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# EXPLORATION OF THE MACROPHAGE – VIRUS INTERACTIONS

# DURING PRRSV INFECTION BY A MODELLING APPROACH

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### Introduction

The Porcine Respiratory and Reproductive Syndrome Virus (PRRSV) responsible for reproductive failures and production losses is a major concern for swine industry. To improve the efficiency of control measures, one challenge is the identification of the immune mechanisms allowing to reduce the infection severity and duration. Several studies discuss the influence of the immune functions of the target cells (macrophages), the role of the cytotoxic cells involving a key anti-viral cytokine (IFN $_{\gamma}$ ) and the humoral response involving a key immuno-modulatory cytokine (IL<sub>10</sub>). The high between-host variability and the heterogeneity of viral strains in the field increase the uncertainties. To unravel these limits, we proposed here a modelling approach.

**Aims : (i)** Provide a detailed representation of the immune and infection dynamics in the infection place, the lung.

(ii) Estimate the model parameters resulting in simulations covering the response variability.

### (iii) Identify the immune mechanisms determining the infection duration in various scenarios of virulence and susceptibility.

## Modelling Approach



**Macrophages** : susceptible macrophages M<sub>s</sub> activation by virus

**Natural killers :** NK destroy the infected cells.





0 50 100 150 200 time [d] FIGURE a.	<b>Conclusions</b> 2 parameter ranges generating contrasted vi- ral dynamics (short duration & high peak vs long duration & low peak) associated with realistic immune dynamics (re- sults not shown).		S1, S2 SA, SB S1B, S2A	+  -	 ++ +- + +	+ + ++ + ++ ++ ++ +++ -	$\Rightarrow$ Take into account the variability between hosts and strains to im- prove the control measures.
	Perspectives						
<b>Model extension</b> to represent the dynamics not only in the lung but in whole pig $\Rightarrow$ integration of dendritic cells and more detailed representation of the adaptive response. Use of the model to : (i) Test the efficiency of <b>individual control measures</b> such as vaccination and propose directions to better control the infection (ii) Identify the key immune mechanisms that drive the infection resolution, to integrate them in an <b>immuno-epidemiological model at the population scale</b> .							



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