

P11

Development of a quantitative PCR method coupled with PMA to quantify viable *Salmonella* spp. cells in the pork supply chain

Jeuge S.¹, Denis M.², Niveau F.¹, Houdayer C.², Boix E.¹, Souchaud F.², Frémaux B.¹

¹IFIP, Maisons-Alfort, France, ²Anses - Laboratoire de Ploufragan, Ploufragan, France

In 2017, *Salmonella* spp. was implied in 30% of foodborne diseases in France (SPF, 2019). Few data on the contamination levels of *Salmonella* spp. are available along the pork supply chain. The protocol of the standard method (ISO/TS 6579-2:2012) is time-consuming and culture-based methods using chromogenic media are less efficient for matrices with high levels of background flora, and for recovering stressed cells. Along the food chain, the cells may be impacted by various stresses (e.g. chemical or thermal), which may lead to physiological changes and the emergence of viable but non-culturable cells (VBNCs).

This study aims to develop a protocol for the quantification of viable *Salmonella* spp. cells from pork carcasses and faeces based on a quantitative TaqMan® PCR (qPCR) method combined with propidium monoazide (PMA) treatment to exclude DNA from dead cells. Performances of the PMA-qPCR method were assayed using different ratios of viable (including heat-stressed cells) and non-viable (heat-inactivated) *Salmonella* cells from pure culture in nutrient broth, and artificially contaminated samples of faeces and pork back fat. Different PMA concentrations and light exposure conditions were tested. For each sample analysis, the concentrations of total, viable and cultivable fractions of *Salmonella* cells were determined by using qPCR, PMA-qPCR and culture-dependent approaches (the standard miniaturized MPN for faeces or chromogenic *Salmonella* plating media for pork back fat), respectively.

The PMA-qPCR reaction developed in the present study exhibited a 100% inclusivity and exclusivity for *Salmonella* spp. For both matrices, the PMA-qPCR allows a quantification of VBNC cells of *Salmonella* spp. even in the presence of dead cells. The limits of quantification of the PMA-qPCR set from artificially contaminated pork back fat and faeces were $1,6 \cdot 10^2$ genome copies/cm² and $5 \cdot 10^2$ genome copies/g, respectively. The PMA-qPCR method was effective to determine the impact of thermal stresses on the behaviour of *Salmonella* spp. cells in artificially contaminated samples of faeces (4°C) and pork back fat (60°C and 100°C). This method will be useful to identify farming practices related to

high/low level of *Salmonella* contamination in pigs. Quantitative data on carcasses and pork cuts are also of interest to qualify slaughtering procedures and their impact on the contamination of meat with *Salmonella* spp.. A development of the method on pork cuts is planned.