EFFECT OF PRE-SLAUGHTER HANDLING AND SEROLOGY ON SALMONELLA IN PIGS

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Summary: This study investigated the combined effect of herd sero-prevalence, time-off-feed prior to slaughter and transport distance to the abattoir on *Salmonella* spp. infection in slaughter pigs under Australian marketing scenarios. Ten herds situated either < 125 km or > 500 km from the abattoirs were monitored at slaughter over a 12-month period both serologically (Australian *Salmonella* spp. mix-ELISA) and by caecal culture. On 4 occasions (seasonally) each farm withdrew feed from three groups of slaughter pigs so they were off feed for 12-18 hours, 18-24 hours and >24 hours prior to slaughter, including transport and lairage times. For herds <125 km from the abattoirs, *Salmonella* spp. infection decreased significantly with an increase in the period between last feed and slaughter. For herds > 500 km from the abattoirs, *Salmonella* spp. infection increased significantly with an increase in the period between last feed and slaughter, other factors apparently overriding the protective effect of fasting. Herd sero-prevalence was not a significant risk factor for caecal positivity.

Keywords: Australia, time-off-feed, transport distance, sero-prevalence, caecal

Introduction: This study investigated the ecology of the major foodborne hazard, *Salmonella* spp. during the period immediately leading up to slaughter. The association between herd sero-prevalence and culture positivity at slaughter has already been established (Dahl and Sërensen, 2001). Rather than duplicating that work, this study aimed to evaluate the relative contribution...
of herd serological status and local marketing procedures (transport distance/time-off-feed). This data would then allow comment on the value of herd sero-monitoring to the Australian pig industry and the importance of other factors.

**Methods:** Initial serological screening was conducted on 24 South Australian herds, selected on the basis of their distance from the abattoirs and their ability to send a minimum of 60 finisher pigs directly to slaughter at one time. Ten of these were selected and their sero-prevalences monitored over a 12-month period using the previously validated Australian *Salmonella* spp. mix-ELISA (van der Heijden, 2001). The ten herds ranged in production capacity from 80 to 1500 sows and were selected to maximise the opportunity for expression of the impact of transport distance. Five herds were situated < 125 km (short-haul) and five > 500 km (long-haul) from the abattoir. On four occasions (seasonally) each farm withdrew feed from three groups of 20 slaughter pigs so they were off feed for 12-18 hours, 18-24 hours and >24 hours prior to slaughter: includes time-off-feed on farm before transport, transport time and lairage time; (10 herds x 4 seasons x 3 treatments = 120 batches of 20 pigs). Therefore, the three time-off-feed treatments were measured within each testing round within each herd. This design is highly powered for the comparison of the three time-off-feed treatments within each transport scenario, which may otherwise be collinear in an observational study. Blood and caecal ingesta (10 g/pig) were collected at slaughter for serology and culture (Australian Standard Method AS1766.2.5-1991) respectively, with results correlated on a batch, not individual pig basis.

**Statistical methods:** The experimental design resulted in a 3-level nested structure in the data. Therefore, effects of time-off-feed treatment, transport distance and serological prevalence on caecal positivity were analysed as a 3-level hierarchical linear model (HLM for Windows, Version 5.04) using the logit link at level 1 and a penalised quasi-likelihood (PQL) estimation method. Average serological prevalence (centred around the mean of 35 %) was measured for each of the three time-off-feed treatments for each batch (testing round) of pigs within each herd (level 1 covariates). Four batches of pigs were tested within each herd (level 2, intercept only), and transport distance was a between herd (level 3) covariate. All intercept terms were treated as random; the remaining parameters were treated as fixed effects. Odds ratios were estimated from the population-averaged (as opposed to unit-specific) regression parameters.

**Results**

**Batch serology and culture results:** There was no significant difference in the serology profile between 125 km and 500 km herds (p = 0.352). Overall 700 (35.4 %) of 1977 blood samples from the 10 study herds were positive in the seasonal sampling rounds. The sero-positive range on a batch basis was 0-100 %. The average culture positive rate over all herds was 5.3 % (2.8, 9.9; 95 % CI), which gave an average sero-prevalence to caecal prevalence ratio of 6.7:1. The culture positive range on a batch basis was 0-70 %.

**Effect of time-off-feed and transport distance:** There was a significant reduction in caecal culture positivity in the < 125 km (short-haul) herds with increasing time-off-feed prior to slaughter (Table 1). The converse was true for the > 500 km (long-haul) herds, where a significant increase was seen with increasing time-off-feed. There was a trend towards a positive correlation between culture positive rate and serological prevalence, which did not reach statistical significance (p = 0.114 [data not shown]). When serological prevalence was excluded as a covariate, the effects of time-off-feed and transport distance were essentially unaltered.
Salmonella serovars: In total there were 109 isolates from 1871 caecal samples. Of these, 52 (48 %) were S. Derby and 25 (23 %) S. Infantis. Only seven (6 %) of the isolations were S. Typhimurium.

Discussion: Regulatory programs have stopped short of mandating specific on-farm control procedures due to inadequate knowledge of the epidemiology of foodborne infections in animal populations. This study adds to the understanding of this complex issue by proposing two models based on the combined effect of time-off-feed and transport distance (Table 1) that may explain some of the apparent contradictions in the literature regarding Salmonella spp. infection in slaughter pigs. Model 1-short haul: For herds < 125 km from the abattoirs, Salmonella spp. infection was found to decrease significantly with an increase in the period between last feed and slaughter. In this model, fasting is a protective factor offsetting any increase in shedding caused by (short distance) transport stress as found by Williams and Newell (1970) and Isaacson et al (1999 a). Model 2-long haul: For herds > 500 km from the abattoirs, the protective effect of fasting is apparently overridden by other factors. There is a significant increase in Salmonella spp. infection with an increase in the period between last feed and slaughter, which is consistent with the findings of Williams and Newell (1967) and Isaacson et al (1999 b). Thus time-off-feed and transport distance appeared to strongly influence caecal positivity at slaughter. However, herd sero-prevalence did not exert a significant effect in this study, indicating that a national serological monitoring programme would have limited application under the Australian marketing scenarios investigated.

The Australian Pork Industry Quality Standards presently advise a fasting period of ‘at least 6 hours’ before slaughter to minimise PSE and gut spillage during processing and slaughtering and ‘no more than 24 hours’ off feed to minimise Salmonella spp. build up. The findings in this study suggest tightening of the pre-slaughter time-off-feed period to 15 to 24 hours, which should include a period of fasting prior to transport where possible, as the best approach to minimising Salmonella spp. in ingesta of slaughter pigs.

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Reference:


Macrolide resistance in porcine streptococci: a human health hazard?

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Summary: In order to obtain better insights into the possible exchange of resistance genes between human and porcine streptococci, macrolide and lincosamide resistant streptococci from tonsillar and colon swabs from pigs and pork carcass swabs were isolated and their resistance phenotypes and genotypes were determined. The sequences of the erm(B) genes of 21 human streptococci, 22 porcine streptococci and 15 streptococci isolated from pork carcasses were compared. From each of the 33 pigs and from 88 of 99 carcass swabs, at least one resistant streptococcal strain was isolated. The predominant phenotype was the constitutively expressed MLSB phenotype, mostly encoded by the erm(B) gene. Identical erm(B) gene sequences were present in strains from humans, pigs and pork carcasses.

Keywords: Macrolide resistance, erm(B), streptococci, swine, resistance transfer

Introduction: Two types of antimicrobial drug resistance transfer from animals to humans might be of importance. The direct way of resistance transfer occurs when resistant zoonotic bacteria infect humans. The contribution of the indirect way of resistance transfer to the antimicrobial resistance problems in human medicine is less clear. Indirect way means that resistance genes from bacteria associated with animals are transferred to bacteria associated with humans. One of the most important antibiotic groups affected by resistance in humans and in pigs is the macrolide-lincosamide-streptogramin B (MLSβ) antibiotic family. The present study was carried out in order to obtain better insights in the possible exchange of resistance genes between human and porcine streptococci.

Materials and methods: Tonsillar and colon swabs were collected from 33 pigs, originating from 33 different farms in Belgium. Ninety-nine swabs were taken by swabbing the entire skin surface of pork carcasses immediately after slaughter in four slaughterhouses. The pigs originated from 35 different