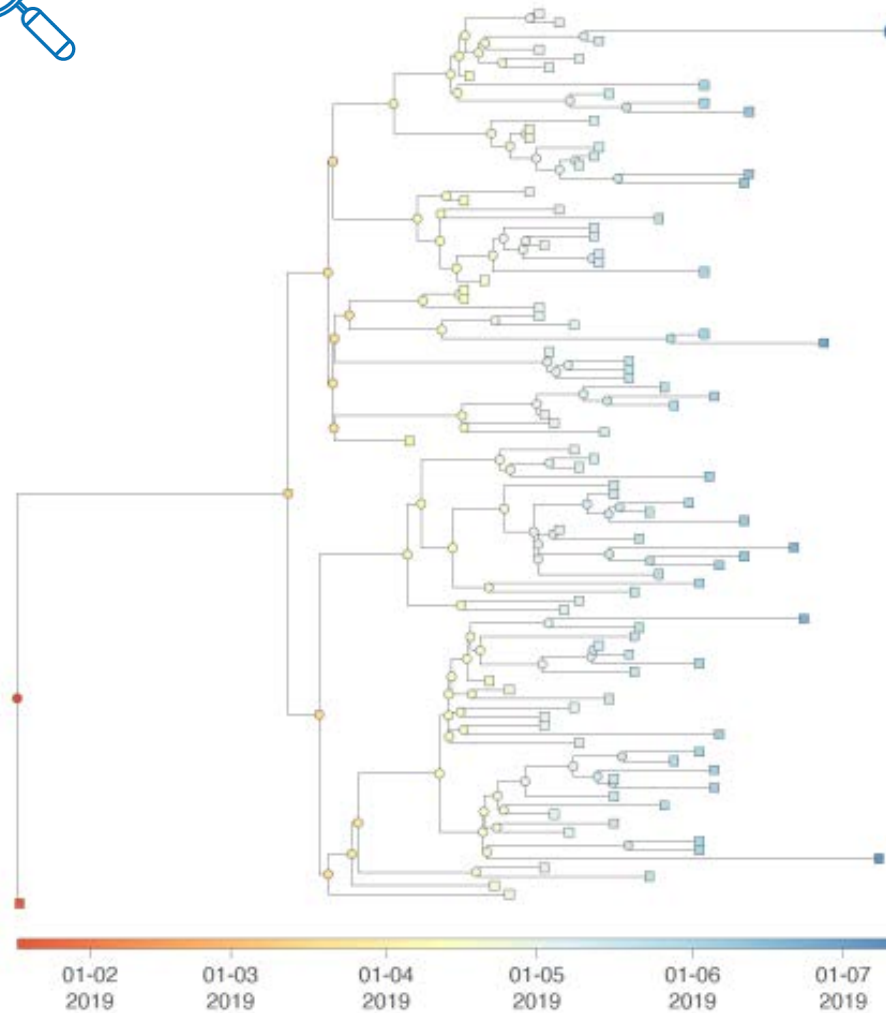


# Spatially explicit phylogeographic reconstruction of H3N1 outbreak



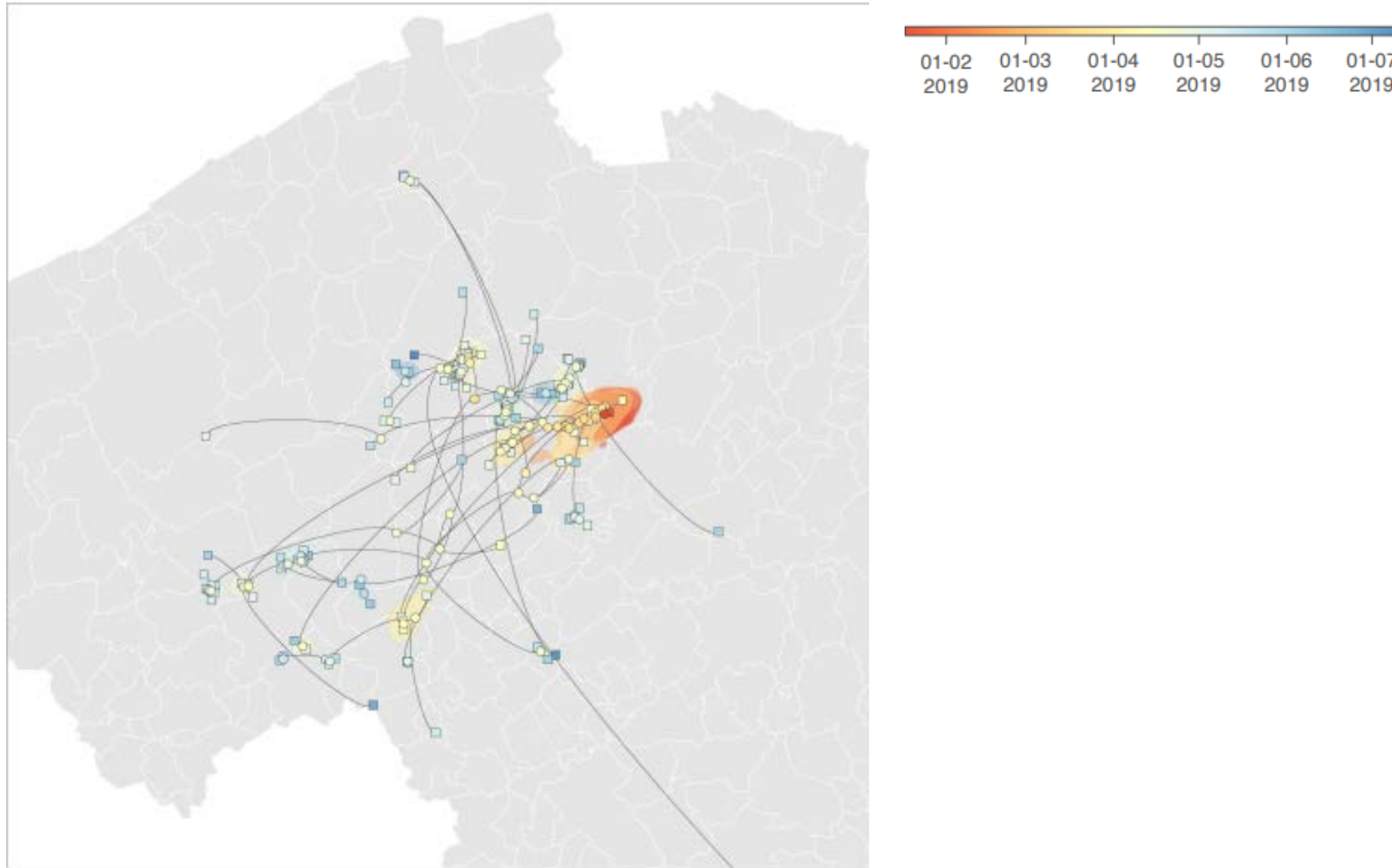
104 AIV genomes (85 % of affected farms)

**B.**



# Spatially explicit phylogeographic reconstruction of H3N1 outbreak

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# Using spatially explicit genetic reconstruction to test epidemiological hypotheses

- Targeted IAV full **genome** sequences (n=104) + sample date  
→ **time**-calibrated phylogenetic reconstruction
- Sample **geographical** coordinates

**1** Spatially explicit outbreak reconstruction = independent dispersal model

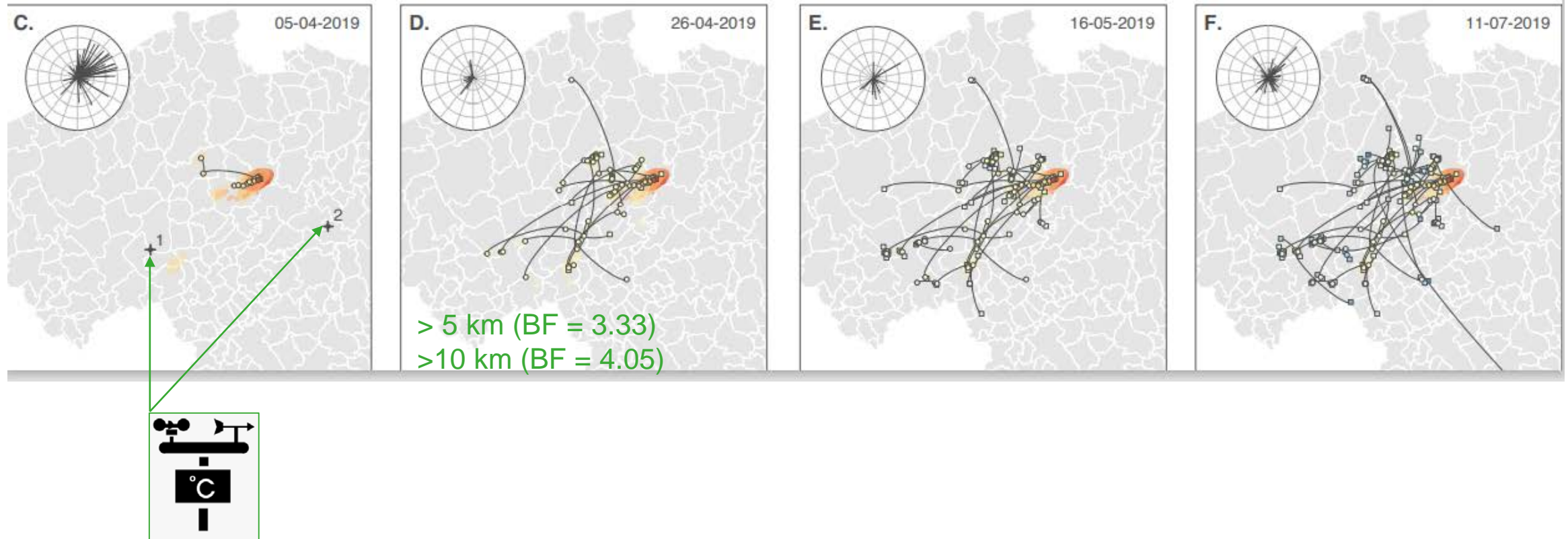
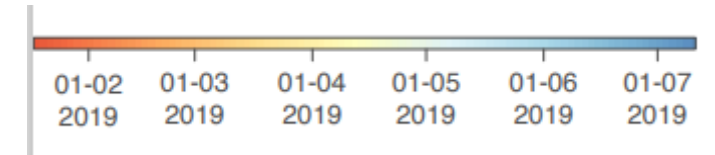
- Meteorological data
- Epidemiological data
  - Transport links (feed, animals, cadavres)
  - Social contacts (vets, family, collaborations, ...)

**Hypothesis testing:**  
assess overall impact of variable on epidemic

**2**

# Wind vectored AIV dissemination?

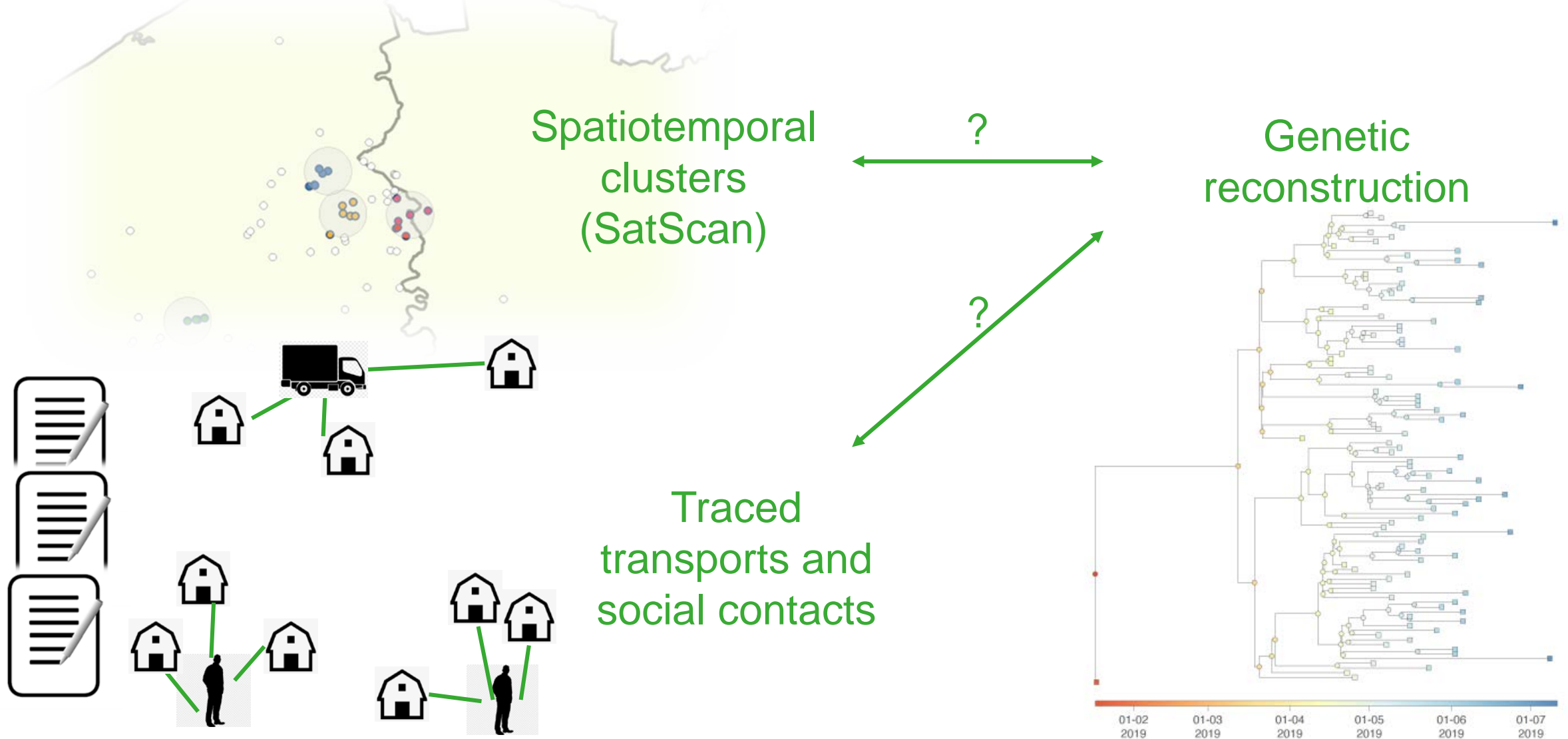
Association virus dispersal direction and wind direction.



$3 < BF < 20$  : moderate support  
 $BF > 20$ : strong support

# Testing hypotheses from epidemiological data

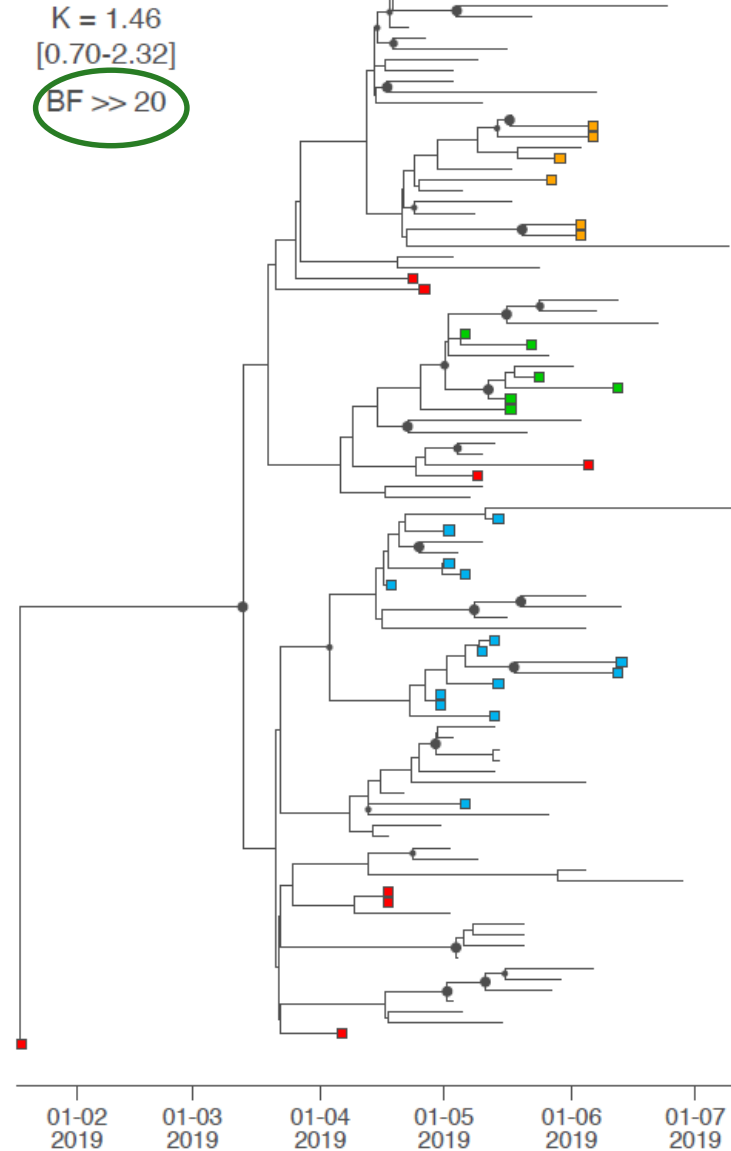
phylogenetic signal associated with three categorical epidemiological covariates



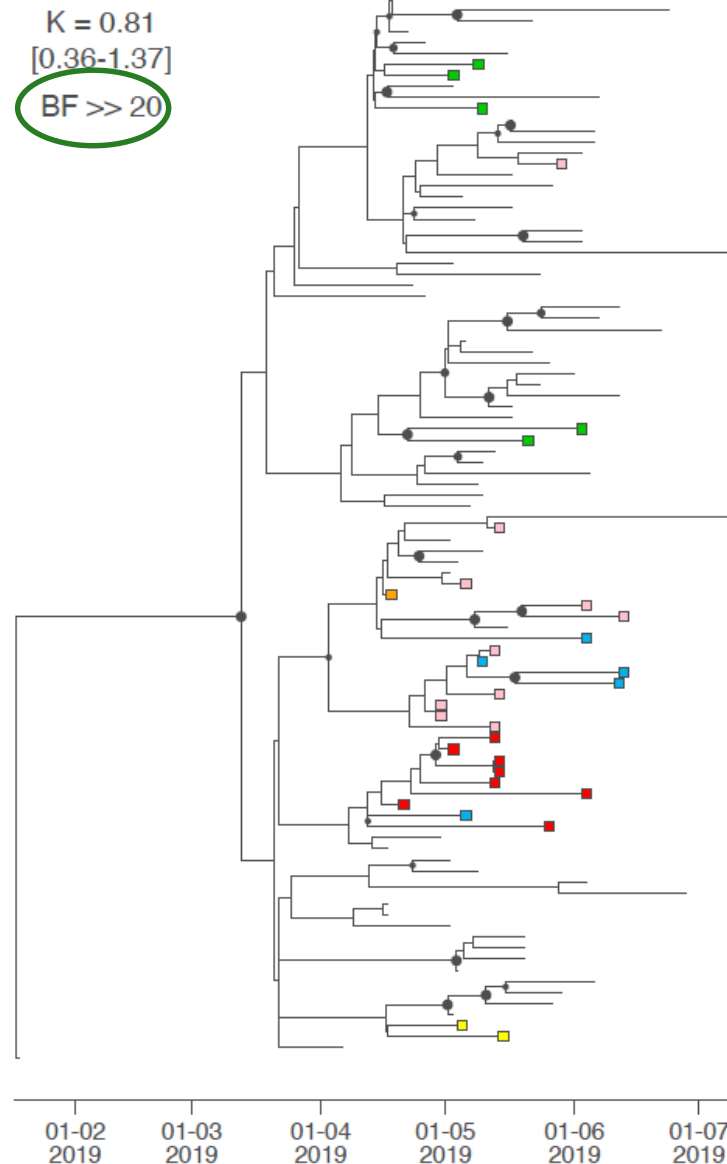


**SatScan:** ■ cluster 1, ■ cluster 2, ■ cluster 3, ■ cluster 4. **Transports** (documented transport contact networks): ■ feed supplier 1, ■ live animal transport 1, ■ cadaver collection 20/04/2019, ■ feed supplier 2, ■ cadaver collection 10/05/2019, ■ feed supplier 3. **Human movements** (documented human contact networks): ■ family collaboration - group 1 + veterinarian 15/04/2019, ■ same owner - group 1, ■ family collaboration - group 2, ■ same owner - group 2, ■ family collaboration - group 3, ■ veterinarian 04/05/2019, ■ family collaboration - group 4, ■ family collaboration - group 5, ■ same owner - group 3. **Node support** (posterior probability): • >0.95, • >0.90, • >0.75.

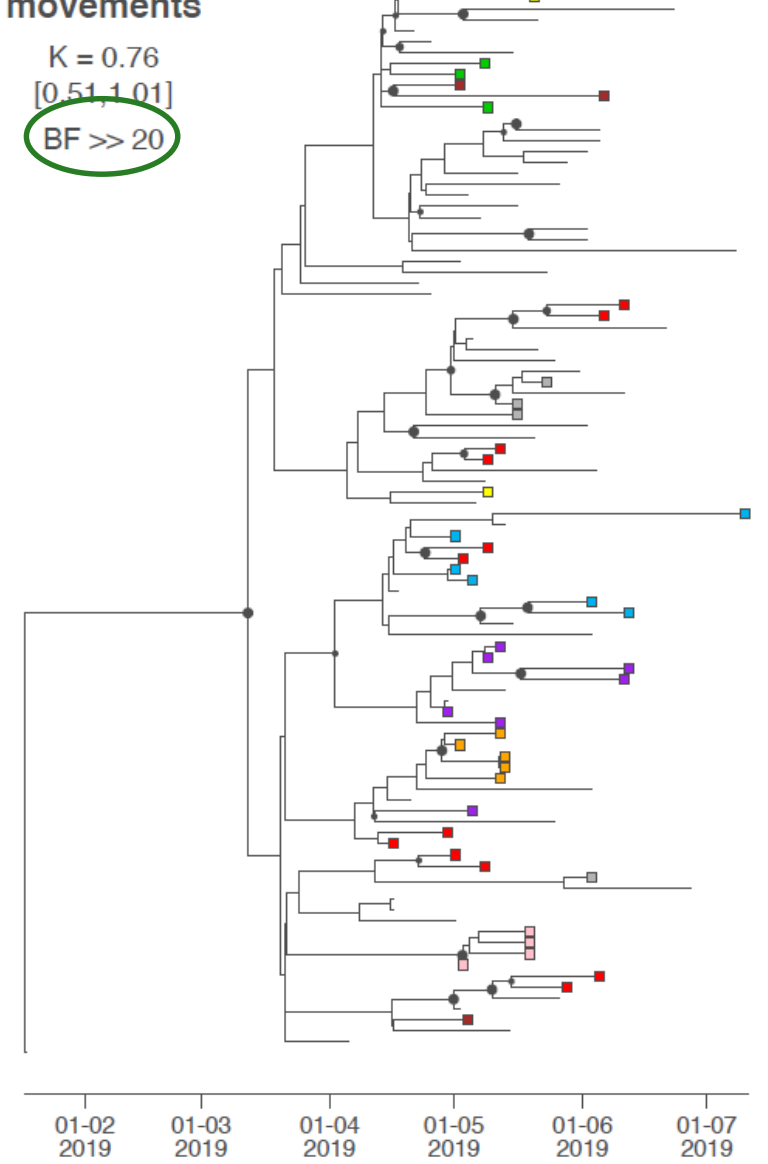
### A. SatScan



### B. Transports



### C. Human movements



## « AIV genomes told us » :

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- Local silent LPAI circulation and re-emergence (more pathogenic)
- Very limited effect of wind direction in early epidemic
- Geographic proximity, transport contacts and social contacts are heavily supported by the genetic reconstruction.
- Phylogeographic reconstruction is **independent dispersal model**:
  - Invalidates some epidemiological connections
  - Suggests additional connections that were not captured by tracing

« AIV genomes told us » :



whole viral genome phylogeography  
+detailed epidemiological data



beyond outbreak description:  
investigate drivers of an epidemic



## Contact

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### Details:

Van Borm S., Boseret G., Dellicour S., et al. 2022. Combining phylogeographic analyses and epidemiological contact tracing to characterize an atypically highly pathogenic H3N1 avian influenza epidemic (Belgium, 2019). *Emerging Infectious Diseases*. In Press.