

Implantation of a strain of *Salmonella* Typhimurium and a strain of *Salmonella* Rissen in a pig herd with recurrent clinical salmonellosis

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Abstract

Clinical salmonellosis is rare, even though it can occur in pig herds. The aim of this study was to investigate the diversity of *Salmonella* strains isolated in a farrow-to-finish pig herd suffering from recurrent clinical salmonellosis from 2018-2022. Different areas were sampled, such as farrowing, post-weaning and fattening rooms (with animals or after cleaning and disinfecting), feeding systems, corridors, the entry room, and the loading platform. Only three serotypes were identified: *S. Typhimurium*, *S. Rissen* and *S. Livingstone*. Because *S. Livingstone* was identified only at the farrowing level, we performed epidemiological monitoring of only *S. Typhimurium* and *S. Rissen*. DNA profiles were determined by molecular pulsotyping. It revealed that the same *Xba*I DNA profile was identified over the five year period for each serotype followed. We assumed that both strains have colonized the herd through either live species (sows, rodents, humans) or the farm building, dust or equipment. To our knowledge, this is the first time that a molecular epidemiological investigation of *Salmonella* strains has been performed in a pig herd suffering from recurrent clinical salmonellosis.

Introduction

Salmonella is one of the most common bacterial pathogen worldwide in human and animal infections, leading to 52,702 cases of human gastroenteritis in Europe in 2020 (Efsa, 2021). In European pig herds, asymptomatic carriers are frequent despite robust prevalence data are difficult to obtain (Corrége & Minvielle, 2013). Epidemiological studies have shown that several serotypes could be detected from the same animal, or an identical batch, according to its physiological development or in the course of time.

Clinical salmonellosis are considered to be rare and short time events even if they can occur in pig herds (Beloeil, 2007). However, some pig herds are exposed to recurrent clinical salmonellosis with consecutive involvement of several batches or with regular occurrence of clinical episodes. The aim of this study was to investigate the diversity of *Salmonella* strains isolated in a farrow to finish pig herd suffering from recurrent clinical salmonellosis between 2018 and 2022.

Materials and Methods

In a farrow-to-finish pig herd suffering from recurrent clinical salmonellosis, sampling was performed between 2018 and 2022 in pig feces and by swabbing in different areas such as nursery, farrowing and fattening rooms, feeding systems, corridors or loading platforms before or after cleaning and disinfection procedures. *Salmonella* detection and strain serotyping was performed according to methods NF U47-102 and ANSES SEL LSA-INS-0413 respectively. Determination of the DNA profiles of the strains panel was performed using PGFE with the *Xba*I enzyme according to the standardized PulseNet Protocol (Ribot et al., 2006).

Results

Over a 40 strains panel, three serotypes were identified, *S. Typhimurium*, *S. Rissen* and *S. Livingstone*. *S. Livingstone* was only detected at the nursery level. Thus, we only performed

the epidemiological monitoring of both *S. Typhimurium* and *S. Rissen*. The table 1 represents the distribution of detected strains of serotypes *S. Typhimurium* and *S. Rissen* by year and by sampling site.

Sampling site	Sampling year				
	2018 N=7	2019 N=1	2020 N=9	2021 N=10	2022 N=10
Sanitary air lock				1 R*	
Nursery CD*				1 R	
Post-weaning with animals				1T, 1R	
Pig feces fattening	1 T*		3 T		
Fattening room - with animals - after CD - feeding system	2 T, 3 R 1 R	1 T	3 T, 3 R	1 T, 2 R 2 R 1 R	2 T, 1 R 3 T, 3 R
Loading platform					1 T

* R : Rissen, T : Typhimurium, CD : cleaned and desinfected

The DNA profiles were determined for 37 strains of *S. Typhimurium* (N= 18) and *S. Rissen* (N= 19) by pulsotyping. It revealed that the same *Xba*I DNA profile was identified over the five years period for each followed serotype.

Discussion and conclusion

Pulsotyping revealed that two strains of *S. Typhimurium* and *S. Rissen* have colonized the pig herd to the detriment of new strains of *Salmonella* and that the contamination cycle continues to be self-sustaining in the farm. Although our work was undertaken on a single pig herd, these results may appear in contradiction with previous data which showed that several serotypes could be isolated on the same animal (sow or pig), the same batch, according to its physiological development or in the course of time (Corrégé et al., 2002; Davies et al., 1998). We assumed that both strains have colonized the herd through either live species (sows, rodents, humans) or the farm building, dust or equipment. To our knowledge, this is the first time that a molecular epidemiological investigation of *Salmonella* strains is undergone in a pig herd suffering from recurrent clinical salmonellosis.

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