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Summary

Information about the proportion of truly *Salmonella*-free herds is required for an evaluation of the epidemiological situation, the development of control strategies and their implementation. Findings regarding the presence of salmonellas in faeces and intestinal lymph nodes as well as the presence of *Salmonella* antibodies in meat juice from slaughtered pigs were obtained in the context of a study conducted by a number of institutes. These data were used for an analysis of the validity of data on the prevalence of infected animals within herds and on the prevalence of infected herds. The proportion of batches or herds with exclusively negative individual findings was found to depend not only on the true proportion of truly *Salmonella*-free animals within herds but quite essentially also on the distribution of the proportion of infected animals within herds, the sensitivity of the methods of examination and sample sizes. When taking into account the existing dependencies, it was found that among the swine, the real numbers of *Salmonella* carriers were much higher than shown by bacteriological and serological examination. Regarding salmonellosis in swine, also a number of contaminated herds must be expected which is far higher than that shown by the number of herds with positive findings in at least one animal. Even a low contamination of all or almost all herds would result in the numbers of ‘negative’ batches observed, i.e. batches with exclusively negative individual findings. A rating of the salmonella exposure of herds as high, low, or very low is possible and may, and should be, used for measures of consumer protection, irrespective of the proportion of truly *Salmonella*-free herds.

Introduction

Prevalence data regarding a specific agent may refer to the proportion of infected individuals among the animals belonging to an epidemiological population unit, e.g. a herd, or the proportion of infected units among the total number of epidemiological units of a country.

Surveys to estimate the presence of a specific agent in a territory are mostly based on the examination of a sample of animals within a sample of herds for the presence of the agent. The herd is considered as infected if at least one of the animals examined has been recognized as a carrier of the infection. The proportion of infected herds in the territory examined is characterized by the number of infected herds as referred to the total number of herds.

To be able to evaluate the epidemiological situation, to develop and implement control strategies, it is important to know the proportion among the herds found to be ‘negative’ which in fact are free of the agent. For this reason, the findings made within a comprehensive study on the presence of salmonella in pigs (Käsbörer et al., 1997; Protz et al., 1997) were used to obtain information on the specificity and sensitivity of salmonella detection and to examine whether and to what extent it is possible to conclude the proportion of truly salmonella-free units from examinations of individual animals and herds.

Data

The data evaluated refer to a total of about 12 000 pigs slaughtered in seven slaughter houses in different parts of Germany. The animals originated from 679 slaughtering batches or herds. One faeces sample and one intestinal lymph node per animal were examined for the presence of salmonellas (Käsbörer et al., 1997; Protz et al., 1997). In parallel, meat pieces was sampled from the animals to determine the level of antibodies to *Salmonella* in meat juice (Steinbach and Staak 1997).

Definitions used for the *Salmonella* Status of Epidemiological Units and Areas

We used the following parameters of prevalence (P) for the discription of the epidemiological situation of *Salmonella* infections:

- **PA**<sub>a</sub> Proportion of animals which harbour *Salmonella* spp. (actually infected animals) **PA**<sub>a</sub> = number of infected animals in the unit divided by the total number of animals in the unit.
- **PA**<sub>b</sub> Proportion of animals which harbour or had harboured *Salmonella* spp. (history of *Salmonella* infection) **PA**<sub>b</sub> = number of animals which are or had been infected in the unit divided by the total number of animals in the unit.
- **PU**<sub>a</sub> Proportion of epidemiological units with *Salmonella* harbouring animals. **PU**<sub>a</sub> = number of epidemiological units with at least one infected animal in an area divided by the total number of units in the area.
- **PU**<sub>b</sub> Proportion of epidemiological units with animals which harbour or had harboured *Salmonella* spp. (history of *Salmonella* infection) **PU**<sub>b</sub> = number of epidemiological units including at least one animal with a present or a
Estimating Salmonella Prevalence in Swine Herds

A sensitivity of nearly 100% would mean that all animals with negative finding are free of the examined characteristics in reality. The sensitivity of Salmonella detection, however, is substantially lower than 100%.

Contrary to the common understanding, specificity and sensitivity of a diagnostic method are determined not only by the respective bacteriological or serological method of examination but also by the situation to which the animals examined are exposed. Thus, the specificity of serological detection of Salmonella may become reduced by an elevated frequency of microorganisms not belonging to Salmonella spp. but inducing antibodies which react with Salmonella antigen. Likewise, the sensitivity of a diagnostic method is not only determined by the method of examination but also by the infection status of the animals. Sensitivity regarding bacteriological detection will be relatively high where the animals examined suffer from an acute infection and harbour a high number of microorganisms, and it will be low if only a small number of microorganisms remains in the animal body. Regarding serological diagnosis, there may be differences in sensitivity depending on the intensity of the infection process among the herd and the time lag between infection and examination.

Sensitivity and Specificity of Bacteriological and Serological Diagnostics

Reliability of the detection of existing and/or preceding infections is characterized by the sensitivity and specificity of the methods of detection used.

The sensitivity of the diagnostic method with regard to PA\(_a\) or PA\(_h\) is defined by the probability that an animal being infected at the time of the examination or having been infected before will lead to a positive result of examinations. It is ascertained by the proportion of animals shown to be positive among the animals examined and being infected at the time of the examination (PA\(_a\)), and being infected or had been infected (PA\(_h\)).

The specificity of the method is defined by the relative frequency of negative findings in animals without a present and without a present or past infection.

Thus, specificity and sensitivity indicate the probability of a defined finding, e.g. the surpassing of a specific antibody level; to occur in the event of a defined situation, e.g. an existing infection. Erroneously, specificity and sensitivity are often interpreted as probability of the factual absence or presence of a defined situation, e.g. the Salmonella infection in the case of a negative or positive finding. In reality, however, probability can be inferred only with much reservation that a negative finding established represents an animal or a herd that is in fact free from the infection; or a positive finding, an animal that is in fact infected or has been infected. In principle, exact statements on this issue can be made only if in addition to specificity and sensitivity of the method of examination, the relative frequencies of truly infected and truly non-infected animals, or truly infected and truly non-infected herds among the total populations of animals or herds are known (Steinbach 1997). Only in the case of 100% or nearly 100% specificity a positive finding gives sure evidence that the characteristic examined, e.g. the harbouring of Salmonella spp., is in existence. Under this condition, the real prevalence \(P\) equals the product of seeming prevalence (AP) and sensitivity (S).

\[
P = AP \times S \quad (1)
\]

former Salmonella infection in an area divided by the total number of units in the area.

Depending on the question to be answered the different parameters of prevalence may be of different importance. Estimating the danger caused by Salmonella spp. from pig population for food chain and consumer, the proportion of actually infected slaughter pigs (PA\(_a\) and PU\(_u\)) is decisive. For the evaluation of fattening units, the actually infected and formerly infected animals among the delivered slaughter pigs (PA\(_h\)) may also be useful to recognize. Correspondingly the proportion of actually contaminated herds (PU\(_h\)) or the proportion of all herds with a history of infection (PU\(_u\)) can be of interest.

The relative frequency of positive findings obtained by the application of a diagnostic method or a combination of methods does not reflect directly the real value of prevalence parameters defined above. Therefore, the found frequencies of positive findings are designated as apparent prevalences (AP). The estimation of real prevalences (P) also requires the knowledge of sensitivity and specificity of diagnostic methods used.

Specificity of bacteriological and serological examination with regard to actually infected animals (PA\(_a\)) and animals which are or had been infected (PA\(_h\)) on bacteriological examination, an animal is classified as positive in the sense of Salmonella detection if salmonellae are found. As salmonellae cannot be detected in a Salmonella-free animal, an almost 100% specificity (proportion of negative bacteriological findings in non-infected animals) of bacteriological diagnosis can be taken for granted.

With regard to the serological findings, the specificity depends on the frequency of values defined as positive in the enzyme-linked immunosorbent assay (ELISA) procedure used in animals without any history of Salmonella infection. We cannot refer to animals which are grown under field conditions and guaranteed free of present or former Salmonella infection. Within the slaughter batches, however, were several batches of a minimum of 25 animals examined, all with exclusively negative bacteriological findings. The distribution of antibody levels among such animals showed antibody levels of more than 30% in only 88 (3.2%) of 2782 meat juice samples. As will be shown later, even among those animals with negative bacteriological findings throughout, single animals with present or past infection may have to be expected as it can be assumed that the percentage antibody levels above 30% without a previous exposure to salmonellae may occur, if at all, only in exceptional cases. Where serological findings are rated as positive only at levels above 30%, also an almost 100% specificity of the serological detection will result as well with regard to PA\(_a\) and PA\(_h\).

Sensitivity of bacteriological examination with regard to actually infected animals (PA\(_a\)) and animals which are or had been infected (PA\(_h\)) can be estimated by the ratio of the number of positive
bacteriological findings \( I_{\text{pos}} \) to the total number of infected animals \( I \) having been examined bacteriologically.

\[
S = \frac{I_{\text{pos}}}{I}
\]  

(2)

To be able to state the total number of infected animals required for a calculation of sensitivity, it would be necessary to know the number of animals in which salmonellae could not be demonstrated despite an existing infection. As in principle, it is not possible to indicate this figure, we chose another approach to estimate the sensitivity of bacteriological detection.

The unknown number of all infected animals \( I \) among the examined animals is composed of infected animals with positive lymph node findings \( I_{\text{pos}} \) and with negative lymph node findings \( I_{\text{neg}} \). The following applies:

\[
I = I_{\text{pos}} + I_{\text{neg}}
\]  

(3)

When assuming the average proportion of positive findings in the faeces of Salmonella carriers exhibiting detectable amounts of the agent in their intestinal lymph nodes \( I_{\text{pos}} \) to be at least equal to that among Salmonella carriers with negative lymph node findings \( I_{\text{neg}} \), the following inequation may be formulated:

\[
\frac{I_{\text{pos}} + I_{\text{neg}}}{I} \geq \frac{I_{\text{pos}} + I_{\text{neg}}}{I_{\text{pos}}}
\]  

(4)

where \( I_{\text{pos}} \) is the Number of Salmonella carriers in whom the agent was detected in the lymph nodes; \( I_{\text{neg}} \) the number (unknown) of Salmonella carriers with negative lymph node findings; \( I_{\text{pos,Fpos}} \) the number of Salmonella carriers in whom the agent was detected in the lymph nodes as well as in faeces; \( I_{\text{neg,Fpos}} \) the number (unknown) of Salmonella carriers with negative lymph node findings but evidence of the agent in faeces.

If equation (4) is valid

\[
\frac{I_{\text{pos,Fpos}}}{I_{\text{pos}}} \geq \frac{I_{\text{neg,Fpos}} + I_{\text{pos,Fpos}}}{I_{\text{neg}} + I_{\text{pos}}}
\]  

(5)

also applies.

As the sum of positive faeces carriers with positive lymph node findings and with negative lymph node findings \( I_{\text{pos,Fpos}} + I_{\text{neg,Fpos}} \) corresponds to that of the total number of positive faeces findings \( I_{\text{pos,Fpos}} \) in Salmonella carriers, the following results for the sensitivity \( S_F \) of the bacteriological examination of faeces:

\[
S_F = \frac{I_{\text{pos,Fpos}}}{I_{\text{pos}}} = \frac{I_{\text{neg,Fpos}} + I_{\text{pos,Fpos}}}{I_{\text{neg}} + I_{\text{pos}}}
\]  

(6)

Among the total of 391 animals involved in the study which exhibited positive findings in the lymph nodes \( I_{\text{pos}} = 391 \), 91 showed positivity in their faeces as well \( I_{\text{pos,Fpos}} = 91 \). Thus, the resulting estimate of the sensitivity of faeces examination \( S_F \) will show a maximum of 23.3%.

In a corresponding way, it has been possible to refer the sensitivity of lymph node examination to the Salmonella carriers with positive faeces findings. Among the number of 445 swine involved in the study which had been demonstrated to be Salmonella carriers on the basis of the findings in faeces \( I_{\text{pos}} = 445 \), there were again 91 animals which yielded positive findings in faeces as well as in the intestinal lymph nodes \( I_{\text{pos,Lpos}} = I_{\text{pos,Fpos}} = 91 \). The sensitivity \( S_L \) of lymph node examination is calculated as

\[
S_L \leq \frac{I_{\text{pos,Lpos}}}{I_{\text{pos}}} = 20.4\%
\]  

(7)

In a strict sense, the estimates of sensitivity refer only to those Salmonella carriers which yielded a positive result in at least one of the two bacteriological examinations, i.e. to animals which, on an average, would seem to be more loaded with salmonellae than carriers exhibiting two negative findings. However it cannot be clearly stated as to what degree the sensitivity of detecting the agent is smaller among the total population of infected animals.

The sensitivity of bacteriological examination with regard to \( PA_h \) must be less than with regard to \( PA_a \) because animals which have recovered from the infection cannot reveal a positive bacteriological finding. Of a total of 1178 swine which because of their antibody value of more than 30% could be regarded as being or having been infected, only 162 (13.8%) were recognized by the examination of faeces and 156 (13.2%) on account of the lymph node findings. Even a combination of both types of examination would have resulted in positive bacteriological findings in a mere 267 animals (22.7%).

As a consequence, the true number of pigs which are or have been infected must be assumed to be much higher than initially suggested by the proportion of positive bacteriological findings.

The frequency of detection of salmonellae in the swine involved in the study and the resulting estimates of the true prevalence \( PA_a \) and \( PA_h \) established in association with the sensitivity are shown in Table 1.

### Sensitivity of serological examination with regard to the prevalence of actually infected animals (\( PA_a \))

Statements as to the sensitivity can be made only in dependence on the cut-off level. In favour of a high specificity we have chosen an antibody level of 30% as cut off. Among the 749 swine reliably confirmed as carriers of infection on the basis of the bacteriological findings in faeces or lymph nodes, only 267 revealed an antibody level of more than 30% and were classified as positive. With regard to the recognition of bacteriologically confirmed Salmonella carriers, this corresponded to a sensitivity level of 35.7%. Again, the true sensitivity will be even lower, taking into account all Salmonella carriers. The estimates of the true prevalence resulting from the apparent prevalence and the sensitivity have also been listed in Table 1. It is shown that the proportion of carriers, recognized by serological examination is higher than the proportion recognized by bacteriological examination of faeces or lymph nodes. The results underline the possibility to estimate the risk of Salmonella introduction into the food chain on the basis of serological examination of slaughter pigs (Nielsen et al. 1995; Christensen et al. 1999; Steinbach and Staak 2001).

### Evaluation of the Salmonella Status of a Herd

As a measure of the quantitative Salmonella contamination of a herd, the proportion of animals with positive bacteriological findings among the animals of the herd having been examined offers itself. It is also referred to as seeming prevalence (AP). If
the specificity of examination is nearly 100% the expected value for AP equals the product of the real proportion of infected animals (PA) and the sensitivity (S) of examination (equation 1).

Consequently, the real prevalence PA can be estimated by the ratio of seeming prevalence AP to the sensitivity of bacteriological examination. Using the same method with the same sensitivity it is possible to evaluate and compare the Salmonella status of herds directly by the seeming prevalence (AP). It is possible even without exact knowledge of the sensitivity.

Serological findings may also be used for a quantitative evaluation of the Salmonella situation in a herd. Both the mean antibody levels determined in the serum or meat juice from animals of a herd, and the proportion of animals exhibiting an antibody level above a given cutoff may serve as quantitative measures of a serologically defined Salmonella status. In contrast to bacteriological evaluation of a herd, animals in whom there has been a complete elimination of salmonellae after previous exposure may show positive findings. On the other hand, animals having become infected only a short period ago may lack, despite the presence of salmonellae, reactions that can be demonstrated by serology. Despite these potential errors, there is a good correlation between the serological Salmonella status and Salmonella contamination of a batch to be slaughtered or a herd (Steinbach and Staak, 2001). This correlation will suffice to use the results of serological meat examination to control the risk of infection for the consumer originating from the pig population involved (Nielsen et al., 1995; Christensen et al., 1999).

Bacteriological diagnosing of herds
In the context of epidemiology and epizootics control, it is necessary to distinguish between infected herds and herds being completely Salmonella-free, i.e. a qualitative distinction between contaminated and non-contaminated herds. Only an absolute absence of the agent will exclude a potential for spreading the agent within the herd or a risk of infection originating from the herd.

The results of the bacteriological examination of faeces and intestinal lymph nodes, and the combined results of both examinations served as criteria for a qualitative evaluation of herds. In Table 2, these parameters have been listed together with the conditions of classification and the resulting frequencies for slaughter batches or herds classified as positive or negative.

However, without knowledge of the sensitivity of the underlying diagnosis for a herd, it is not possible to estimate, even with an approximative reliability, the proportion of herds which are truly Salmonella-free (1 – PA a) or the proportion of herds even without even a history of Salmonella infections (1 – PA h). The sensitivity of the detection of contaminated herds will be limited because usually it is not possible to examine all animals of a herd. An examination of random samples always involves the risk of selecting, by chance, only Salmonella-free animals from a herd which also includes infected animals. In the following, this risk will be referred to as ‘sampling error’ (SRS). Under conditions of equal proportion of infected animals within a herd, the sample sensitivity, i.e. the probability that the selected animals include at least one infected animal, will increase with an increasing sample size. With a decreasing proportion of infected animals among the herd, this sensitivity will decrease. It may become negligibly small if only single animals of a herd harbour the agent. (If within a herd of 1000 animals, only three are infected, the probability of detecting at least one carrier of the infection by examining a sample of 10 animals would be a mere 3%). Although the herd was an infected one, 97% of all examinations referring to 10 animals would classify the herd as Salmonella-free.)

However, even if an infected animal was examined, this would not necessarily yield a positive result. This error has already been referred as sensitivity (S) of the examination.

**Table 1. Estimate of true prevalence of Salmonella free animals among the swine covered by the study**

<table>
<thead>
<tr>
<th>Criterium of prevalence</th>
<th>Animals covered</th>
<th>No. of positive findings</th>
<th>Seeming prevalence (%)</th>
<th>Existing infection*</th>
<th>Existing or preceding infection**</th>
<th>PA a</th>
<th>PA h</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Bacteriological findings</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Faeces positive</td>
<td>11 960</td>
<td>444</td>
<td>3.7</td>
<td>≤23.3</td>
<td>≤13.8</td>
<td>15.9</td>
<td>26.8</td>
</tr>
<tr>
<td>Lymph nodes positive</td>
<td>11 960</td>
<td>396</td>
<td>3.3</td>
<td>≤20.5</td>
<td>≤13.2</td>
<td>16.1</td>
<td>25.0</td>
</tr>
<tr>
<td>Faeces or lymph nodes positive</td>
<td>11 960</td>
<td>748</td>
<td>6.3</td>
<td>***</td>
<td>≤22.7</td>
<td>***</td>
<td>27.8</td>
</tr>
<tr>
<td><strong>Serological findings</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Antibody level &gt; 30%</td>
<td>11 896</td>
<td>1178</td>
<td>9.9</td>
<td>≤35.6</td>
<td>***</td>
<td>34.2</td>
<td>***</td>
</tr>
<tr>
<td><strong>Combined findings</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Antibody level &gt; 30 or faeces positive or lymph nodes positive</td>
<td>11 896</td>
<td>1134</td>
<td>13.9</td>
<td>***</td>
<td>***</td>
<td>***</td>
<td>***</td>
</tr>
</tbody>
</table>

*Refers to bacteriological findings made independently.  **Refers to serological findings made independently. ***Cannot be stated for lack of an independent reference parameter.
In the context of serological diagnosis of herds, not only herds including at least one current Salmonella carrier should therefore be regarded as Salmonella-exposed but also all herds including animals with antibodies attributed to Salmonella infections. As antibody levels above 30% indicate a preceding Salmonella exposure (specificity approaching 100%, cf. 4.1), we defined a herd as serologically positive if at least one animal in that herd had exhibited an antibody level of more than 30%.

The results of qualitative diagnosis in herds based on serological examination has been listed in Table 2, as well as a classification of herds based on a combination of bacteriological and serological findings.

### Relation between Seeming and True Frequency in Salmonella-free Swine Herds

The epidemiological evaluation of the situation and strategic considerations regarding Salmonella control require an answer to the question as to which proportion of the herds shown to be negative by the examination can be regarded as truly Salmonella-free.

The classification of a herd as infected or free from the agent is decided upon by establishing whether examination has resulted in positive findings in at least one animal or whether the samples examined have yielded exclusively negative results. Thus, the probability (L) that examination will result in negativity for a herd is determined by the true prevalence (PAi) of actually infected animals and the prevalence (PAi) of animals having been or being infected within the herd, the number (n) of animals examined (sample size = n) and the sensitivity (S) of the examination. If the animals examined are considered as random samples of very large statistical populations, the resulting value for L will be

\[
L = [1 - (PA \times S)]^n \tag{8}
\]

If z herds exhibiting prevalence figures PA1, PA2, ..., PAz, ..., PAz, examination sensitivity values S1, S2, ..., Sz, ..., Sz, and sample sizes n1, n2, ..., nz, ..., nz, are examined, the expected value of the number \(N_z\) of herds with exclusively negative individual findings will be calculated as

\[
N_z = \sum_{i=1}^{z} L_i = \sum_{i=1}^{z} [1 - PA_i \times S_i]^{n_i} \tag{9}
\]

Table 3 depicts the relationship between the true prevalence (PAi), the sensitivity (S), the sample size and the probability of a false-negative classification of a herd. It becomes evident to what extent the frequency of infected herds being falsely classified as negative is influenced by the level of the true prevalence and the sensitivity of the examination. Even if the sensitivity of the examination was 100%, a sample size of >20 would be necessary to detect a herd with a true prevalence of 10% and confirm it as infected with an adequate reliability. In the case of herds with only 0.5% infected animals, 67% of the herds would still be erroneously classified as negative, even at a 100% sensitivity of the method and a sample size of 80.

As the proportion of positive findings (APA) determined in the sample from a herd constitutes an estimate of the product \(PA_i \times S_i\) (equation 1), the above mentioned equation (9) allows to calculate the expected number of consistently negative findings in the examination of herds, depending on the APAi values and sample sizes \(n_i\).

Using this connection, we tried to obtain information on the true status of the batches or herds which had consistently produced negative results in the context of the study.

We set out from the formulation of a null hypothesis. The distribution of the proportions of positive findings revealed in slaughter batches represents the true distribution of prevalence and batches designated as negative are truly Salmonella-free. With the aid of equation (9), we calculated the expected number of herds with exclusively negative findings, assuming the hypothesis to be valid. As an estimate of the values, \(PA_i \times S_i\), we used the seeming prevalence values (APAi values, c.f. 3) established for the herds. The calculated expected values have been listed in column 3 of Table 4. With regard to all five ways of examining and parameters of prevalence, respectively, the expected figures for negative or positive herds showed highly significant \((2 \times 2\ table, \ chi-squared\ test, P < 0.001)\) differences from the true frequencies observed (column 2). As a second step, we calculated the expected values that would have resulted if in reality, the product of true prevalence and sensitivity of the examination \((PA_i \times S_i)\) for all batches

### Table 2. Parameters used for qualitative evaluation of the Salmonella status of slaughter batches or herds and resulting numbers of positive and negative herds

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Conditions for classification of a herd</th>
<th>No. of batches classified as:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Positive</td>
<td>Negative</td>
</tr>
<tr>
<td>Bacteriological parameters</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Faeces</td>
<td>Salmonella detected in faeces of at least one animal</td>
<td>All faeces specimens bacteriologically negative</td>
</tr>
<tr>
<td>Lymph node</td>
<td>Salmonella detected in intestinal lymph nodes of at least one animal</td>
<td>All intestinal lymph nodes bacteriologically negative</td>
</tr>
<tr>
<td>Serological parameter</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Antibody level</td>
<td>Antibody level in at least one animal &gt;30%</td>
<td>Antibody levels in all animals ≤30%</td>
</tr>
<tr>
<td>Combined findings</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Faeces and lymph node</td>
<td>Faeces or lymph node positive</td>
<td>Faeces and lymph node negative</td>
</tr>
<tr>
<td>Antibody level, faeces and lymph node</td>
<td>Faeces or lymph node or antibody level positive</td>
<td>Faeces and lymph node and antibody level negative</td>
</tr>
</tbody>
</table>

\[
N_z = \sum_{i=1}^{z} L_i = \sum_{i=1}^{z} [1 - PA_i \times S_i]^{n_i} \tag{9}
\]

\[
L = [1 - (PA \times S)]^n \tag{8}
\]
This would mean that the true prevalence level was at least 0.1, 0.5, 1.0 or 2.0%, respectively. The resulting expected values have been listed in columns 4–7 of Table 4. Even if assuming that all batches classified as negative came from infected herds with a very low prevalence (seeming prevalence \(= P_A \times S_i = 0.1\%\)), the expected number of consistently negative findings (column 4) would have been higher than the one we found (column 2). Only if the product of prevalence and sensitivity (seeming prevalence) in herds classified as negative was at a level of 0.5–2.0%, the number of negative batches expected would be in conformity with the expected number. This means that the number of batches (280 or 41.2%) with exclusively negative findings with regard to bacteriology and serology (prevalence parameter \(P_{FLH}\)) is consistent with the assumption that all herds covered were Salmonella-infected and the true prevalence in the herds designated as negative were at least 2% \(P_A \times S_i = 2\%\), \(S_i < 1\).

We repeated the same considerations and calculations including only those slaughter batches from which at least 10 animals had been examined. The frequencies found and calculated have been listed in Table 5. On principle, the result obtained has been the same.

The analysis made has shown that even a Salmonella contamination of all herds would be in harmony with the data observed and the frequency of detection in the study. However, it does not yet prove that this is in fact the case. Theoretically, the high number of negative batches could also result from a true absence of the agent from a larger number of the herds designated as being free from the agent and that instead, other batches designated as negative were in reality exposed to salmonellae by more than 2%. In a first view, the concepts of an absence of the agent adopted from the epidemiology of classical epizootics suggest such a situation. They are based on the idea that the agent having become introduced into a herd will spread most rapidly and affect a large part of the population (e.g. at least 10% of the animals) within a short period. If this is the case, very low prevalence rates will be rare because these occur only immediately after introduction of the agent. Practically, under such circumstances, there will be only herds truly free from the agent and herds in which at least 10% of the animals are, or were, infected. However, the distribution of the seeming prevalence of animals being or having been infected (positive bacteriological finding or antibody level >30%) has shown that, contrary to such expectations, the relative frequencies of lower prevalences were even higher than for all other prevalence ranges (Fig. 1). The high proportion of slaughter batches with an existing but very low prevalence disproves the concept adopted from the epidemiology of classical epizootics regarding Salmonella infections in swine being of interest in the context of consumer protection. Obviously, salmonellae often occur at a very low

<table>
<thead>
<tr>
<th>Parameter</th>
<th>No. of batches found with negative findings only</th>
<th>Expected frequency of batches with exclusively negative findings assuming the following true prevalence levels in batches with negative findings only</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bacteriological findings</td>
<td>568</td>
<td>559*</td>
</tr>
<tr>
<td>Lymph node</td>
<td>573</td>
<td>564*</td>
</tr>
<tr>
<td>Faeces and lymph node</td>
<td>513</td>
<td>505</td>
</tr>
<tr>
<td>Antibody level</td>
<td>465</td>
<td>459</td>
</tr>
<tr>
<td>Combination of all bacteriological and serological findings</td>
<td>395</td>
<td>391</td>
</tr>
</tbody>
</table>

*Area of correspondence between found and expected frequency.

### Table 4. Frequencies observed and expected values for slaughter batches with exclusively negative findings on examination (679 batches examined by serology)

<table>
<thead>
<tr>
<th>Parameter</th>
<th>No. of batches found with negative findings only</th>
<th>Expected frequency of batches with exclusively negative findings assuming the following true prevalence levels in batches with negative findings only</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bacteriological findings</td>
<td>543</td>
<td>559*</td>
</tr>
<tr>
<td>Lymph node</td>
<td>549</td>
<td>564*</td>
</tr>
<tr>
<td>Faeces and lymph node</td>
<td>479</td>
<td>505</td>
</tr>
<tr>
<td>Antibody level</td>
<td>429</td>
<td>459</td>
</tr>
<tr>
<td>Combination of all bacteriological and serological findings</td>
<td>353</td>
<td>391</td>
</tr>
</tbody>
</table>

*Area of correspondence between found and expected frequency.

### Table 3. Influence of sample size and product of true prevalence (\(P\)) and sensitivity (\(S\)) of the examination on the proportion of infected herds with exclusively negative results

<table>
<thead>
<tr>
<th>No. of animals examined per herd</th>
<th>Expected percentage of infected herds with negative findings on examination only</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>99.5</td>
</tr>
<tr>
<td>10</td>
<td>97.5</td>
</tr>
<tr>
<td>20</td>
<td>95.1</td>
</tr>
<tr>
<td>40</td>
<td>90.4</td>
</tr>
<tr>
<td>80</td>
<td>77.4</td>
</tr>
<tr>
<td>160</td>
<td>59.0</td>
</tr>
<tr>
<td>320</td>
<td>32.8</td>
</tr>
<tr>
<td>0</td>
<td>7.8</td>
</tr>
<tr>
<td>0.60</td>
<td>1.0</td>
</tr>
<tr>
<td>0.80</td>
<td>0.03</td>
</tr>
<tr>
<td>1.00</td>
<td>&lt;0.001</td>
</tr>
</tbody>
</table>

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prevalence over extended periods, or with a prevalence that varies between 0 and low values.

Irrespective of the problem of distinction between exclusively negative findings and truly Salmonella-free herds which is of importance for epidemiology and epizootics control, it has remained meaningful to assess the intensity of Salmonella exposure among herds and the resulting risk for the consumer. Even if a qualitative presence of salmonellae has to be expected in a very large share of swine herds, the existing correlation between serological findings and intensity of Salmonella exposure originating from a herd may be put to use in the sense of consumer protection.

### References


