

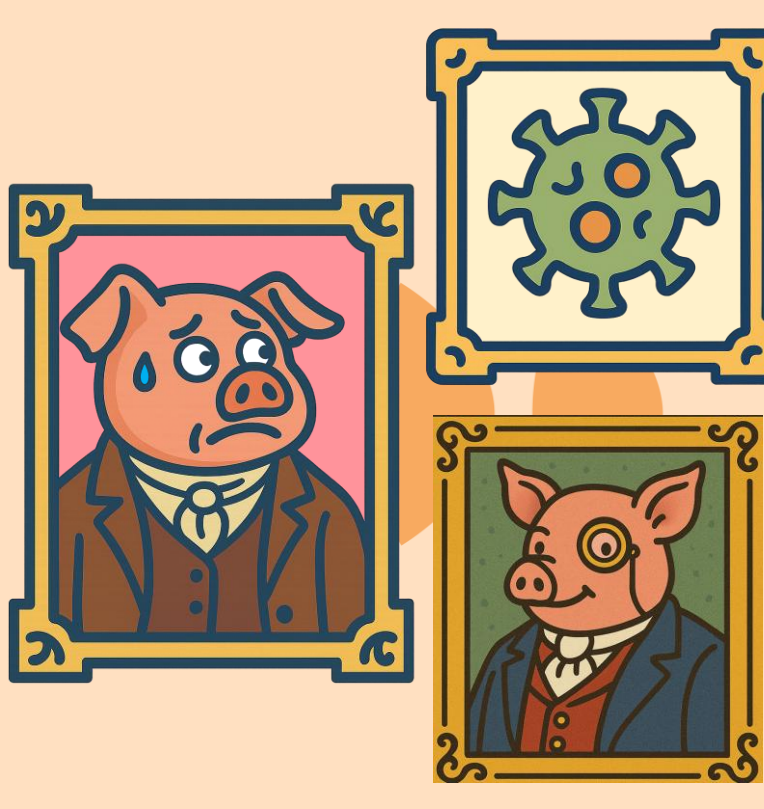
The *Porcine Reproductive and Respiratory Syndrome* virus transmission parameters: A systematic review and a deterministic MSEIR-type modelling

Salma Ettahri^{1,2}, Morgane Salines², Sébastien Picault¹, Mathieu Andraud²

1: Oniris, INRAE, BIOEPAR, 44300 Nantes, France

2: Anses, Laboratory of Ploufragan-Plouzané-Niort, EpiSabe, 22400 Ploufragan, France

Context



Protagonist

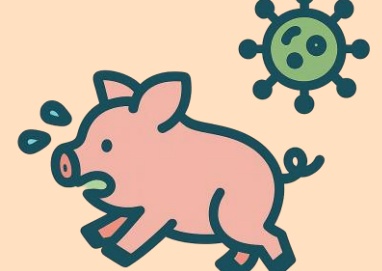
The *Porcine Reproductive and Respiratory Syndrome (PRRS)* is a swine disease

Genotype 1
Endemic and mainly present in Europe

Genotype 2
Endemic and mainly present in North America and Asia


Main symptoms

Immune dysregulation




risk of co-infections

Respiratory issues



Reproductive failure



fertility, risk of abortions and stillborn

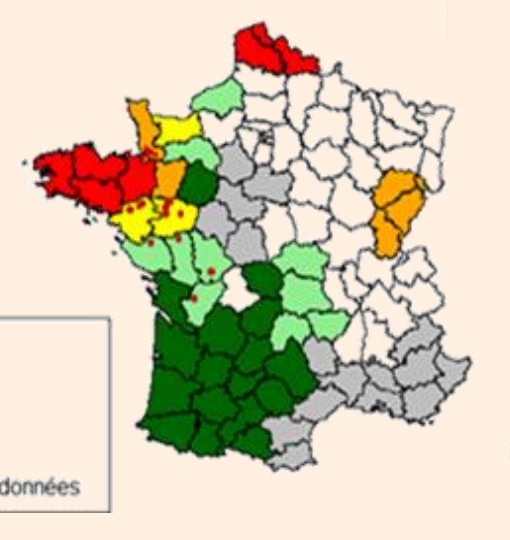
Scientific challenge

Literature reviews on this disease remain scarce, particularly those focusing on the European strain of the virus.

Economic challenge

Porcine Reproductive and Respiratory Syndrome is considered the most costly disease affecting the swine industry worldwide. In the United States, it is estimated to cause approximately \$664 million in annual losses (Holtkamp et al., 2013).

Health challenge



In France, more than 50% of herds are infected with PRRSV (Rose et al., 2015). PRRSV exhibits a high mutation rate and modulates the host immune response (Eclercy, 2020).

Objective

- ✓ To synthesize current data on PRRSV-1 transmission parameters and model the within-herd infection dynamics of a finisher batch in a conventional system, accounting for the different infection sources.

Goal: better understand PRRSV spread within herds and build a reference database of transmission parameters.

Literature review

Literature review of studies estimating PRRSV transmission parameters, based on the following search query:

(Porcine Reproductive and Respiratory Syndrome) AND (parameter OR model)

Identification of studies using PRISMA guidelines

Records identified from:

- Pubmed database (n=1393)
- Scopus database (n=1495)
- Given by experts (n=6)
- Citation search (n=9)

Records removed before screening:

- Duplicate records removed (n=867)
- Records marked as ineligible by automation tools (n=5)

Records screened on title, abstract and full text. Then, assessed for eligibility (n=1966)

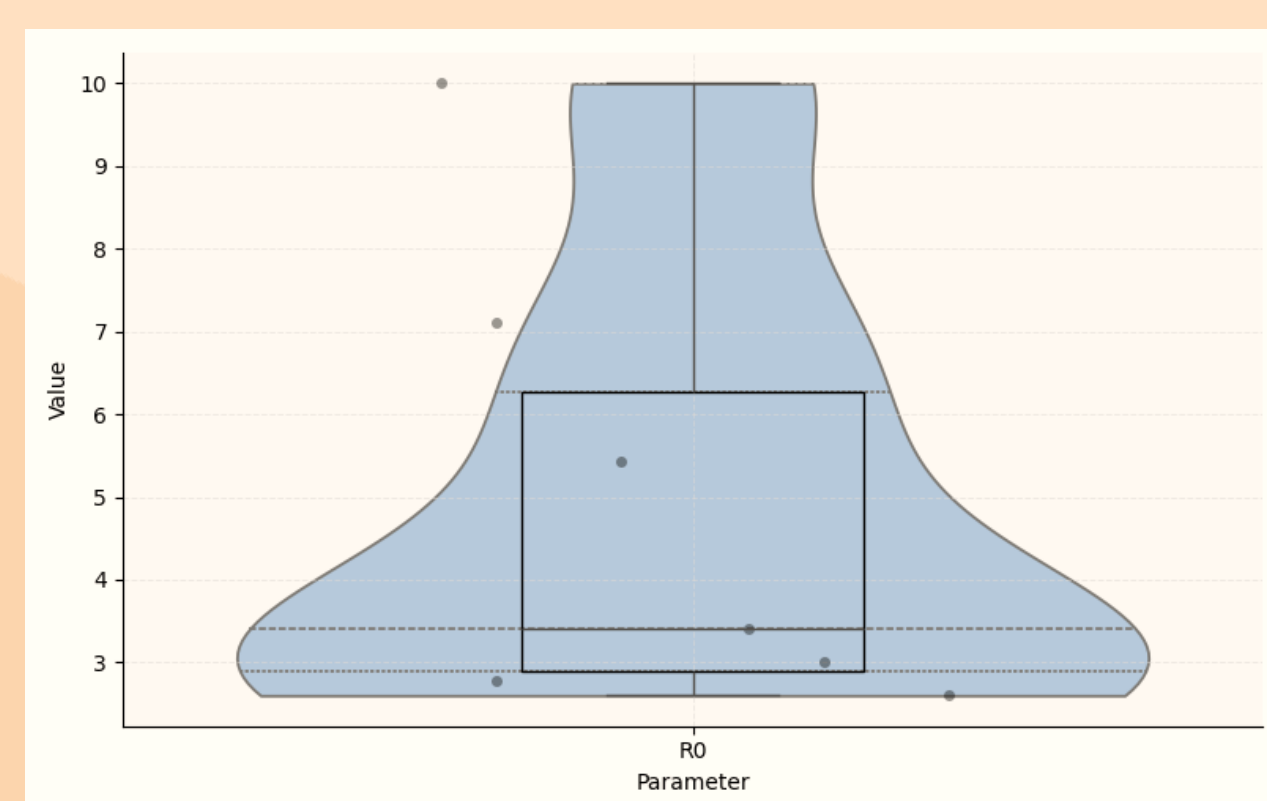
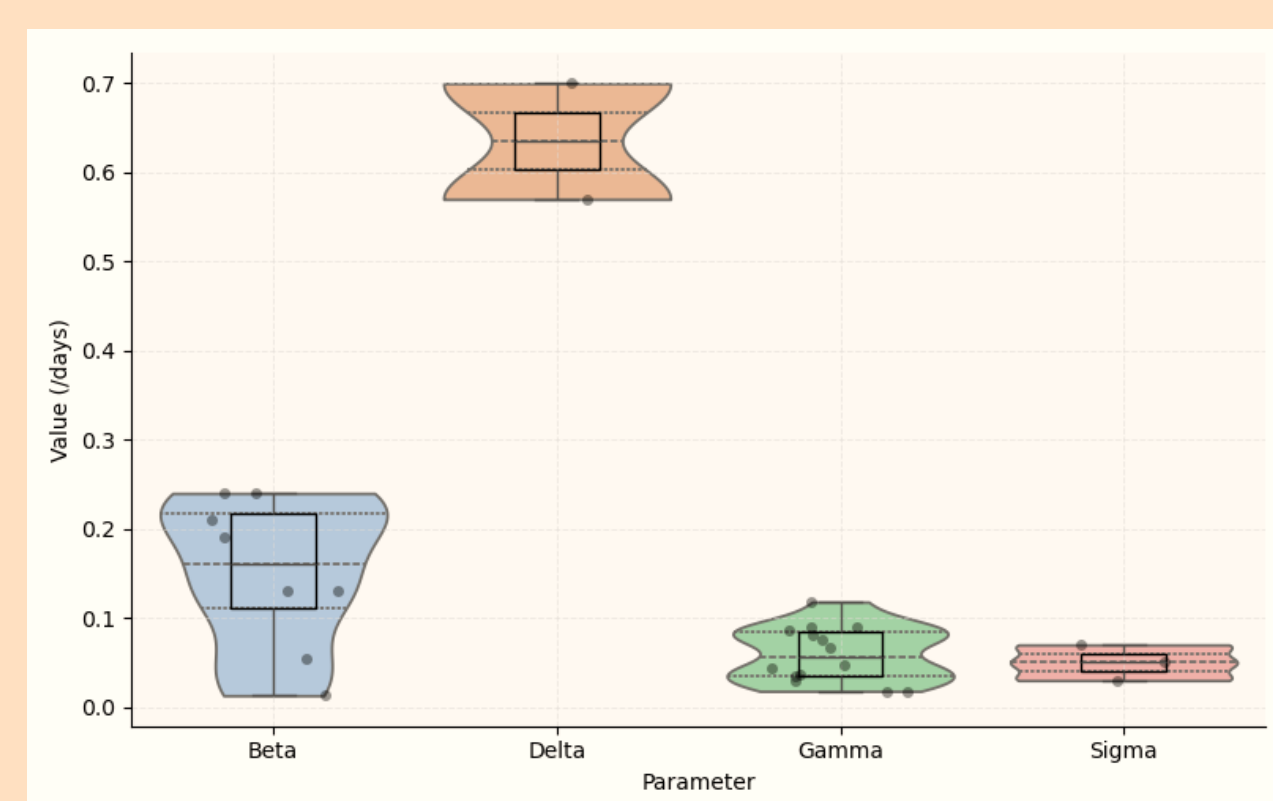
Records excluded:

- Virology or genomic study
- Not genotype 1 viral strain
- Transmission between herds
- No data on PRRSV alone

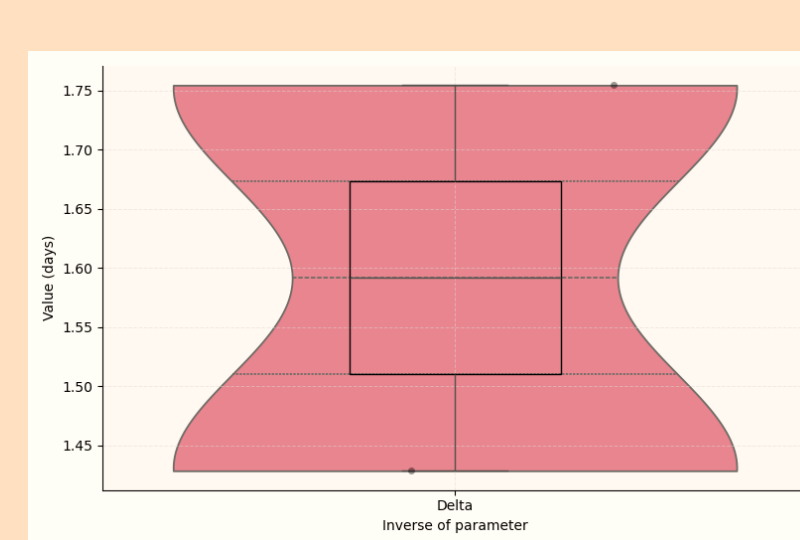
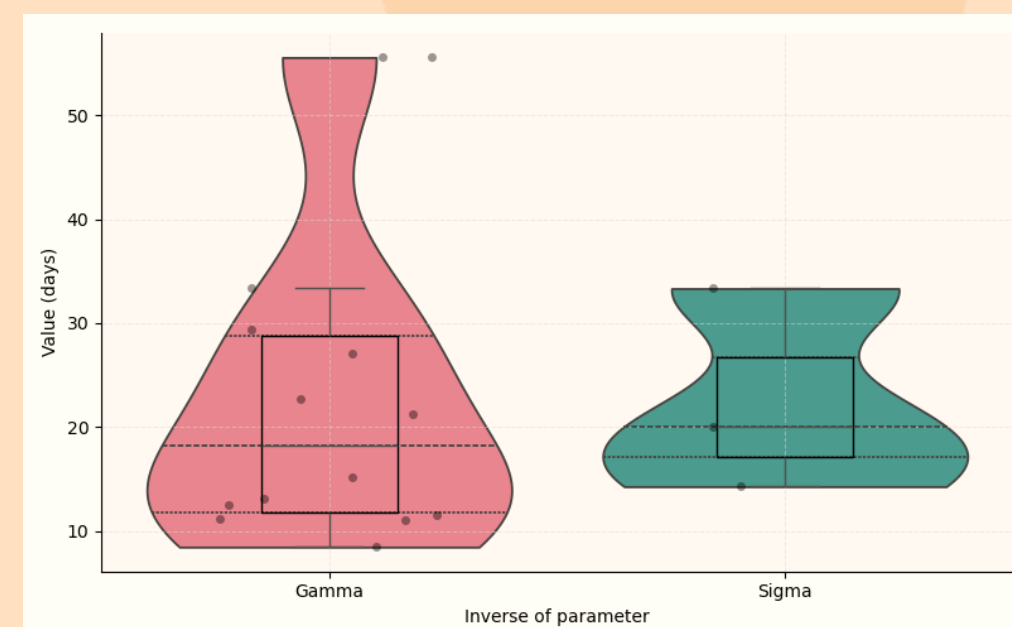
Total studies included in review (n=14)

Results and data distribution

We present a summary of our results for the transmission rate (β), recovery rate (γ), latency rate (δ), maternal antibody decay rate (σ) and basic reproduction ratio R_0 in unvaccinated swine..



Those last figures illustrate the duration of the infectious and latency periods, as well as the average persistence of maternal antibodies

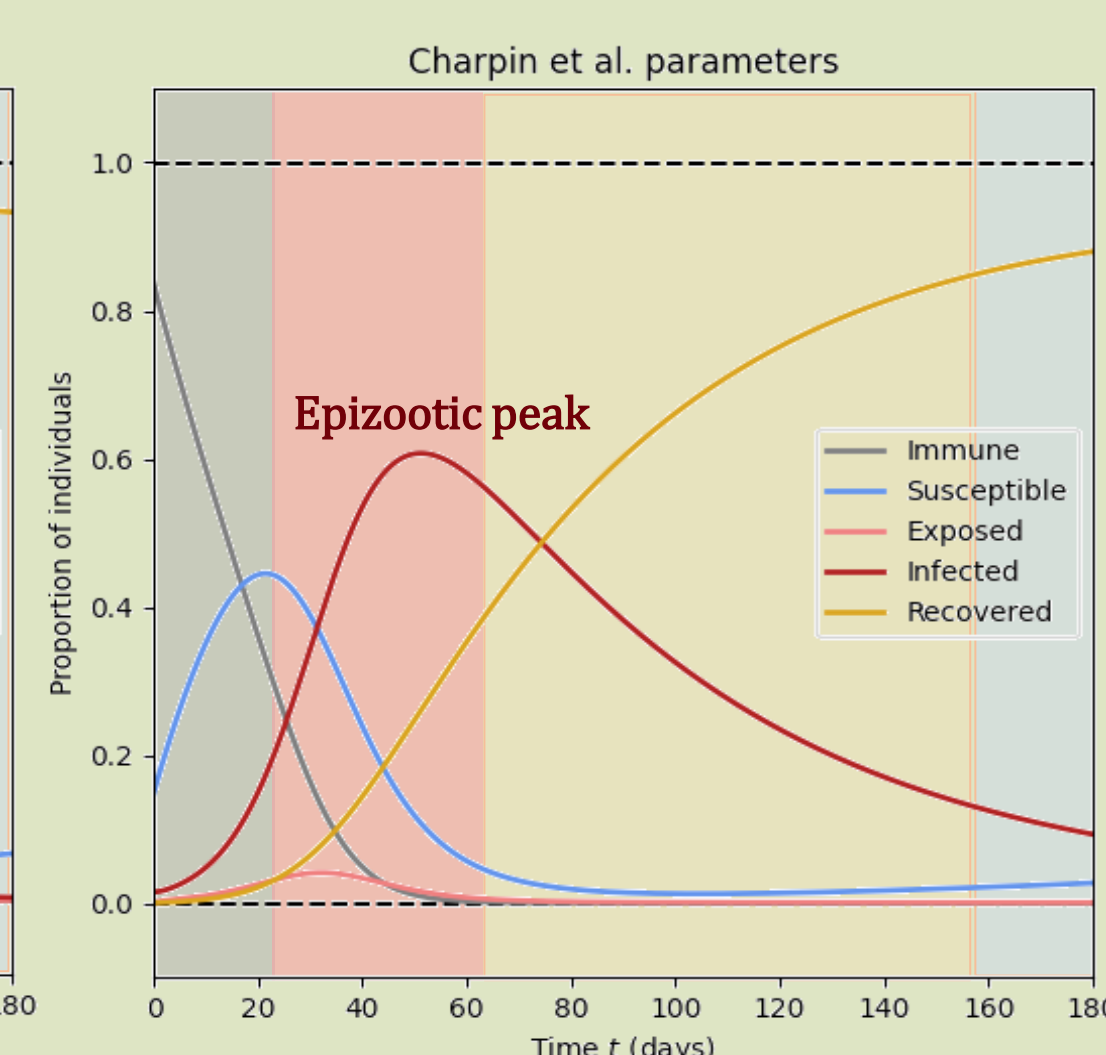
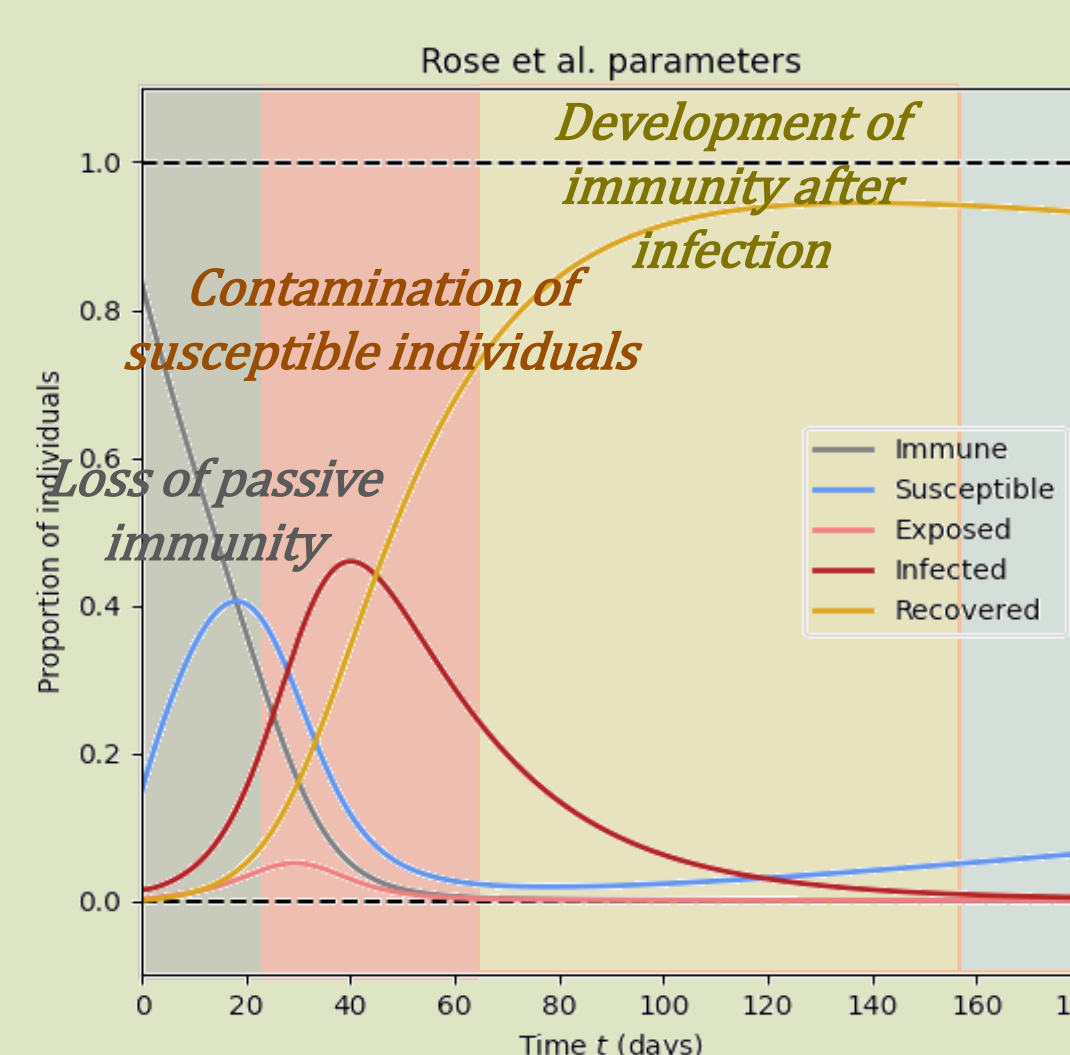
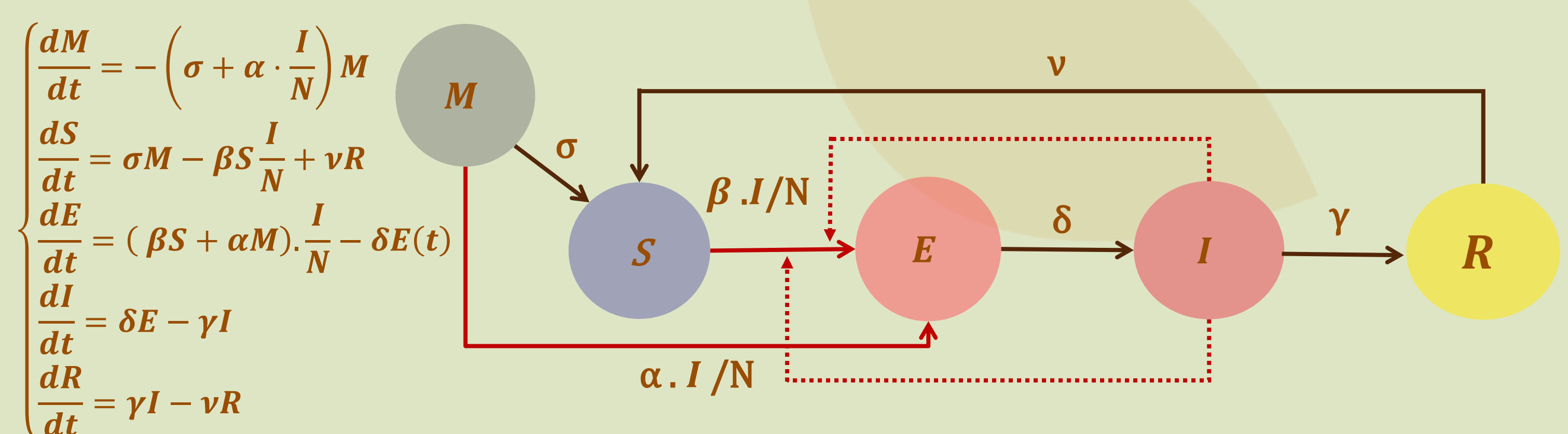


Deterministic MSEIR model

A deterministic MSEIR model was used to describe the infection dynamics of PRRSV within a batch of finisher pigs.

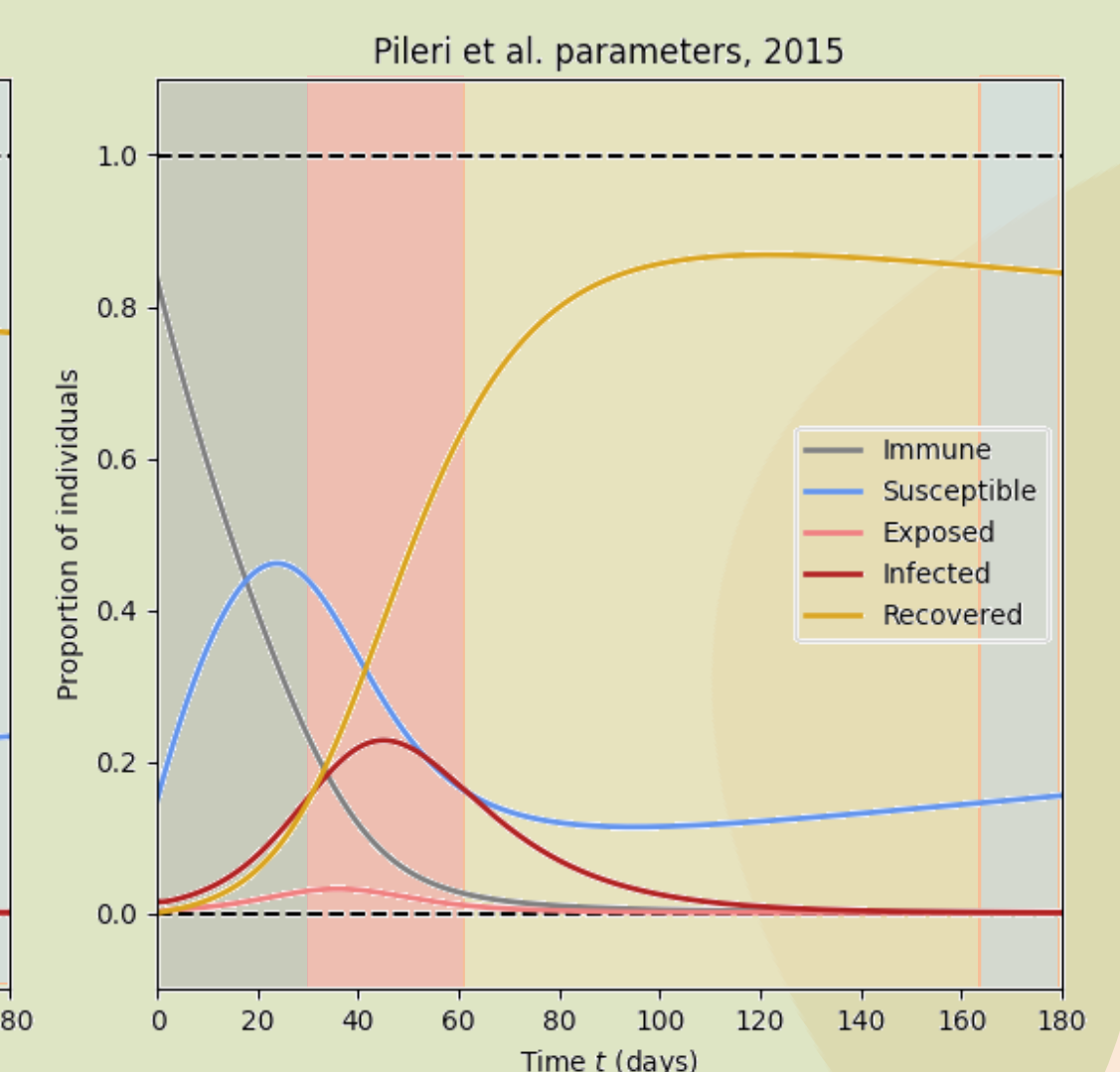
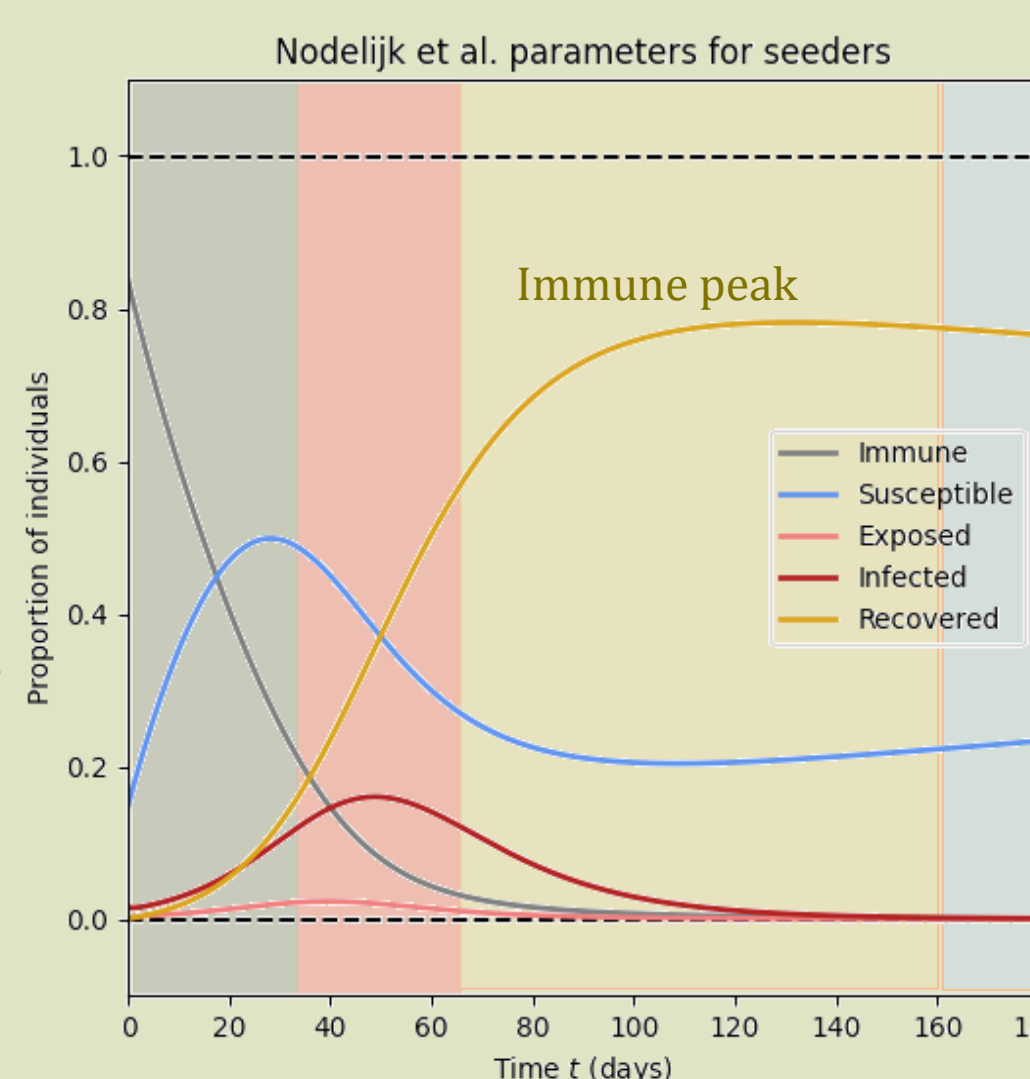
The model includes re-susceptibility but excludes demographic processes (births or deaths). The simulation spans from birth (day 0) to slaughter (day 180), assuming an initial group of vertically infected piglets (I_0).

Flow diagram, equation and figures



In these visual representations, each figure is divided into areas representing the spreading dynamics within the batch, with colors corresponding to the different compartments of the MSEIR model.

From these dynamics, we observe that the Rose and Charpin studies assumed a much higher proportion of infectious individuals than Nodelijk's study. This difference may reflect the study designs: Nodelijk conducted a 6-year longitudinal study on sows, whereas Rose was based on an experimental setup.



Discussion and Perspectives

- Available data on PRRSV transmission remain scarce and highly variable across studies. These discrepancies do not appear to be related to housing type (experimental vs conventional) or to the estimation method used.
- These findings underline the importance of considering herd structure and individual variability when modeling PRRSV transmission. Deterministic approaches provide a useful first approximation, but more complex models integrating within-herd structure and stochasticity are needed to better capture the true infection dynamics.

To be continued...