

# A Transport & Lairage model for Salmonella transmission in pigs for individual EU Member States

A. A. Hill<sup>1</sup>

R. R. L. Simons<sup>1\*</sup>, A. Swart<sup>2</sup>, E. L. Snary<sup>1</sup>

<sup>1</sup> Veterinary Laboratories Agency, Woodham Lane, New Haw, Surrey, UK

<sup>2</sup> National Institute for Public Health and the Environment (RIVM), Bilthoven, The Netherlands.

\* Veterinary Laboratories Agency, Woodham Lane, New Haw, Surrey, UK

e-mail: r.simons@vla.defra.gsi.gov.uk

fax: +44(0) 1932 357445

## Abstract

A model for the transmission of salmonella in finisher pigs during the transport and lairage stages of the farm-to-consumption chain has been developed, specifically designed with the aim of modelling potentially important risk factors and interventions. As such, the model includes factors such as environmental contamination and the effect of stress. The model forms part of a Quantitative Microbiological Risk Assessment, funded by EFSA as part of the evidence base for the development of National Control Plans for control of Salmonella in pigs, to support the scientific opinion requested by the EC and adopted by the EFSA BIOHAZ Panel. This poster describes the modelling methodology and demonstrates the parameterisation of the model for two case-study member states (MSs). For both MSs, the model predicts a small increase in the average lymph node positive batch prevalence during both transport and lairage. While the average change in prevalence over all batches is small, closer analysis shows that there is wide variation in the change in prevalence in individual batches, with some batches showing an increase of up to 70%. Sensitivity analysis (variation inherent in the baseline model) of the model suggests that stress is the most important factor during transport, while a number of parameters including the rate of carryover between batches of pigs and one of the dose-response parameters are important during lairage. This model suggests that the transport and lairage stages of the farm-to-consumption chain can have a large effect on an individual level, potentially being the cause of a large increase in the prevalence within a batch of pigs and also providing an opportunity for previously uninfected batches of pigs to become infected. However, large individual changes at a batch level are infrequent enough to not cause a similarly large change in the average national prevalence between farm and the point of slaughter.