Rift Valley fever virus hosts are not equal

Modelling infectiousness at the individual level

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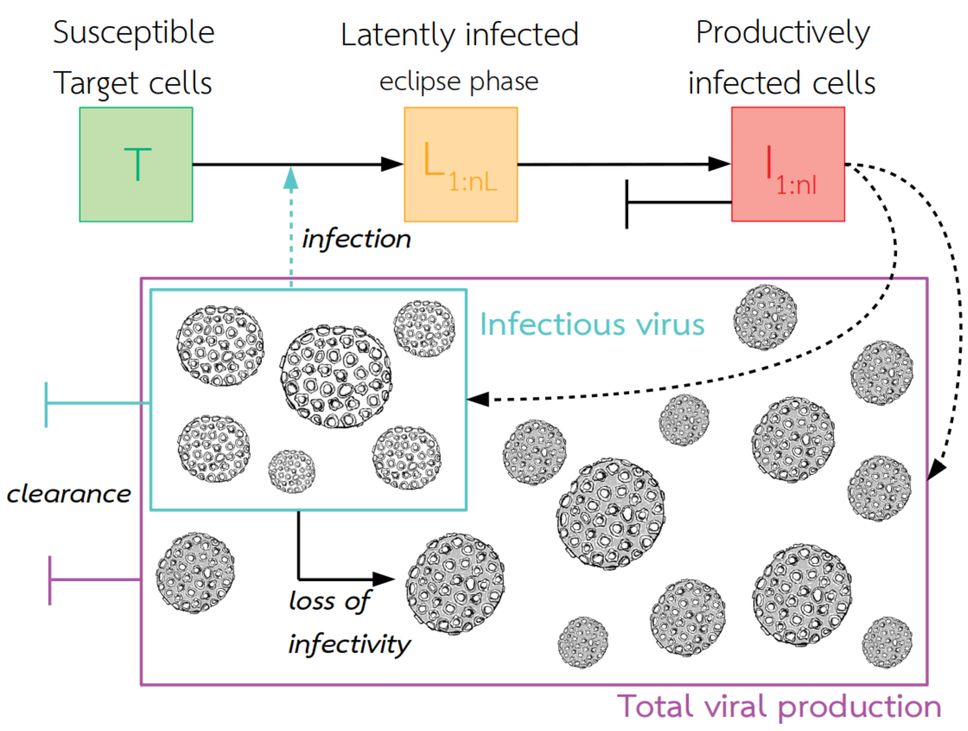
I - Context

- Rift Valley fever virus (RVFV) is vector-borne and zoonotic
- RVFV affects sheep, goats, cattle, and humans
- The main mosquito genera involved in RVFV transmission are Aedes and Culex
- We suspect livestock species do not play an equal part in onward transmission
- At the population level, vector feeding preferences, husbandry and trading practices might induce different contributions

Goal: investigate whether some livestock species are more infectious than others, possibly due to different viral load dynamics and associated probabilities to infect mosquitoes

II - Within-host model

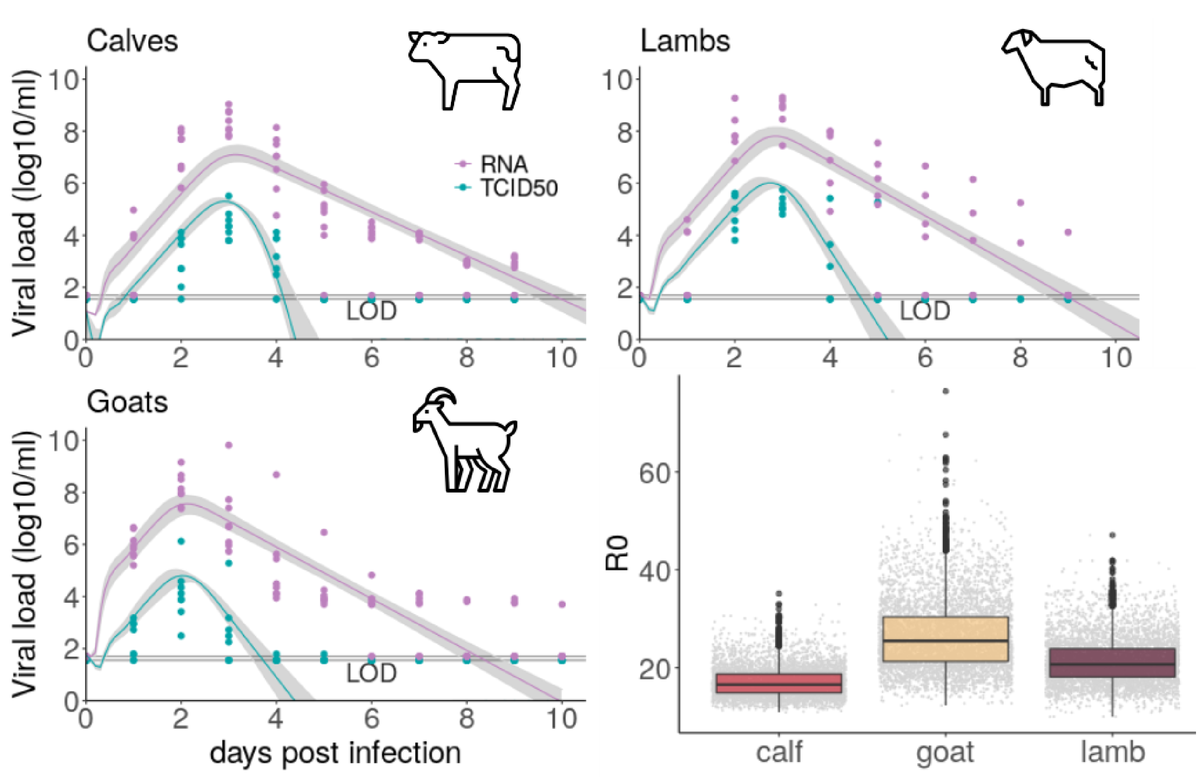


III - Infection of livestock hosts

Data : total viral loads (RNA measured by RT-qPCR) and infectious titers (measured by $TCID_{50}$) in plasma following laboratory infection by RVFV
Infected hosts : calves, young goats, and lambs

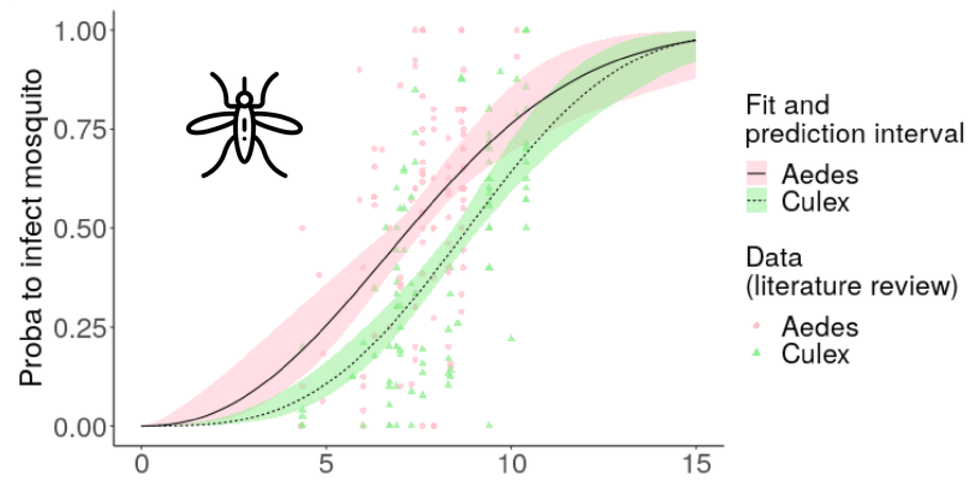
→ **Within-host model fitted to data using Metropolis Hastings MCMC**

IV - Infection features

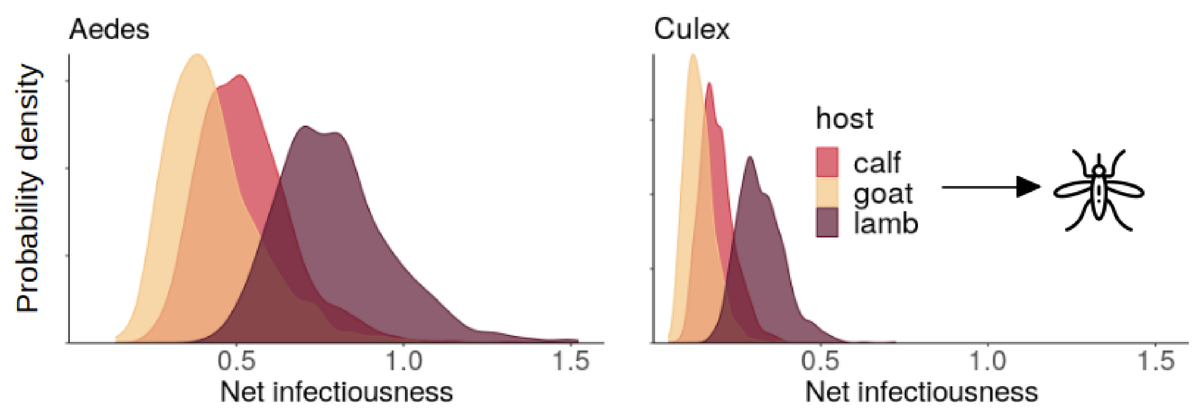


LOD : limit of detection
R_0 : average number of cells getting infected following the introduction of a single infected cell into a population composed entirely of susceptible cells

V - Probability to infect mosquitoes



VI - Infectiousness



Net infectiousness : extent of infectiousness of an individual over the entire course of their infection

VII - Take-home messages

- For similar infectious titers, there's a **higher probability to pass RVFV on to Aedes than to Culex mosquitoes**
- **Lambs have the highest infectiousness to mosquitoes**, due to higher peak viremia and a longer infection

→ **Perspective : How does this impact transmission at the population level?**

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