Development in within herd prevalence, between herd prevalence and carcass prevalence in Danish pigs and pork compared to number of attributable human cases from 1995 to 2012.

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Abstract
The Danish Salmonella program for pigs and pork has been running for 20 years, and has resulted in a 90 % reduction of human cases attributed to Danish pork from 1993 to 2012 (Anonymous, 2013). The development in prevalence in breeding herds, sow herds, finisher herds and at carcass level was analysed as part of the ongoing preparations for the fifth Danish Salmonella plan for pigs and pork, which will be initiated from January 2014.

Analyses of the serological surveillance of the prevalence in breeding herds showed an increase in positive herds from 25 % in 1998 to 50 % in 2012. The within-herd prevalence in positive breeding herds fluctuated between 3 and 6% seropositive samples (cut-off 40 OD%) with no clear pattern.

Prevalence in sow herds could not be analysed directly, but two microbiological surveys in 1998 and 2008 showed an increase in positive sow herds.

The serological surveillance in finisher herds showed an initial decrease from 1995 to 1998. From 1998 the number of positive herds increased from 30 % to 65 %. Within herd prevalence in positive finisher herds fluctuated between 6 and 9 % (cut-off 40 OD%) with no clear pattern.

The carcass surveillance program was initiated in 2001. The carcass prevalence on slaughterhouses affiliated with the Danish Agriculture and Food Council dropped from 1.7 % in 2001 to 1.2 % in 2010. In 2010 the sampling area per carcass was increased from 300 cm² to 400 cm², which coincided with an increase in carcass prevalence to 1.5 % for 2011 and 2012. The relative and absolute prevalence of Salmonella Typhimurium dropped from 0.8 % in 2001 to 0.4 % in 2012, consistent with the development in human cases attributed to pork, whereas the prevalence of Salmonella Derby increased from 0.2 % to 0.4 %, making it more prevalent than Typhimurium in 2012. This increase has not been followed by an increase in the number of human cases of Derby, which remains low at around 5-10 cases each year.

Overall the results indicate a steady increase in the number of positive herds in primary production. But improved hygiene in the slaughter house kept the carcass prevalence low, and the number of human cases attributed to Danish pork has remained at a low level since 2000 (Anonymous, 2013).

Introduction
In the spring of 2013 the Danish Veterinary and Food Administration initiated an analysis of the results of the Danish Salmonella program for pigs and pork as part of the planning of the fifth Salmonella plan. The development in salmonella prevalence in breeding herds, sow herds, finisher herds and at carcass level was analysed using surveillance data from the ongoing program.

Material and Methods
Breeding and multiplying herds
Ten blood samples are collected each month from 4-7 months old gilts on all Danish breeding and multiplying herds. The blood samples are analysed using the Danish Mix-ELISA (Mousing, 1997).

The surveillance data were analysed in the period from 1996 to 2012. The cutoff for positive samples was OD% >40.

The data were analysed using a zero-inflated binomial model, as described by Stevenson (2005). The zero-inflated model can in one step handle overdispersion caused by excess zeros, due the existence of truly negative herds, and estimate the prevalence in positive herds. Herd effects were included by adding a herd effect as a random effect.

Sow herds
Salmonella surveillance in Danish sow herds is risk based, and the results cannot be used for analyses over time. Instead two bacteriological screenings of sow herds from 1998 (Anonymous, 1999) and 2008 (Anonymous, 2009) were used to evaluate the progress.
**Finisher herds**
Serological results from the meat-juice Mix-ELISA (Mousing, 1997) from 1995 to 2012 were analysed using the same statistical model as for breeding and multiplying herds (Stevenson, 2005).

The sampling frame was changed several times over the period. To standardise results over the years, only the first sample obtained per herd-month was used for the evaluation. The cut-off was OD% 40.

**Carcass swabs**
From 2001 to 2010 3*100 cm² per carcass was swapped on 5 different, randomly chosen carcasses per day per slaughterhouse. The 5 swabs were analysed as one pooled sample. Individual carcass prevalences were estimated by dividing the pool prevalence by 3, following Sørensen (2007).

In 2011 swapping was extended to 4*100 cm² per carcass to comply with EU-standards. Over the years, microbiological methodology has changed, and PCR-based methods have replaced standard microbiological methods.

**Results**
**Breeding and multiplying herds**
After an initial drop from 1996 to 1998, the proportion of positive herds has increased from 25 % in 1998 to 50 % in 2012. The within-herd prevalence has fluctuated over the years, with no clear trend (figure 1). 682 breeding and multiplying herds were active in the period. The number of herds active per year ranged from 208 to 354. The number of breeding and multiplying herds declined over the years, from 354 in 1999 to on average 220 herds per year from 2007 to 2012.

**Sow herds**
A bacteriological screening based on fecal samples in 1998 found at least one positive sample in 17 % of the sow herds. A screening in 2008 found at least one positive sample in 41 % of the sow herds.

In 1998 the most frequent serotype was *S. Typhimurium*. In 2008 *S. Typhimurium* was found in 29 % of the herds, but *Salmonella Derby* was now just as frequent as *S. Typhimurium*.

**Finisher herds**
Figure 2 represent results from all herds (from 16000 herds in 1995 to 5000 in 2012). After an initial drop from 1995 to 1998, the proportion of positive herds has doubled from 1998 to 2012 (figure 2). But the average prevalence in positive herds has been fairly constant over the period.

**Carcass prevalence**
Figure 3 shows the carcass prevalence from 2001 to 2012 from Danish slaughterhouses affiliated to the Danish Agriculture and Food Council (figure 3). From 2001 to 2010 the prevalence of salmonella positive carcasses dropped from 1.7 % to 1.2 %. In 2011, the swabbed area was extended from 3*100 cm² to 4*400 cm². The apparent prevalence increased to 1.7% the first year.

*Salmonella Typhimurium* decreased from 0.8 % in 2001 to 0.4 % in 2012. In the same period *Salmonella Derby* increased, and exceeded the *S. Typhimurium* prevalence in 2012.
Discussion

The zero-inflated model showed a steady increase in the number of sero-positive breeding herds and finisher herds from 1998 to 2012.

A more detailed analysis of data from 1998 and 2012 showed that herd-size had increased considerably, and the proportion of specialized finisher herds had increased from 50% in 1998 to 75% 2012 (details not shown).

The increase in positive herds could not be explained by the increase in herd size, but part of the increase could be attributed to the increase in specialized finisher herds. Specialized finisher production had a higher proportion of positive herds in both years compared to integrated herds (sow herds with production of finishers).

Focus in the Danish salmonella program in primary production has been on reducing high prevalence herds, based on the idea, that buying gilts, weaners and growers from high prevalence herds was more problematic than buying from medium to low prevalence herds.

This allowed for a continued spread of infection from herd to herd.

In 2010 the declaration system for breeding, multiplying herds and sow herds was changed to positive or negative status for each herd, making it easier for sow herds or finisher herds to get salmonella-free replacement animals.

The increase in herd prevalence has not resulted in an increase in carcass prevalence and in human cases. Baptista (2010) showed that the association between herd prevalence and carcass prevalence is positive, although not very strong for large slaughterhouses. The improvement in slaughterhouse technology and hygiene more than compensated for the increase in salmonella prevalence in primary production.

References


Stevenson, J. D. Analysis of presence/absence data when absence is uncertain (false zeroes) : An example for the Northern Flying Squirrel using SAS. Extension note 74, July 2005.