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Exploring the impact of B cell responses on influenza virus epidemiology in pigs - A rule-based simulation model

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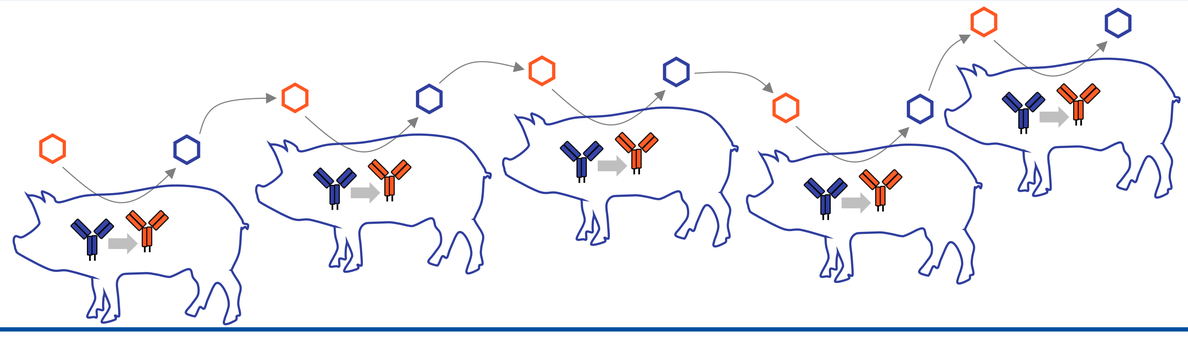
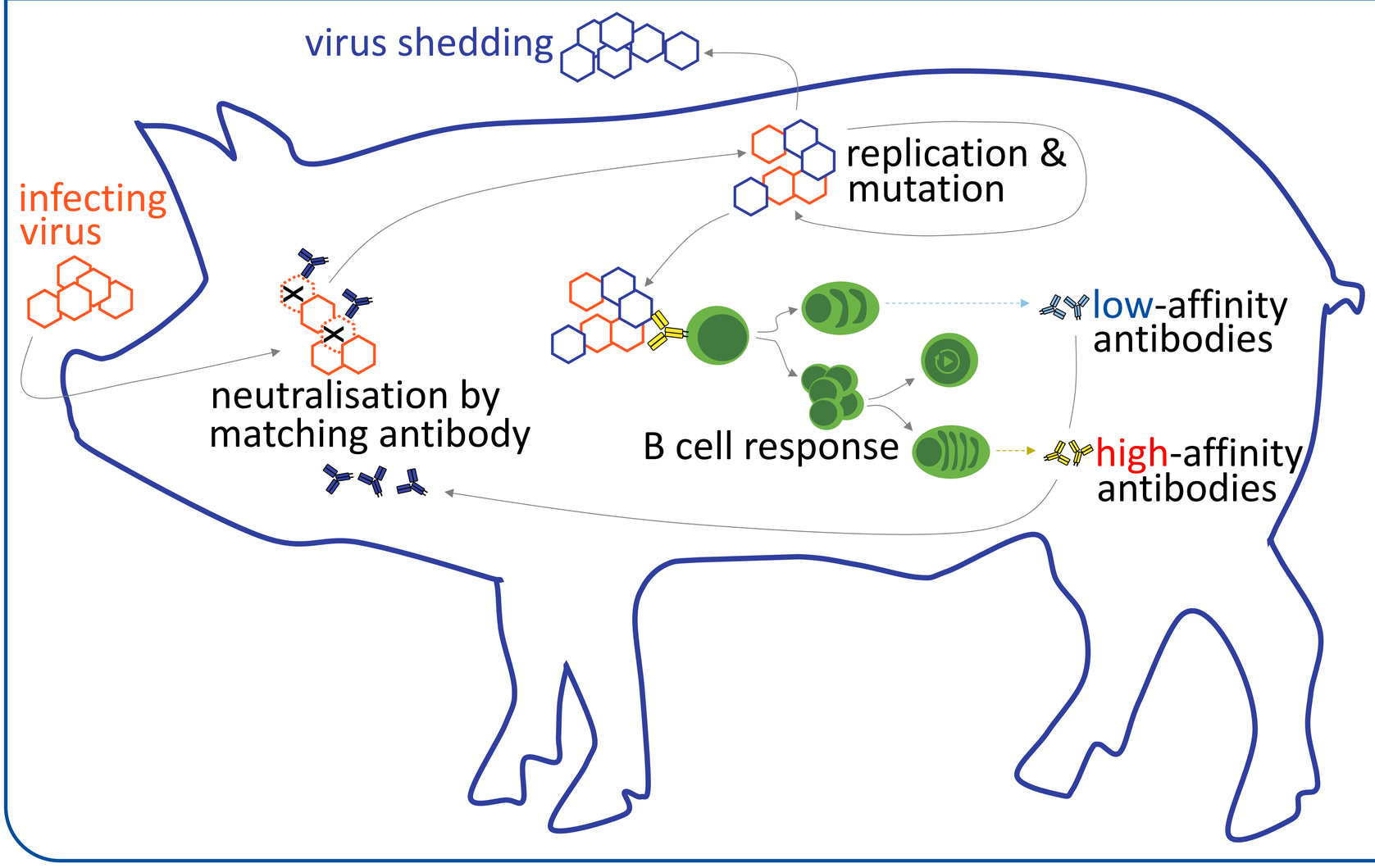
1. Aim

The aim of this project is the development of a computer simulation model that allows us to explore how changes in individual B cells responses could influence viral disease epidemiology and host pathogen co-evolution on a population level.



2. Materials and Methods



An intra-host part of the model simulates viral infection and B cell responses in individual pigs. Influenza virus HA1 protein sequences were used to model the infection, antibody-mediated virus neutralisation through sequence alignments, viral replication and different types of B cell responses. The model explicitly records emerging viral sequences and the development of a B cell receptor repertoire.
Several intra-host models are then linked to describe viral transmission chains between multiple pigs. The model is currently implemented in R.

3. Results

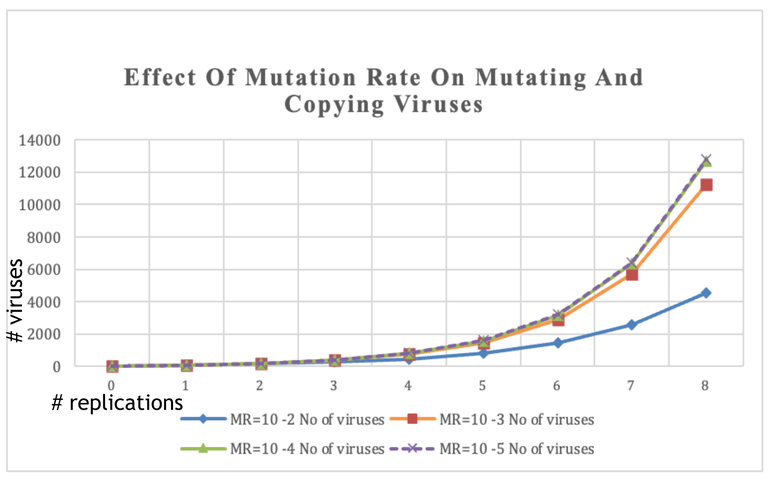


Fig. 1: Effect of viral mutation rate on simulated viral load

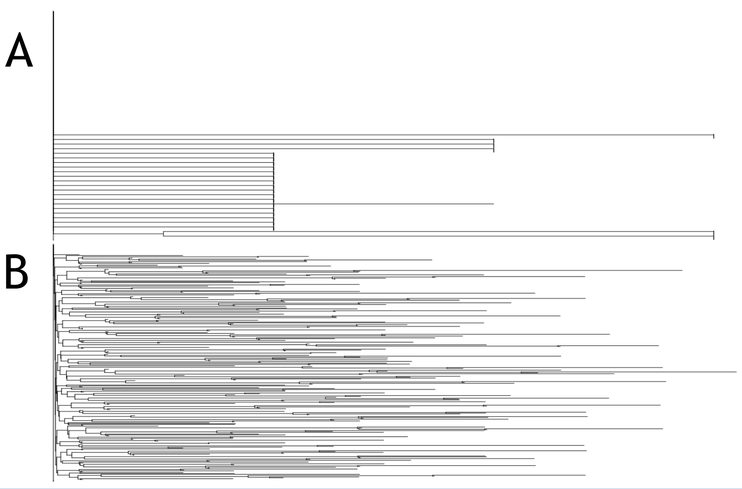


Fig. 2: Viral sequence diversity in the model with low (A) and high (B) mutation rate.

4. Conclusions

- This work helps to provide fundamental insights into the role of B cell development for the sustainable health of populations exposed to threats by highly variable pathogens, such as influenza viruses.
- Further development of the model is needed, particularly to manage viral and antibody sequences generated during the modelling process.

EUP AH&W European Partnership on Animal Health and Welfare

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