

Role of wild birds and environmental contamination in the epidemiology of *Salmonella* infection in an outdoor pig farm

Highlights

- *Salmonella* was isolated from a field left empty by pigs for more than 2 years.
- Wild birds and pigs had the same *Salmonella* serotypes and phage types.
- The close relatedness of a selection of monophasic *S. Typhimurium* and *S. Rissen* isolated from wild birds and pigs was confirmed using whole genome sequencing.
- Pigs are the likely to be the original source of *Salmonella* infection in wild birds.
- Wild birds are likely recycling and contributing to the persistence of *Salmonella*.

Introduction: In the European Union in 2015, 13% of the strong evidence foodborne outbreaks caused by *Salmonella* were attributable to the consumption of pork and pork products. *Salmonella* contamination of retail pork is directly linked to the prevalence on farm. The infection can be introduced into a pig herd by many routes, for example through the purchase of *Salmonella*-infected pigs, contaminated feed or other animals. Movements of pigs between premises at different life stages represent a risk because during transport pigs are subjected to stress. Furthermore, especially for outdoor and organic farms, wild fauna, synanthropic and domestic animals living on the farm can constitute a source of introduction and transmission of *Salmonella* through direct contact with pigs or indirectly through faecal contamination of feed, water troughs or farm equipment.

Aim of this study was to investigate the role of wild birds in the epidemiology of *Salmonella* in one outdoor pig farm.

Materials and methods: Three sampling visits were carried out at monthly intervals to an outdoor pig farm consisting of two adjacent fields, one left empty of pigs for more than 2 years (field A)

while the second was occupied by pigs during the first visit only (field B). Faeces from wild bird droppings, environmental samples and pig faeces were tested for the presence of *Salmonella*. *Salmonella* was isolated according to ISO6579 Annex D, and serotypes were determined according to the White-Kauffmann-Le Minor scheme. Phage typing and whole genome sequencing (WGS) were also carried out.

Results and Discussion: *Salmonella* spp. was isolated from environmental samples also in field A that had not been occupied by pigs more than 2 years. Interestingly, the wild bird population accessing the fields increased considerably once the pigs had left the farm and the proportion of *Salmonella* positive wild bird droppings increased over time with 7.4%, 15.8% and 44.3% at the first, second and third visit, respectively. The levels of *Salmonella* identified in some of the wild bird droppings were unusually high ($10^5 - 10^6$ CFU/g) suggesting that *Salmonella* was actively replicating in the gastrointestinal tract of these birds. Monophasic *Salmonella* Typhimurium DT193 was the predominant serotype isolated in pigs as well as in wild bird droppings and the environment suggesting that the pigs were the original source of infection, as this serovar is typically associated with pigs. The close relatedness among wild bird and pig *Salmonella* isolates, was also confirmed using WGS, supporting the hypothesis that pigs can act as a source of wild bird salmonellosis.

Significance of findings: This study suggests a possible cyclical dissemination of *Salmonella* between pigs and wild birds, and that wild birds are capable of contributing to the persistence of *Salmonella* between batches of pigs.

Adequate management practices to minimize the contact between pigs and wild birds (e.g. cover feed and water sources, use of nets) should be implemented in outdoor pig units.