Modelling HPAI within-farm transmission using viral load distributions, to evaluate biosecurity effectiveness and to support management policies

Sophie Planchand[1], Timothée Vergne[1], Sébastien Lambert[1]

[1]UMR IHAP, ENVT INRAE, Université de Toulouse, Toulouse, France

sophie.planchand@envt.fr

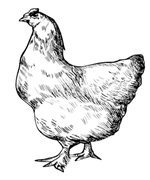
DVM, MSc

1st year PhD student

Background

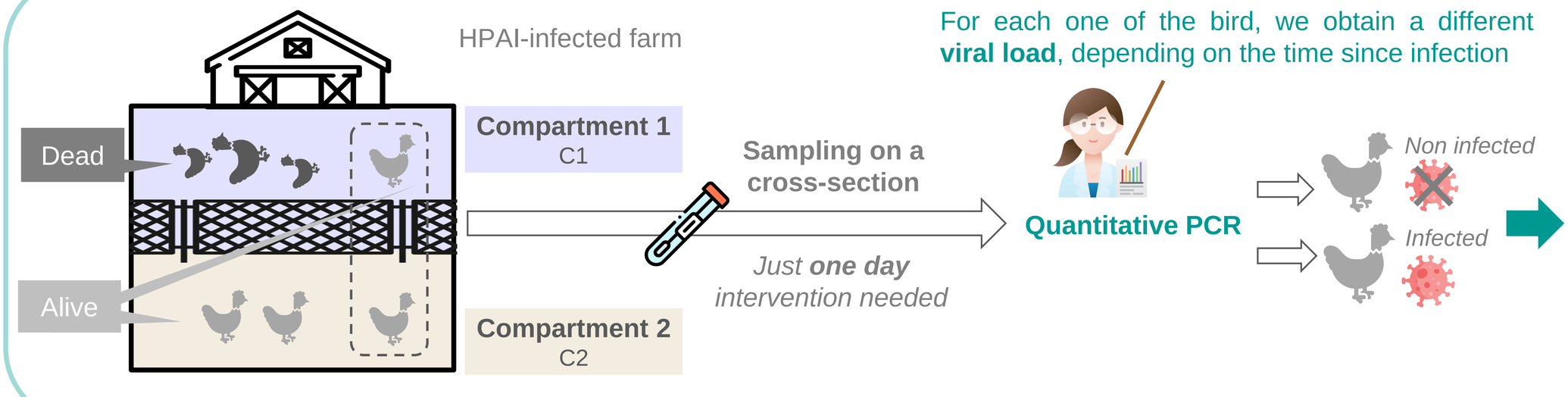
- Managing a HPAI epidemics = **race against time: high and rapid lethality** *(up to 90-100%, often within 48 hours)*
- **HPAI models:** based on **daily mortality,** which is often a **missing value**
- **Biosecurity:** a method of choice to slow down viral spread, but **effectiveness of within-farm measures** (e.g., compartmentalization) is **underdocumented**

Research questions



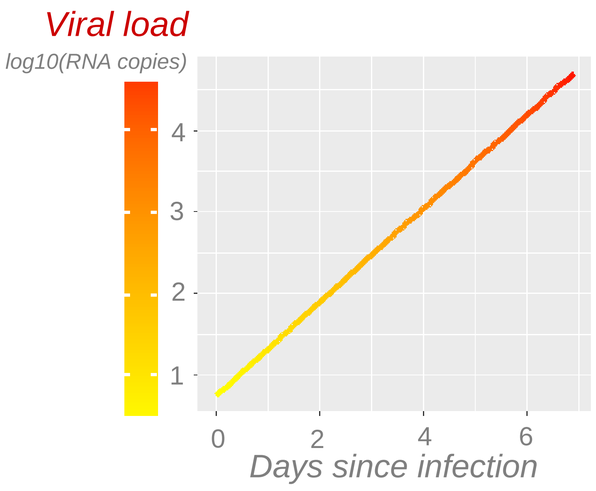
1. How to develop a **HPAI model,** estimating the **day of** introduction of the virus and its within-farm dynamics, using an **innovative** approach : **cross-sectional viral load distribution**[1] ?
2. Is within-houses **compartmentalization efficient to limit viral spread** ?

Data we need

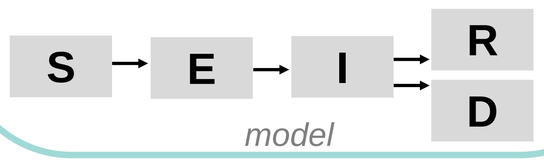


Models we need

The **individual** evolution of the **viral load** over **the time since infection**[2]



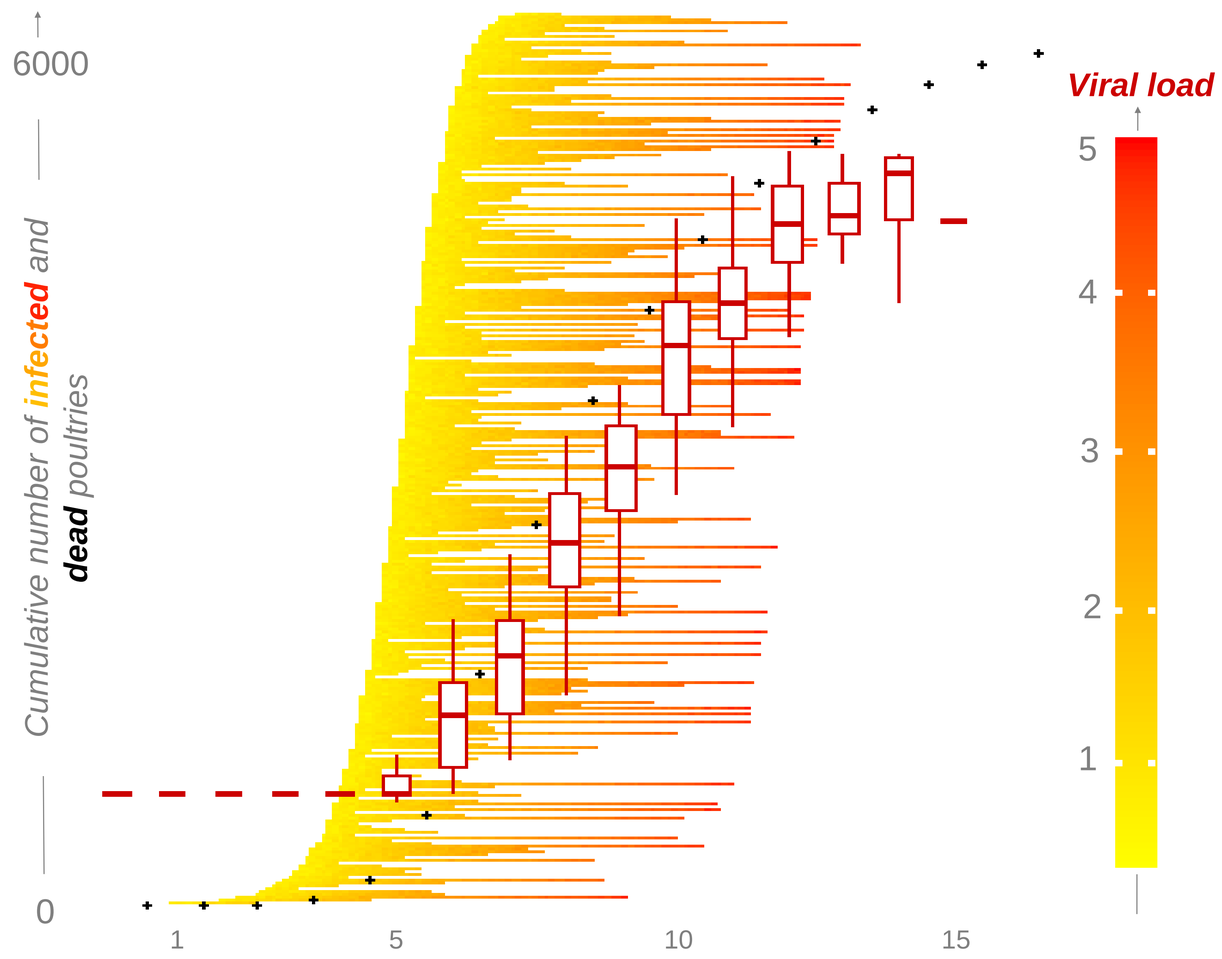
The **number of infected poultries** since the introduction of the virus in the farm



model

Expected results

Each **boxplot: simulated** cross-sectional viral load **distribution**



Comparison with the observations

Estimation of :

- → **Date of the first infection** in the farm
- → Viral **dynamics within** the farm
- → Viral **diffusion between compartments**

C1 ⇆ C2

Expected impacts

✓ Identifying **risk factors**, and directing **epidemiologic investigations**

✓ Estimation of the within-houses **compartmentalization effectiveness**

→ **Supporting management policies**

Perspectives

Using this method to test the effectiveness of different surveillance methods, in a context of **avian influenza vaccination**

[1] Hay *et al.*, 2021, Science [2] Bessière *et al.*, 2021, Journal of Virology