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Theoretical value of pre-trade testing for *Salmonella* in Swedish cattle herds

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ABSTRACT

The Swedish *Salmonella* control programme includes mandatory action if *Salmonella* is detected in a herd. The aim of this study was to assess the relative value of different strategies for pre-movement testing of cattle.

Three fictitious herds were included: dairy, beef and specialised calf-fattening. The yearly risks of introducing *Salmonella* with and without individual serological or bulk milk testing were assessed as well as the effects of sourcing animals from low-prevalence areas or reducing the number of source herds.

The initial risk was highest for the calf-fattening herd and lowest for the beef herd. For the beef and dairy herds, the yearly risk of *Salmonella* introduction was reduced by about 75% with individual testing. Sourcing animals from low-prevalence areas reduced the risk by >99%. For the calf-fattening herd, the yearly risk was reduced by almost 50% by individual testing or sourcing animals from a maximum of five herds.

The method was useful for illustrating effects of risk mitigation when introducing animals into a herd. Sourcing animals from low-risk areas (or herds) is more effective than single testing of individual animals or bulk milk. A comprehensive approach to reduce the risk of introducing *Salmonella* from source herds is justified.

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1. Introduction

The aim of the Swedish Salmonella control programme is to keep food originating from Swedish animals free from Salmonella, in order to protect the consumers (Sundström et al., 2014; Wahlström et al., 2014). The programme covers all livestock species and Salmonella serotypes. The legislation on Salmonella involves mandatory action from the Swedish Board of Agriculture in any case of confirmed Salmonella infection in a livestock herd (Swedish Ministry of Enterprise and Innovation, 2014). Restrictions (on movements of animals and animal products) are put on the herd and compulsory eradication measures are instituted (Swedish Board of Agriculture (2014)). Although it has been concluded that the overall costs of the programme are outweighed by the public health benefits (Sundström et al., 2014; Wahlström et al., 2014), the costs are substantial, and unequally divided between farmer categories (Sternberg Lewerin et al., 2013). The feed control incurs the highest costs, followed by Salmonella control in cattle (Sternberg

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Lewerin et al., 2013; Sundström et al., 2014). Analyses of the costs of *Salmonella* control in cattle farms have shown the average cost per herd for on-farm *Salmonella* control to amount to approximately 490,000 EUR with a median of about 110,000 EUR (Ågren et al., 2015). Surveys indicate a very low overall prevalence in cattle (Ågren et al., 2016) but, due to challenges to on-farm eradication especially in large herds, a number of farms remain restricted for long periods (National Veterinary Institute, 2014).

The challenges linked to large herds are reflected in an association between eradication costs and herd size (Ågren et al., 2015). *Salmonella* in cattle herds, particularly *Salmonella* Dublin infection, is associated with production losses and impaired animal health (Dahl Nielsen, 2012; Hughes and Jones, 1973; Peters, 1985; Rosenbaum Nielsen, 2009; Visser et al., 1997). Despite the low prevalence of *Salmonella* in Swedish cattle, there are areas where the seroprevalence of *S.* Dublin may be as high as 17% (National Veterinary Institute, 2014; Ågren et al., 2016). To protect farmers from the risk of *Salmonella* introduction, a voluntary testing scheme for cattle was planned in the Safe Livestock Trade programme, one of the voluntary preventive animal health programmes run by the farmer-owned animal health organisations (Växa Sweden, 2016).

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Any pre-trade testing programme faces the dilemma of balancing costs and consequences of false negative and false positive results when choosing what animals to test, how many animals to test and what diagnostic test to use. The cost-benefit of pre-trade testing for infectious diseases can be questioned (Clegg et al., 2008). Pre-trade testing can lead to a false sense of security that affects risk awareness and creates new trading patterns, but it can also reduce high-risk movements by making them more costly and complicated (Gates et al., 2013).

The aim of this study was to assess the relative value of different strategies for pre-movement testing for *Salmonella*, by applying an import risk assessment model to three fictitious Swedish cattle herds.

2. Material and methods

Three previously used fictitious model herds: one dairy, one beef and one specialised calf-fattening herd were included (Sternberg Lewerin et al., 2015). The dairy farm consisted of 180 lactating cows and introduced on average 10 new animals (pedigree heifers) per year. The beef herd included 65 suckler cows with an introduction of 2 new animals every year. The calf fattening herd had 120 animals and brought in on average 100 new animals every year.

The model was built in Microsoft Excel (Microsoft Co., Redmond USA), with Monte Carlo simulation in @Risk (Palisade Co., Ithaca, USA) with 10,000 iterations. The yearly risks of introducing *Salmonella* with and without serological testing of individual animals or bulk milk testing were assessed as well as the effects of sourcing animals from low-prevalence areas or reducing the number of source herds. Calculations for each strategy are shown in Table 1.

Input data included expected prevalence of Salmonella in Swedish cattle herds, in regions of high and low prevalence, estimates of within-herd prevalence and test sensitivity. The overall herd prevalence was allowed to vary, in a uniform probability distribution, between the value for the region with lowest prevalence to the regions with the highest prevalence, to reflect that with no specific sourcing strategy cattle could be sourced from any region. The within-herd prevalence was allowed to vary between one infected animal, a most likely proportion and a maximum proportion, to reflect that animals could be selected in any phase of the herd infection. In the absence of validated test characteristics, estimates of test sensitivity were based on assumptions in previous studies (Veling et al., 2001; Wedderkopp et al., 2001). Prevalence assumptions were based on a serosurvey (National Veterinary Institute, 2014; Ågren et al., 2016) and re-calculated as previously described, using sensitivity and specificity estimates from previous studies (Ågren et al., 2016). The input values used are shown in Table 2.

Further, it was assumed that when batch-wise introduction was used to reduce the number of source herds, fattening calves were

sourced from 5 different herds. Most importantly, it was also assumed that the *Salmonella* type in infected herds would be detectable by serological tests (mainly *S*. Tyhimurium and *S*. Dublin, see e.g. Ågren et al., 2016).

Sensitivity testing was performed in @Risk, by examining tornado graphs.

3. Results

The risks of Salmonella introduction with the different strategies in the three herds are illustrated in Fig. 1. There were large variations in the results, but the initial risk was highest for the calffattening herd (about four times that of the dairy herd) and lowest for the beef herd (about a fifth of that of the dairy herd). For the dairy herd, the yearly risk of Salmonella introduction via animal purchase from any area was reduced to 25-30% of the initial risk by testing individual animals or bulk milk once. Sourcing animals from a low-prevalence area reduced the risk to 0.5-1% of the initial risk and with testing this risk was reduced further by 90%. For the beef herd, the yearly risk was reduced to about 25% of the initial risk by testing individual animals and to <1% of the initial risk by sourcing from a low-prevalence area. This risk was further reduced by 75% by testing the animals from low-prevalence areas. For the calffattening herd, the yearly risk was reduced to 45-50% of the initial risk by testing individual animals before introduction or sourcing animals from a maximum of five herds. Sourcing animals from a low-prevalence area reduced the risk to about 1% of the initial risk with a further 80% reduction of the risk by testing or batch-wise sourcing of animals.

Tornado graphs revealed that the input with the highest effect on model results was the herd prevalence while the second most important assumption was within-herd prevalence (see Fig. 2).

4. Discussion

The difference in the size of the risk between the different types of herds is logical as it is highly dependent on the number of animals introduced. Due to various uncertainties and variability in the input data, the results should be regarded as estimates of the size of the probabilities, not as actual likelihood of introduction. The variation in the input data is reflected in the large variation in the model outputs, as demonstrated by the error bars in Fig. 1. Although some of this variability is in fact uncertainty and may be reduced by further studies strengthening the scientific basis for the input data, some variability is inherent and the results should be interpreted with this in mind. Although the figures are not useful as risk estimates per se, they may be used to compare risk mitigation strategies for different herds under different circumstances. For instance, if regional prevalence figures are available, these could form a basis for decisions on source herds when buying animals and, depending on type of production and number of animals introduced, different

Table 1

Risk mitigation strategies assessed for the risk of introducing Salmonella into a herd via live animals.

Strategy	Description	Risk of introduction calculated as ^c
No risk mitigation ^a Bulk milk testing ^b Individual serology ^b Batch-wise sourcing	Introduction via animals without any testing or sourcing strategy A single bulk milk test, from source dairy herds, before introduction A single serological test from each introduced animal, before introduction Fattening calves sourced from 5 herds	$\begin{array}{l} 1-(1-HP^*WHP)^n \\ 1-(1-((HP^*(1-Se))/((HP^*(1-Se))+(1-HP))^*WHP)^n \\ 1-(1-(((HP^*WHP^*(1-Se))/(HP^*WHP^*(1-Se))+(1-HP^*WP)))^n \\ (1-(1-HP)^{nb})^*(1-(1-WHP)^{nab}) \end{array}$

^a With no risk mitigation, herd prevalence was assumed as the national prevalence. When sourcing from only low-prevalence regions, the herd prevalence figure was changed.

^b Assuming animals are only introduced after a negative test.

^c HP = herd prevalence, WHP = within-herd prevalence, n = yearly number of animal introductions, Se = test sensitivity, nb = number of batches, nab = number of animals per batch.

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