Association between carcass-swab-positivity and seroprevalence in herd of origin and estimation of the importance of cross-contamination on the slaughterline for salmonella-negative herds

Jan Dahl¹, Lene Lund Sørensen¹

¹: Danish Bacon and Meat Council, Axeltorp 3, DK-1609 Copenhagen V, Denmark,
Phone: ++4533116050, Fax: ++4533145756, E-mail: jd@danishmeat.dk,
lls@danishmeat.dk.

Abstract: The aim of this study was to investigate the correlation between Salmonella positive herds and microbiological results from carcasses from the same herd. The results showed, that there was an increasing risk of salmonella-positivity with increasing seroprevalence in herd of origin. But although the results were highly significant, we found more Salmonella on the low prevalence herd than anticipated, indicating cross-contamination from other herds to add significantly to the number of positive carcasses in low prevalence herds.

Introduction: Denmark has instituted a new surveillance system for Salmonella on pig carcasses. Three different areas of the carcass are swabbed, and the swab is cultured for Salmonella. For app. one year the system was used on 9 different slaughterhouses to investigate the performance of the test. For most of the carcasses it was possible to identify herd of origin, so it was possible to investigate the correlation between seroprevalence in herd of origin and salmonella status of the carcass.

Materials and Methods: From 9 different slaughterhouses swab-samples were collected from at total of 13591 carcasses. 73 % of the sampling days, 5 swabs were taken pr slaughterhouse, and for the remaining days, between 1 and 15 samples were obtained pr day. From 11265 of the carcasses, the central herd register number was obtained. Swabs were analysed using standard microbiological techniques.
From each of the herds, serological results from the ongoing surveillance system were obtained from the same month as the carcass was sampled.
For comparison we looked at results from two studies, were caecal samples had been taken at the slaughterhouse, and analysed for salmonella content. From 2136
herds, approximately 10 caecal samples pr herd were taken. From each caecal sample, 25 gram were analysed using standard microbiological techniques. Also from these herds, we obtained serological results from the surveillance system from the same month as the caecal samples were obtained.

Serological samples were analysed using the Danish Salmonella-Mix-ELISA. Positive samples were samples with and OD% above 20. This is the cut-off used in the Danish surveillance system.

For the statistical analyses, we used the MIWiN-package for analysing the association between carcass-positivity, slaughterhouse and seroprevalence. For association between caecal samples and seroprevalence, we used the SAS-procedure Proc Genmod.

**Results:** 1.44 % of the carcasses were positive for *Salmonella*. The number of positive carcasses ranged from 0.1 % to 2.9 % at the 9 slaughterhouses in the study. In figure 1 is shown the association between carcass positivity and seroprevalence of the herd from 9 slaughterhouses and association between positivity of caecal samples and seroprevalence of the herd. Seroprevalences are from the same month as the carcass and caecal samples.

**Figure 1. Association between carcasspositivity in 9 slaughterhouses (thick line=average), prevalence of positive caecal samples and the seroprevalence from herd of origin**

Statistical analyses showed a highly significant (p<0.0001) association between caecal prevalence and seroprevalence in herd of origin. The association was stronger between *Salmonella* Typhimurium and seroprevalence than between exotic serotypes and seroprevalence, although both were highly significant.

For carcass positivity we found a significant difference between slaughterhouses. There was a highly significant association (p<0.0001) between carcass-positivity and seroprevalence. This association was not different between slaughterhouses, meaning that although the level of *Salmonella* on the slaughterhouse differed, then
for all slaughterhouses, there would be an increase in positive carcasses with increasing seroprevalence in herd of origin.

**Figure 2. Indirectly assessed association between caecal prevalence and carcass positivity**

The described studies do not compare caecal prevalence with carcass positivity directly. But given the fact, that we have found a strong association between seroprevalence and both carcass positivity and caecal prevalence, we can construct the association between carcasses and caecal samples. In figure 2 the assessed association between the caecal samples and carcasses is shown. A regression line is drawn, and there seems to be a near linear association between caecal samples and positive carcasses. Extrapolating the line to 0 percent positive samples shows, that the regression line crosses the y-line at approximately 0.75 percent.

**Discussion and conclusion:** There is a significant difference in number of *Salmonella* positive carcasses between slaughterhouses. This difference could not be explained by the difference between *Salmonella* status in the herds delivering to the slaughterhouse. But for all slaughterhouses we found a higher risk of carcass positivity, when the herd of origin was a high seroprevalence herd. By extrapolating the line in figure 2, we would expect around 0.75 % positive carcasses, even when the herd of origin is a microbiologically negative herd. This could be interpreted as cross-contamination of pigs/carasses during transport, lairage and slaughter. Care should be taken not to over interpret the result, since it is based on extrapolation, and the level differs between slaughterhouses, but it indicates, that cross-contamination might contribute significantly to the number of positive carcasses.