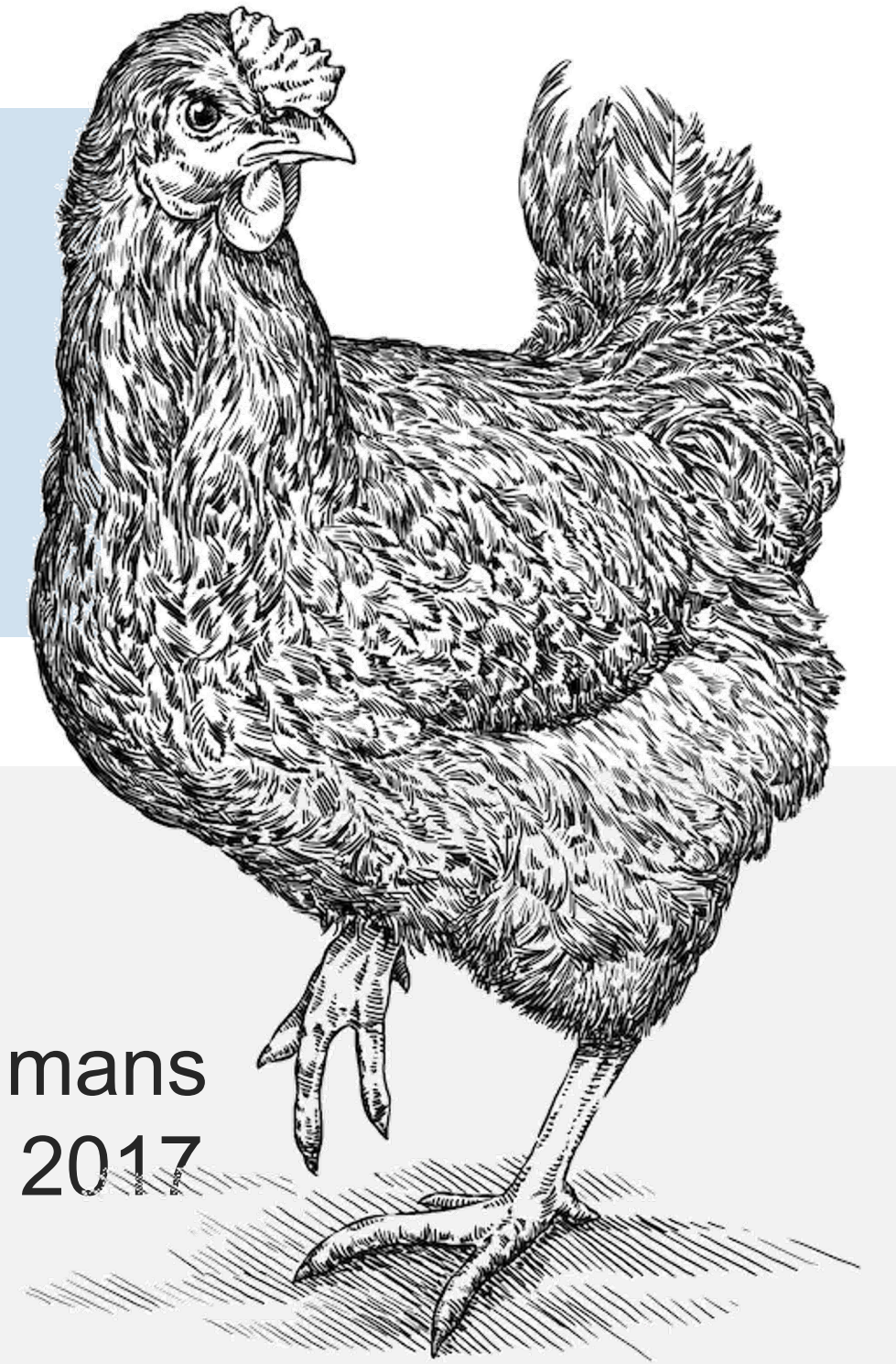


Bayesian phylodynamics of avian influenza A(H7N9) virus at the human-live bird market interface in China

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Why unraveling H7N9's past with phylodynamics?

- H7N9 caused **severe epidemics** in China in 2013-17
- Persistence** despite vaccination, further research needed
- Role of live bird markets (LBMs) in transmission **unclear**
- Case surveillance data **do not provide complete picture**



Sequence data and phylodynamic analysis

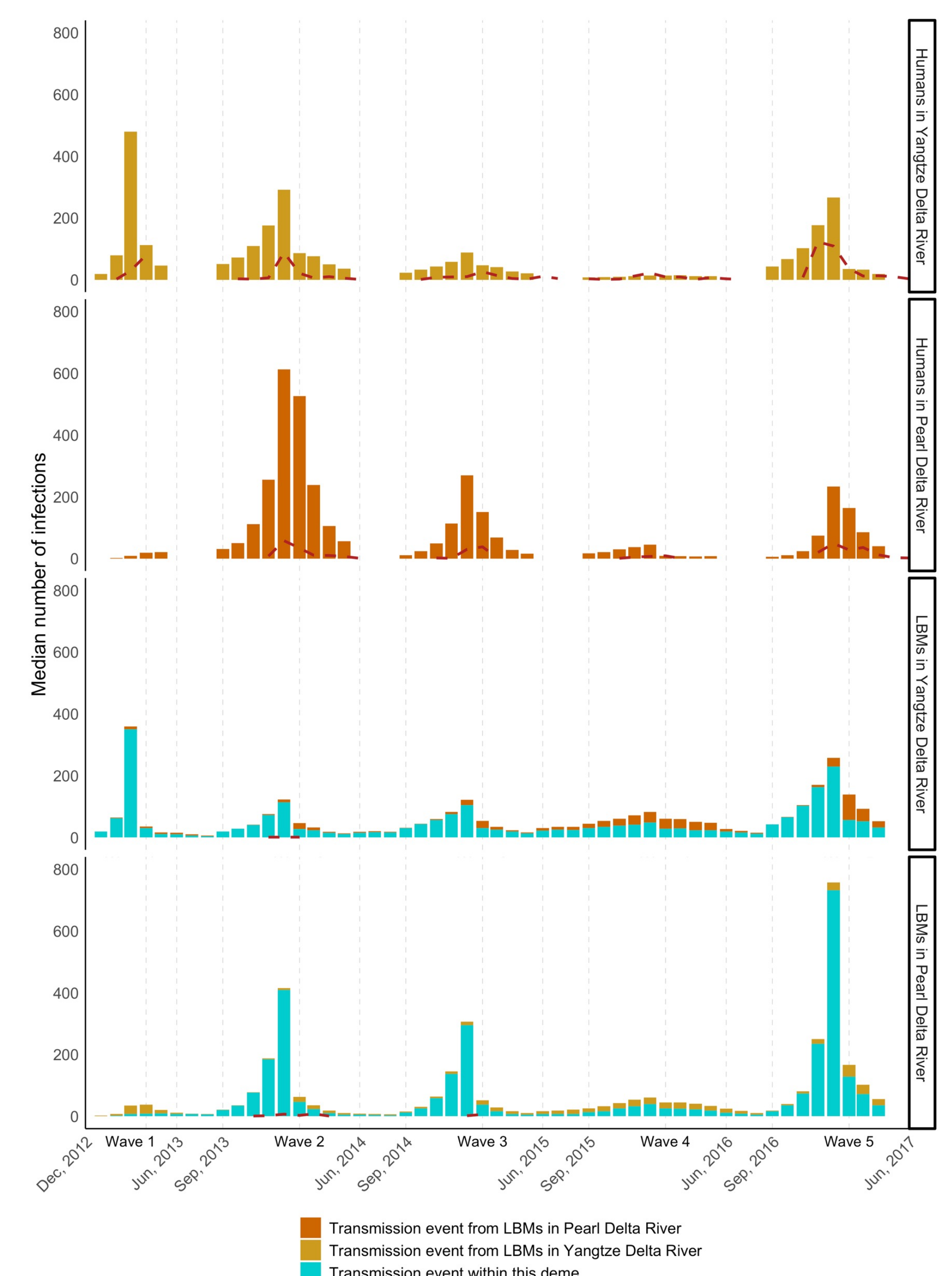
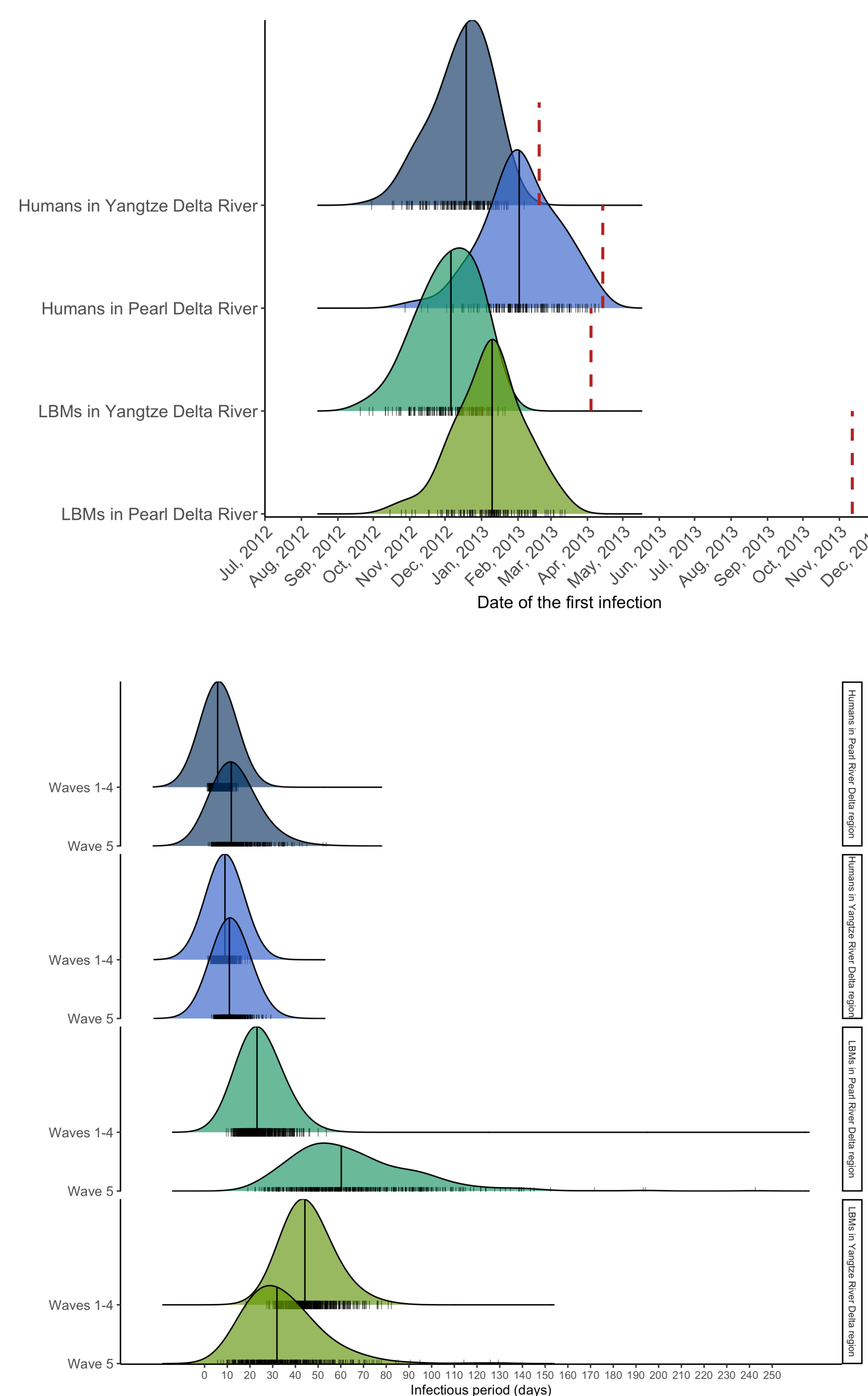
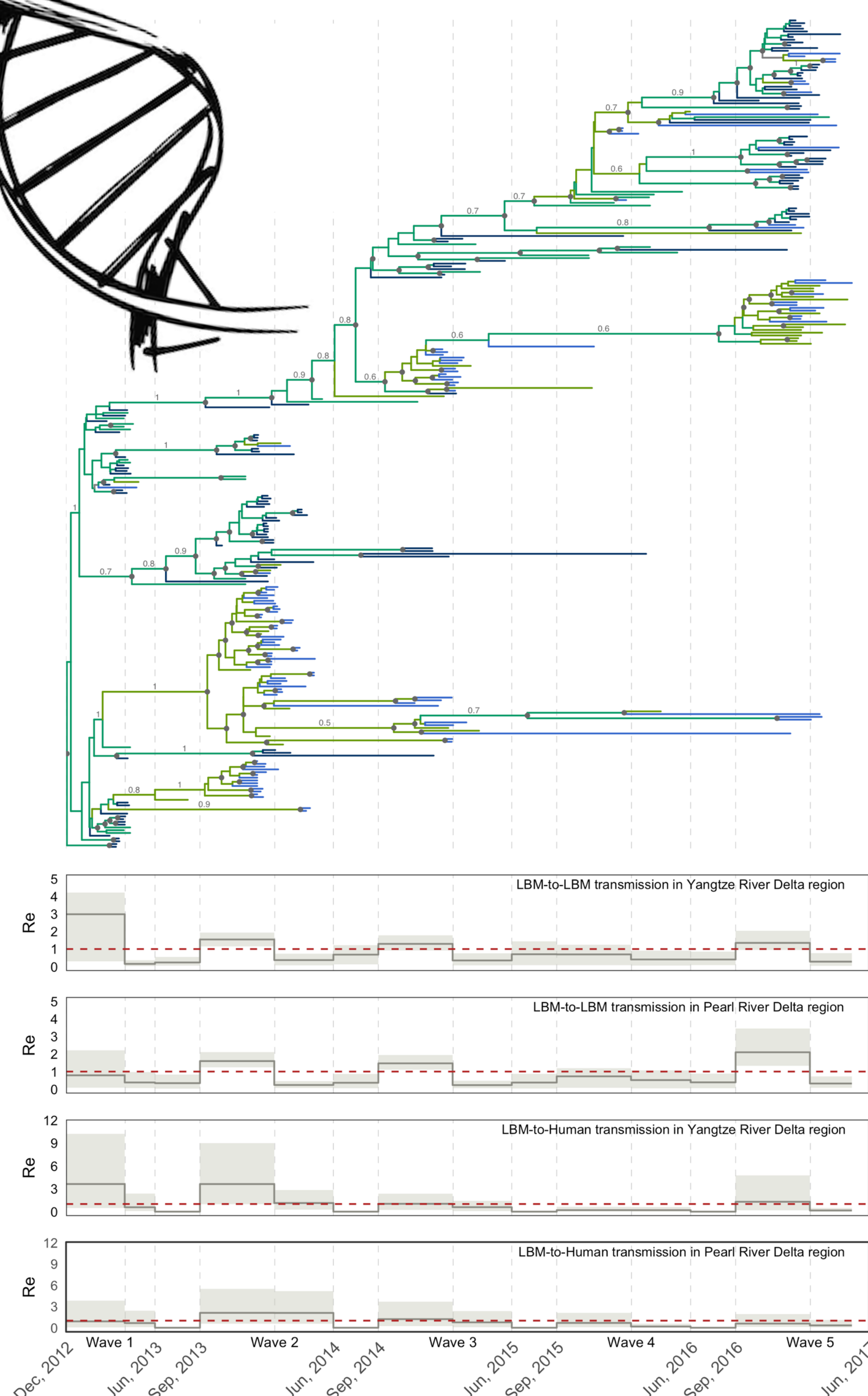
- 238 and 62 **sequences of H7N9** from infected poultry at LBMs and humans in Yangtze and Pearl River Delta regions between February 2013 to April 2017
- BDMM-Prime package** for BEAST v2.6.3
- Inference of epidemiological and clinical parameters using **multi-type birth-death model**, relaxed molecular clock model, HKY+G4 nucleotide substitution model
- Demes defined according to **host and location** of sequences
- Model **extension** with inference of incidence trajectories



BEAST2

Insights into H7N9 transmission dynamics

- H7N9 circulated **concurrently** in Yangtze and Pearl R.D. regions
- Regional structure** for H7N9 spread among LBMs
- H7N9 circulated in humans and LBMs **before being detected**
- High number of **under-reported** infections, particularly in LBMs
- Differences in transmissibility between LP and HP H7N9



Impact for public and animal health

- ✓ **First estimates** of H7N9 transmission at LBM level to improve future surveillance efforts
- ✓ Phylodynamics: key for **understanding** and **responding** to emerging infectious diseases
- ✓ Findings **inform response efforts** to protect animal and public health

