Observations on the distribution of *Salmonella* on pig multiplier breeding farms

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Abstract

Centralisation of the structure of pig production in the UK has resulted in the development of large integrated companies which supply finishing pigs as well as centralised services such as compound feed, transport and veterinary services to the whole company. Typically the integration will comprise an indoor multiplier farm which supplies gilts, and other boars, to a range of large outdoor commercial breeding farms. Usually artificial insemination is used on the multiplier farm rather than natural service. Each commercial breeding farm then supplies weaned pigs either to a range of nursery farms or direct to finishing farms. It is therefore possible to disseminate *Salmonella* to tens or hundreds of other farms if the multiplier herd is infected. Longitudinal studies were carried out on the multiplier farms for two large companies and a single investigative visit was made to the multiplier farm from a third company. On one of the farms (X) *Salmonella* Typhimurium and other serovars were widespread in all age groups of pigs and environmental samples. There was a sustained reduction in *S.* Typhimurium after ongoing tetracycline medication for sub-fertility was removed but the improvement for other serotypes was transient. On the second farm (Y) *S.* Typhimurium was intermittently detected, against a background of *S.* Panama. *S.*Typhimurium DT104b and *S.*Derby were found in batches of new replacement gilts, originating from a primary breeding company, which had just been delivered to this farm. On the third farm (Z) S. Ohio was predominant, although *S.* Derby was present in post weaning accommodation for gilts and *S.* Typhimurium was detected in several groups. It was necessary to sample individual pens to detect *S.* Typhimurium on the site because of masking by the other serovars in pooled samples. All three of the companies had a high prevalence in their commercial breeding and finishing herds of the same *Salmonella* serovars found on the respective multiplier farms.

Introduction

Despite the potential importance of multiplier herds in the maintenance and dissemination of *Salmonella* amongst production herds, there is limited data on *Salmonella* colonisation above the commercial production tier of the breeding pyramid. Serological examination of a small number of Dutch multiplier herds by ELISA (van der Wolf et al., 2001) revealed that 100% and 91% of herds were seropositive at 10% and 40% optical density (OD) cut-offs, respectively. Similar values were obtained for production breeding sows. One of four Greek multiplier herds proved seropositive with an ELISA similar to that used in Danish monitoring (Grafanakis et al., 2001). Bacteriological sampling of 10 animals per herd in Denmark (Christensen et al., 2002) showed similar herd-level prevalences of *Salmonella* in genetic breeder herds (12%) and in finished pigs before slaughter. The present report concerns intensive sampling for *Salmonella* on three multiplier herd premises in England.

Materials and Methods

Farms X, Y and Z were, respectively, 800-, 200- and 1100-sow multiplier units. All 3 farms were multiplier units for large integrated companies and supplied maiden gilts for service on commercial breeding farms throughout the organisations.

The strategy was to sample all groups of pigs from all age groups present, plus empty and cleaned accommodation, equipment, walls and floors in pig-handling and staff areas, and wildlife vectors, particularly rodents. Samples taken on each unit included 25 g bulked faeces from groups of pigs, swabs of sterile medical gauze soaked in buffered peptone water (BPW) from empty pens and surfaces (approx 0.5 m^2), plus rodent droppings and dead mice. Faeces and swabs were placed directly into 225 ml BPW. Rodent droppings (1-10 g) and the liver, intestine and spleen from aseptically dissected mouse carcases (2-3 g) were placed in an approximately tenfold volume of BPW at the processing laboratory. Samples were taken to the laboratory under ambient temperature conditions and processed on the day of collection.

Samples in BPW were pre-enriched for 24 h, inoculated onto modified semi-solid Rappaport-Vassiliadis agar with 0.01 % novobiocin (MSRV; Difco 218681) and incubated at 41.5 °C for 16 to 24 h. A 1 µl loop from the edge of any opaque growth on MSRV was inoculated onto Rambach agar (Merck 107500). Rambach and associated MSRV plates were incubated at 37 °C and 41.5 °C respectively for 24 h. Any MSRV plates on which the growth had spread widely, but which were negative for *Salmonella* on the Rambach plates, were subcultured again onto Rambach agar. Serotyping of representative *Salmonella* isolates was performed at the *Salmonella* reference laboratory at VLA – Weybridge.

Analyses included consideration of prevalence rates (number of positive samples or pools / number of same collected) within certain sample categories, i.e. boars/service areas, sows, farrowing accommodation, weaner pens/decks, grower/finisher pens, gilt pens, rodent samples, and surfaces after cleaning and disinfection (C&D). In addition, for each visit there was an overall prevalence rate that additionally included results from samples of equipment, other wildlife and the wider farm environment.

Results

Farm X was sampled on seven occasions over seven years (Figure 1), and routine tetracycline medication ceased between the first and second visits. *S.* Manhattan was stably persistent in most sample categories throughout the seven years and *S.* Derby was widespread on the first visit and the last four visits, but not detected in the intervening period. Other non-Typhimurium serotypes were detected within several categories on two consecutive visits (Bredeney, Muenchen), or in one or two categories on one visit only (Newport, Heidelberg, Montevideo). The temporal variation of non-Typhimurium *Salmonella* prevalence was marked and without regular patterns. Of the age-group categories, weaners showed oscillations between zero and 15 to 40% detected prevalence on consecutive visits, whereas other age groups were more consistently positive, at prevalences up to 90%. *S.* Typhimurium initially was prevalent and widespread, it declined after three years and in the last eighteen months of the study was found only amongst growers or finishers, at modest prevalences of up to 15%. A number of different definitive phage types and untypable strains were isolated, some concurrently (Figure 1). Hospital pens were heavily contaminated, first with *S.* Typhimurium and latterly with other serotypes. Samples following C&D yielded zero prevalence on only three of five occasions. Initially, rodent faeces were heavily contaminated with herd serotypes, but opportunities to sample declined sharply as rodent control improved.

Farm Y was visited on five occasions over three years and showed an alternating pattern of dominance by serotypes Panama and Typhimurium (Figure 1). Initially, *S.* Panama was prevalent in the farrowing accommodation (25%) and present at a lower level amongst sows, boars and weaners. On this first visit *S.* Typhimurium DT208 was found only in wild bird faeces on site, but on the second visit nine months later it was prevalent (30%) among gilts and detected also from boars, farrowing accommodation and weaners. *S.* Panama was not found on this occasion, but a year later it was heavily prevalent in all age groups plus rodents, and no Typhimurium was found. A novel serotype (Derby) was found amongst incoming and established gilts on one occasion, and on another occasion *S.*Typhimurium DT104b was found. Five months later, the overall *Salmonella* prevalence was much lower with Panama, Derby and Typhimurium DT104b being isolated at modest frequency (3-10%) from weaners, dry sows and gilts respectively. Higher levels of contamination and excretion were once again evident a year later, dominated by *S.* Typhimurium DT208, which was heavily prevalent (30-80%) amongst farrowing and young stock

but present also in older animals. A low level of *S.* Panama was found among sows. C&D proved to be inconsistently effective, with 8 of 43 swabs taken post-C&D throughout the study yielding *Salmonella*, and cleaning equipment itself being found to be contaminated on one visit. Few rodent faeces samples were taken, but *S.* Panama was found in four of five samples on one occasion.

A single visit was made to **Farm Z**, where *Salmonella* was found to be widespread, with 53% prevalence overall (Figure 2). The exception was farrowing sows, yielding no positives from 151 individual faeces samples. The commonest serotype was Ohio, but Derby was found amongst weaners and associated rodents, plus in water and effluent associated with sows and the farrowing house. Ohio was very widespread, extending to staff clothing and rooms, vehicles and a public road. *S.* Typhimurium was also present, although sometimes difficult to detect due to masking by other serotypes. It was found amongst weaners, rodents and in service and hospital pens, but not in sow groups. Phage type U288 was predominant.

Discussion

The three multiplier herds examined showed distinctly differing patterns of *Salmonella* contamination. Farm X had multiple serotypes simultaneously present, but only three of eight (Manhattan, Derby and Typhimurium) were persistent and recurrent. The prevalences varied widely between visits, and a reduction in prevalence of *Salmonella* spp. after the withdrawal of tetracycline medication proved to be short-lived. *S.*Typhimurium was the only persistent serotype to show a progressive decline over time, ultimately being restricted to less than 2% prevalence among growers only. Hospital pens consistently showed heavy contamination and might prove to be a sensitive site for detection on occasions when sampling opportunities are limited.

Farm Y had a much smaller herd, with fewer serotypes present in an apparently more dynamic relationship, oscillating between periods of dominance by *S.* Panama and *S.* Typhimurium DT208. It is difficult to estimate the relative influences of pig immunological responses and bacterial ecological competition upon the patterns observed but it is likely that some strains fell below the limits of detection rather than disappeared. *S.* Typhimurium DT208 was initially found only in wild bird faeces, but nine months later it was the dominant strain in the herd. This is consistent with a role for wild birds as sentinel and/or reservoir species for *Salmonella* in pigs. A further factor was the introduction of *S.* Derby by incoming gilts, it being found subsequently in sows. *S.* Typhimurium DT104B was uniquely found amongst gilts and may have been another such import.

The investigation on Farm Z provided an interesting snapshot of an untypical serotype (Ohio) appearing dominant, against a background of serotypes more typically found as residents, i.e. Derby and Typhimurium. Ohio can be found as a feedstuff contaminant, which may be the route by which it attained dominance. As there was just one visit, it is unknown whether it was persistent, but it had achieved extensive spread on the farm, even into staff areas and a roadway. The absence of *Salmonella* in the farrowing accommodation was surprising, but this area was relatively isolated from effluent and faeces from elsewhere and had a good foot-dip system in place.

Conclusions

Multiplier herds are well-placed to disseminate *Salmonella* to production herds via movement of young breeding stock, and the introduction of *S.* Derby, and possibly *S.* Typhimurium DT104B, into Farm Y by gilts illustrates the point. Reductions in *Salmonella* contamination of slaughter pigs will be difficult to achieve without good controls higher up the production pyramid. The present data shows fluctuating but persistent contamination of multiplier herds by several serotypes, including Typhimurium. Prevalence rates were similar to those found amongst slaughter-age pigs in the UK (Davies et al., 2004). As in production herds, wildlife, ineffective C&D and importation of infected stock appear to be significant factors in the maintenance and re-introduction of *Salmonella* within multiplier herds.

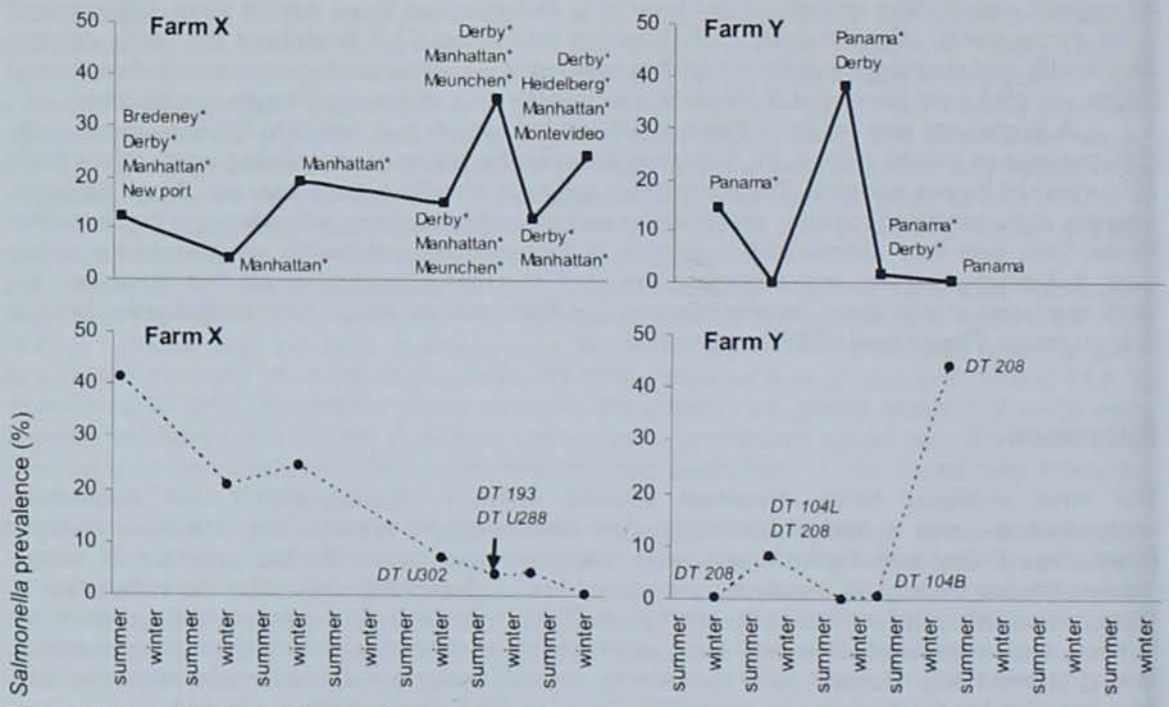

Figure 1: Overall *Salmonella* prevalence values of non-Typhimurium (solid lines) and Typhimurium (dotted lines) serotypes over time. Time scales apply to all charts. * Predominant serotypes.

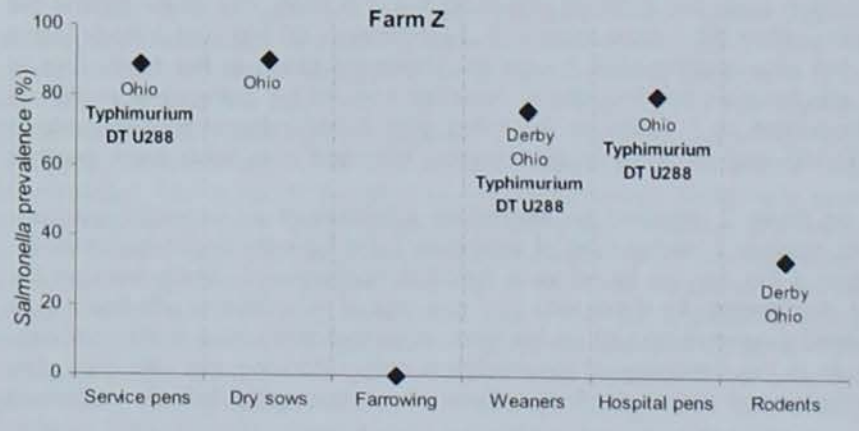

Figure 2: *Salmonella* prevalence within categories on Farm Z.

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