Annual incidence, prevalence and transmission characteristics of Streptococcus agalactiae in Danish dairy herds

Marshal M. Mweu a,*, Søren S. Nielsen a, Tariq Halasa b, Nils Toft a

a Department of Large Animal Sciences, Faculty of Health and Medical Sciences, University of Copenhagen, Grønnegårdsvej 8, DK-1870 Frederiksberg C, Denmark
b Division of Veterinary Diagnostics and Research, National Veterinary Institute, Technical University of Denmark, Bulowsvej 27, DK-1790 Copenhagen V, Denmark

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ABSTRACT

Contagious mastitis pathogens continue to pose an economic threat to the dairy industry. An understanding of their frequency and transmission dynamics is central to evaluating the effectiveness of control programmes. The objectives of this study were twofold: (1) to estimate the annual herd-level incidence rates and apparent prevalences of Streptococcus agalactiae (S. agalactiae) in the population of Danish dairy cattle herds over a 10-year period from 2000 to 2009 inclusive and (2) to estimate the herd-level entry and exit rates (demographic parameters), the transmission parameter, β, and recovery rate for S. agalactiae infection.

Data covering the specified period, on bacteriological culture of all bulk tank milk samples collected annually as part of the mandatory Danish S. agalactiae surveillance scheme, were extracted from the Danish Cattle Database and subsequently analysed. There was an increasing trend in both the incidence and prevalence of S. agalactiae over the study period. Per 100 herd-years the value of β was 54.1 (95% confidence interval [CI] 46.0–63.7); entry rate 0.3 (95% CI 0.2–0.4); infection-related exit rate 7.1 (95% CI 5.6–8.9); non-infection related exit rate 9.2 (95% CI 7.4–11.5) and recovery rate 40.0 (95% CI 36.8–43.5). This study demonstrates a need to tighten the current controls against S. agalactiae in order to lower its incidence.

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1. Introduction

Streptococcus agalactiae (S. agalactiae) is a contagious obligate pathogen of the bovine mammary gland, which primarily causes subclinical mastitis. Subclinical mastitis causes a substantial economic impact to dairy producers owing to production losses and its detrimental effects on milk quality (Keefe, 1997). Transmission of the pathogen within dairy herds may occur during milking via milkers’ hands, liners and use of common udder cloths contaminated with milk from infected cows (Keefe, 1997). Hiring of relief milkers and purchase of cows or heifers have been associated with the spread of infection between herds (Ager et al., 1994; Edmondson, 2011).

In Denmark, a surveillance and control programme for S. agalactiae has been in place for decades. This was initiated against a backdrop of worrisome infection prevalences in the early 1990s (c.f. Andersen et al., 2003). The control programme was compulsory until 1988 (though the mandatory surveillance carried on) and entailed the identification of infected cows by bacteriological culture of quarter milk samples with subsequent treatment or culling. These measures were supplemented with improved milking practices and hygienic measures to control within-herd spread of infection. Afterwards, there was a switch to a voluntary programme but still with a prohibition to sell cows...
and pregnant heifers from herds declared to be infected (Andersen et al., 2003). These concerted efforts saw a drastic decline in the herd-level prevalence of S. agalactiae from 30 to 40% in 1950 (Anonymous, 1981) to about 2% in 1992, with a 1–2% annual incidence of herd infections (Anonymous, 1980–1992). However, since 2000 the proportion of infected herds has been rising steadily. Monitoring of infection incidence and prevalence is central to evaluating the performance of control programmes (Neave et al., 1966). Given the prohibitive costs and impracticalities of assessing the effectiveness of control measures in field trials, mathematical models have increasingly been employed to play this role (Zadoks et al., 2002; White et al., 2006). Furthermore, these models provide unique opportunities for the description of the dynamics of mastitis transmission (Barlow et al., 2009). The within-herd transmission dynamics of mastitis pathogens, in particular, Streptococcus uberis and Staphylococcus aureus have previously been investigated (White et al., 2001, 2006; Zadoks et al., 2001, 2002). However, to date and to the best of our knowledge, there are no published studies describing the between-herd transmission dynamics of S. agalactiae. An often used parameter to quantify transmission is the transmission rate, $\beta$ which is defined as the average number of secondary infections caused by one infectious individual per unit of time (Keeling and Rohani, 2008). When exploration of the long-term persistence of a pathogen in a population is of interest, it is necessary to take into consideration demographic changes (entries and exits) that occur in the population over time. Knowledge of this transmission characteristic and demographic parameters can be used in modelling the effectiveness of control strategies against S. agalactiae and in the estimation of the basic reproductive ratio, $R_0$ (the average number of secondary infections caused by one infectious individual, throughout its infectious period, in an entirely susceptible population (Keeling and Rohani, 2008)), which reflects a pathogen’s potential for spread.

The objectives of this study were: (1) to estimate the annual herd-level incidence rates and apparent prevalences of S. agalactiae in the population of Danish cattle herds over a 10-year period from 2000 to 2009 inclusive and (2) to estimate the herd-level entry and exit rates (demographic parameters), the transmission parameter, $\beta$, and recovery rate for S. agalactiae infection.

2. Materials and methods

2.1. Data

Data covering the period 1998–2009 inclusive, on bacteriological culture of all bulk tank milk (BTM) samples collected as part of the mandatory Danish S. agalactiae surveillance scheme, were extracted from the Danish Cattle Database. The scheme involves an annual collection of BTM samples by truck drivers during milk collection, after which samples are stored on ice. Within 24 h, they are sent to Eurofins Laboratory, Holstebro, Denmark, for processing. Bacteriological culture of the samples follows the National Mastitis Council (1999) standards, but briefly: for each BTM sample, a 120 µl of milk inoculum is mixed with 9 ml of selective media in a Petri dish containing 5% sterile calf blood, 1% (w/v) aesculin supplied with neomycin sulphate and Polymyxin B, sodium fusidate and Staphylococcus aureus $\beta$-toxin. This mixture is incubated for 18–24 h at 37 °C. Any colonies showing $\beta$-haemolytic activity are counted on each plate, following which one of the colonies is selected and recultured on 5% bovine blood agar with the S. aureus $\beta$-toxin to elicit the characteristic CAMP reaction (named after the discoverers of the phenomenon: Christie, Atkins and Munch-Petersen) (Christie et al., 1944). Isolates that are positive in the CAMP as well as in a Lancefield group B latex agglutination test are identified as S. agalactiae. Notably, the sensitivity and specificity of the BTM bacteriological culture have been estimated to be 68.0% and 99.7%, respectively (Mweu et al., 2012).

For some herds in certain years, particularly if the first screening result was positive, upon a farmer’s request repeat testing was carried out. However, to ensure consistency with the rest of the data the first observation for any given herd in a given year was used to define the status of the herd. Any missing observations for herds over the 10-year period were considered to arise from either: (1) an omission from surveillance or contamination of samples prohibiting bacteriological culturing or (2) an exit from the population of herds which could be a permanent or temporary cessation in milk production followed by a re-entry (resumption in production). In that case, an entry into the population could either be a new entry (new dairy enterprise) or a re-entry as formerly explained. For the purpose of this study, we considered an entry to have occurred when it was preceded by at least two years with missing observations and an exit when it was succeeded by at least two years with missing observations.

2.2. Case definition

A case was defined as one from which S. agalactiae was cultured from its BTM sample as previously described. A non-case was that from which the pathogen was not identified by the same bacteriological procedure.

2.3. Statistical analysis

2.3.1. Apparent prevalences

Estimation of the annual apparent prevalences (Ap) and their associated 95% exact binomial confidence intervals was carried out using Stata software (Stata version 11.2, Stata Corporation, College Station, TX, USA).

2.3.2. Incidence, entry, exit, recovery and transmission ($\beta$) rates

Dohoo et al. (2009) contend that in open populations calculation of rates as opposed to risks is befitting. Consequently, we computed the annual incidence rates based on an approximation of the amount of herd-time at risk for the rate denominator as:

$$\text{Rate} = \frac{\text{No. of newly infected herds in a specific year (cases)}}{\text{average no. at risk} \times \text{time}}$$
where average no. at risk = no. at risk at the start of the year + \{0.5 \times (susceptible entries + recoveries – cases – susceptible exits)\}.

The associated 95% confidence intervals (CI) were calculated using an exponential error factor (EF) for incidence rates (Kirkwood and Sterne, 2003):

\[ \text{lower CI limit} : \text{rate} \times EF^{-1}; \]

\[ \text{upper CI limit} : \text{rate} \times EF; \]

where \( EF = \exp(1.96 / \sqrt{d}) \) and \( d \) is the rate numerator.

Based on the pattern given by the annual incidence rates (Fig. 1), we assessed the significance of the difference between pooled incidence rates before and after 2005 by incorporating a time covariate in both Poisson and negative binomial regression models fitted to the data. The fits of the models were compared using likelihood ratio tests (Dohoo et al., 2009).

However, the rates of entry (\( v \)), exit and recovery (\( r \)) were calculated as averages because they were assumed to be constant during the 10-year period (Fig. 2). Both Poisson and negative binomial regression models were used to obtain the average estimates. Notably, a separate exit rate was calculated for non-case (non-infection-related exit rate, \( \mu_e \)) and case herds (infection-related rate, \( \mu_k \)). The proportion of entries into the population of non-cases (\( \theta \)) and cases (1 – \( \theta \)) was derived by dividing the mean numbers joining the respective populations by the mean number of total entries during the entire period, i.e. \( n_{\text{non-cases}} / N_e \) and \( n_{\text{cases}} / N_e \), where \( n_{\text{non-cases}} \) and \( n_{\text{cases}} \) are the mean number of non-case and case entries, respectively, and \( N_e \) is the mean of the total number of entries.

To estimate the parameter \( \beta \), we used the framework of an SIS (Susceptible–Infected–Susceptible) model (Fig. 3) for the transmission of \( S. \) agalactiae between herds. Its use is motivated by the fact that infected herds upon recovery are capable of being re-infected. Thus, the population of dairy herds was accordingly partitioned into \( S \) (non-cases) and \( I \) (cases) states. New herd infections with \( S. \) agalactiae were assumed to occur at the rate \( \beta \times S \times I / N \), where \( \beta \) is the transmission rate, \( S \) the number of susceptible herds, \( I \) the number of infected herds and \( N \) is the total number of herds present in a specific year (Zadoks et al., 2002). As with the average rates, the number of new infections, \( C \), in each year, was modelled assuming both Poisson and negative binomial distributions:

\[ \varepsilon [\ln(C)] = \ln(\beta) + \ln \left( S \times \frac{I}{N} \right) \]

where \( \varepsilon \) is the expected value and \( \ln(S \times I / N) \) was used as a model offset.

Considering the shape of the incidence curve in Fig. 1, we also assessed whether the estimate of \( \beta \) differed before and after 2005 by incorporating a time covariate in the models.

3. Results

A frequency distribution of the number of times herds had been infected during the 10-year period is displayed in Table 1. A total of 765 (7.65%) herds had been infected at least once over the course of the study period. The median duration of infection was 2 years.

Descriptive statistics on the annual entry, exit, recovery, incidence and prevalence of \( S. \) agalactiae are presented in Table 2.

3.1. Apparent prevalences

The annual prevalence estimates of \( S. \) agalactiae are graphed in Fig. 4. The prevalence increased steadily over time with the lowest and highest values recorded in years 2000 and 2008, respectively.

3.2. Incidence rates

The annual herd-level incidence rates of \( S. \) agalactiae are displayed in Fig. 1. As with Ap, there was a general increase in the incidence of herd infections over the 10-year period. However, there were two distinctive incidence patterns observed before and after 2005 (\( P < 0.001 \)). As was the case with Ap, the lowest and highest rates were observed in years 2000 and 2008, respectively.

3.3. Entry, exit, recovery and transmission rates

The herd-level parameter estimates are summarised in Table 3. For all the parameters, a negative binomial regression model provided a better fit to the data than a corresponding Poisson model (\( P < 0.001 \)). The rate at which herds joined the population of dairy herds (0.3 per 100 herd-years [95% confidence interval (CI) 0.2–0.4]) was lower than the rate at which they exited (7.1 per 100 herd-years [95% CI 5.6–8.9]; 9.2 per 100 herd-years [95% CI 7.4–11.5], for infection and non-infection-related rates, respectively). A higher proportion of herds joined the susceptible pool of herds (0.97) as compared to the infected one (0.03). The value of the \( S. \) agalactiae-specific \( \beta \) parameter was estimated to be 54.1 new herd infections per 100 herd-years (95% CI 46.0–63.7). This value remained constant before and after 2005 (\( P = 0.82 \)).

4. Discussion

The rising trend in both the incidence and prevalence after a period of quiescence is indicative of a possible re-emergence of the pathogen in the Danish dairy herd population. In Canada and some North-European countries, \( S. \) agalactiae has been considered to be at the brink of eradication (Pitkalä et al., 2004; Østerås et al., 2006; Piepers et al., 2007; Sampimon et al., 2009; Olde Riekink et al., 2010). The resurgence of this mastitis problem may be suggestive of either: (1) possible emergence of new and better adapted \( S. \) agalactiae strains or (2) a breakdown in the stringent implementation of the ‘5-point plan’ for mastitis control developed in the 1960s (Neave et al., 1969). Recent work by Zadoks et al. (2011) involving multi-locus sequence typing of 111 isolates collected from a 2009 Danish BTM survey revealed that the commonest \( S. \) agalactiae strains were sequence types (ST)1 (28%) and ST23 (23%), which were previously primarily associated with human
Fig. 1. A plot of the annual herd-level incidence rates of *Streptococcus agalactiae* in the population of Danish dairy herds.

Fig. 2. Plots of the annual herd-level recovery, non-infection and infection exit rates from the population of Danish dairy herds.
infection. With respect to adherence to the 5-point mastitis plan, it is particularly noteworthy that only selective dry cow therapy is permitted in Nordic countries (Olsen, 1975; Funke, 1988). In Denmark, the number of dairy herds has been declining with the average herd size steadily increasing. These changing herd dynamics could influence the frequency of S. agalactiae. With increasing herd size, the demand for labour is expected to rise. This may bring about a heightened risk of infection for herds as humans may serve as a source of infection for cattle (Zadoks and Schukken, 2006). This situation is expected if on-farm biosecurity measures are not commensurately beefed up. Moreover, a rapid herd expansion may increase the need for purchasing animals which may result in elevated risk

### Table 1

Frequency distribution of the number of times herds had been infected during the period 2000–2009 in the population of Danish dairy herds.

<table>
<thead>
<tr>
<th>No. of times infected</th>
<th>0</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
</tr>
</thead>
<tbody>
<tr>
<td>Frequency, n (%)</td>
<td>9238</td>
<td>379</td>
<td>142</td>
<td>104</td>
<td>46</td>
<td>35</td>
<td>29</td>
<td>11</td>
<td>4</td>
<td>13</td>
<td>2</td>
</tr>
</tbody>
</table>

Median duration of infection – 2 years.

### Table 2

Descriptive statistics on the annual entry, exit, recovery, incidence and prevalence of Streptococcus agalactiae in the population of Danish dairy herds.

<table>
<thead>
<tr>
<th>Year</th>
<th>N</th>
<th>bENT</th>
<th>cENT</th>
<th>dINI</th>
<th>eANI</th>
<th>fIE</th>
<th>gIEr</th>
<th>hREC</th>
<th>iREC</th>
<th>jINS</th>
<th>kANS</th>
<th>lNIE</th>
<th>mNIEr</th>
<th>nINC</th>
<th>oINCr</th>
<th>pINF</th>
<th>qAp</th>
</tr>
</thead>
<tbody>
<tr>
<td>2000</td>
<td>9886</td>
<td>20</td>
<td>0</td>
<td>113</td>
<td>114</td>
<td>6</td>
<td>5.3</td>
<td>57</td>
<td>50</td>
<td>9947</td>
<td>9559</td>
<td>788</td>
<td>8.2</td>
<td>65</td>
<td>0.7</td>
<td>118</td>
<td></td>
</tr>
<tr>
<td>2001</td>
<td>8207</td>
<td>18</td>
<td>0</td>
<td>118</td>
<td>130</td>
<td>11</td>
<td>8.5</td>
<td>43</td>
<td>33.1</td>
<td>9768</td>
<td>9140</td>
<td>1238</td>
<td>13.5</td>
<td>78</td>
<td>0.9</td>
<td>128</td>
<td></td>
</tr>
<tr>
<td>2002</td>
<td>7662</td>
<td>8</td>
<td>0</td>
<td>128</td>
<td>140</td>
<td>11</td>
<td>7.9</td>
<td>38</td>
<td>27.1</td>
<td>8079</td>
<td>7658</td>
<td>814</td>
<td>10.6</td>
<td>73</td>
<td>1.0</td>
<td>170</td>
<td></td>
</tr>
<tr>
<td>2003</td>
<td>7329</td>
<td>49</td>
<td>0</td>
<td>170</td>
<td>175</td>
<td>12</td>
<td>6.9</td>
<td>65</td>
<td>37.1</td>
<td>7492</td>
<td>7238</td>
<td>534</td>
<td>7.4</td>
<td>8.2</td>
<td>12</td>
<td>180</td>
<td></td>
</tr>
<tr>
<td>2004</td>
<td>6627</td>
<td>10</td>
<td>0</td>
<td>180</td>
<td>164</td>
<td>13</td>
<td>7.9</td>
<td>75</td>
<td>45.7</td>
<td>7149</td>
<td>6807</td>
<td>712</td>
<td>10.5</td>
<td>56</td>
<td>0.8</td>
<td>149</td>
<td></td>
</tr>
<tr>
<td>2005</td>
<td>5416</td>
<td>24</td>
<td>1</td>
<td>149</td>
<td>180</td>
<td>20</td>
<td>11.1</td>
<td>46</td>
<td>25.6</td>
<td>6478</td>
<td>5906</td>
<td>1087</td>
<td>18.4</td>
<td>127</td>
<td>2.2</td>
<td>207</td>
<td></td>
</tr>
<tr>
<td>2006</td>
<td>5231</td>
<td>10</td>
<td>0</td>
<td>207</td>
<td>197.5</td>
<td>7</td>
<td>3.5</td>
<td>92</td>
<td>46.6</td>
<td>5209</td>
<td>5060</td>
<td>319</td>
<td>6.3</td>
<td>80</td>
<td>1.6</td>
<td>195</td>
<td></td>
</tr>
<tr>
<td>2007</td>
<td>4714</td>
<td>21</td>
<td>1</td>
<td>195</td>
<td>196</td>
<td>15</td>
<td>7.7</td>
<td>80</td>
<td>40.8</td>
<td>5036</td>
<td>4782</td>
<td>513</td>
<td>10.7</td>
<td>96</td>
<td>2.0</td>
<td>196</td>
<td></td>
</tr>
<tr>
<td>2008</td>
<td>4430</td>
<td>13</td>
<td>2</td>
<td>196</td>
<td>204.5</td>
<td>10</td>
<td>4.9</td>
<td>76</td>
<td>37.2</td>
<td>4518</td>
<td>4363</td>
<td>298</td>
<td>6.8</td>
<td>101</td>
<td>2.3</td>
<td>213</td>
<td></td>
</tr>
<tr>
<td>2009</td>
<td>4258</td>
<td>20</td>
<td>1</td>
<td>213</td>
<td>205</td>
<td>11</td>
<td>5.4</td>
<td>97</td>
<td>47.3</td>
<td>4217</td>
<td>4129</td>
<td>202</td>
<td>4.9</td>
<td>91</td>
<td>2.2</td>
<td>198</td>
<td></td>
</tr>
</tbody>
</table>

IEn; REC; NIEr; INCr expressed as number of events per 100 herd-years at risk. Ap expressed as a percentage. ANI⁎ INI⁎ [0.5 × (LENT + INC – REC – IE)]; ANS = INS + [0.5 × (S.ENT + REC – INC – NIE)].

| a | Only counts of entries presented as rate denominator was indeterminate.
| b | Susceptible entries.
| c | Infected entries.
| d | Initial no. infected.
| e | Average no. infected.
| f | Infection exits.
| g | Infection exit rate.
| h | Recoveries.
| i | Recovery rate.
| j | Initial no. susceptible.
| k | Average no. susceptible.
| l | Non-infection exits.
| m | Non-infection exit rate.
| n | Incidence.
| o | Incidence rate.
| p | No. infected.
| q | Apparent prevalence.
of introducing *S. agalactiae*. There were 2 constant incidence patterns observed in the dairy herd population with the transition between them marked by a sudden surge in 2005. This observation coincides with a Danish ministerial directive issued in the same year (Anonymous, 2005), which authorised the lifting of a movement ban imposed on *S. agalactiae* infected herds. However, according to the order, farmers with infected herds were thereafter obligated to disclose their herd status to all coming into contact with their respective herds. Indeed, in light of our results, there is a pressing need to review the current policy pertaining to the control of *S. agalactiae*.

The parameter estimates in this study correspond to an $R_0$ value of 1.1 ($\beta/r + \mu_k$). This implies that on average each infected herd leads to more than one new herd infection in a susceptible population of Danish dairy herds. Therefore, given the value of $R_0$ it would be generally expected that incidence would increase as was exemplified by the shape of the incidence curve in Fig. 1. Successful control of transmission is said to be achieved when $R_0$ is reduced to a value below unity, which signifies that infection would not persist. This study thus illustrates a need to strengthen existing control measures against *S. agalactiae* in order to reduce $R_0$, and hence incidence. However, it remains debatable as to whether elimination of *S. agalactiae* in this population is feasible even in the absence of infected animal movements since infection from humans is still a threat.

In the estimation of $\beta$, we implicitly assumed homogeneous mixing of herds. This assumption could have been violated in two ways: (1) the data were overdispersed suggesting the possibility of clustering and (2) the fact that farms are spatially distributed entities, in which case assuming such a mixing pattern would be erroneous (Heath et al., 2008). However, Newman (2002) shows that in a network setting, the $\beta$ parameter can be estimated in an analogous way only that its interpretation would be slightly different; the rate of transmission from an infective node (herd) to a susceptible node along a given edge (e.g. infected movement) per unit of time. Thus, the $R_0$ estimated from a non-network setting would have to be adjusted for the average number of neighbours each farm trades with minus 1. The minus 1 accounting for the fact that every infectious herd, except for the initial infective, must have acquired infection from one of its neighbours.

### Table 3

Parameter estimates for rates of entry, exit, recovery and transmission in an SIS (Susceptible–Infected–Susceptible) model that represents the dynamics of *Streptococcus agalactiae* transmission in the population of Danish dairy herds. Rates of entry, exit, recovery and transmission are expressed as number of events per 100 herd-years at risk.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Symbol</th>
<th>Estimate</th>
<th>95% CI</th>
<th>Alpha</th>
<th>Mean</th>
<th>OF</th>
</tr>
</thead>
<tbody>
<tr>
<td>Entry rate</td>
<td>$\sigma$</td>
<td>0.3</td>
<td>0.2–0.4</td>
<td>0.26</td>
<td>19.8</td>
<td>6.1</td>
</tr>
<tr>
<td>Exit rate unrelated to infection</td>
<td>$\mu_i$</td>
<td>9.2</td>
<td>7.4–11.5</td>
<td>0.12</td>
<td>650.5</td>
<td>79.1</td>
</tr>
<tr>
<td>Exit rate related to infection</td>
<td>$\mu_k$</td>
<td>7.1</td>
<td>5.6–8.9</td>
<td>0.05</td>
<td>11.6</td>
<td>1.6</td>
</tr>
<tr>
<td>Recovery rate</td>
<td>$r$</td>
<td>40.0</td>
<td>36.8–43.5</td>
<td>0.01</td>
<td>66.9</td>
<td>1.7</td>
</tr>
<tr>
<td>Transmission parameter</td>
<td>$\beta$</td>
<td>54.1</td>
<td>46.0–63.7</td>
<td>0.06</td>
<td>85.4</td>
<td>6.1</td>
</tr>
<tr>
<td><em>Proportion of entries that is susceptible</em></td>
<td>$\theta$</td>
<td>0.97</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

* a Fraction.
* b Confidence interval.
* c Overdispersion factor is calculated as: 1 + (alpha × mean).
(Diekmann et al., 1998). Additionally, the computed $\beta$ is an aggregate parameter encompassing all potential sources of transmission. Although calculation of source-specific transmission parameters would have been preferable, this was not possible in our study as only aggregated data on the number of newly infected herds were available. Thus from the estimated $\beta$, it is difficult to deduce the relative importance of the individual sources in the transmission mechanism of the pathogen.

Bacteriological culture does not correctly identify all infected herds because its sensitivity is low (Mweu et al., 2012). We attempted a manual adjustment for misclassification in the parameters of the present study by changing the status of herds that had positive–negative–positive profiles to positive–positive–positive. This adjustment affected incidence, exit and recovery rates (data not shown). For instance, the incidence rate in 2009 decreased from 2.2 cases per 100-herd years to 1.9 per 100 herd-years whereas the infection-related exit and recovery rates reduced to 6.5 and 30.2 per 100 herd-years, respectively. This adjustment method cannot be validated, and there is presently no other available means for adjustment. Nevertheless, the results provide a sneak insight into the magnitude of misclassification inherent in the estimates. Thus, the study findings are “apparent” and can only be strictly treated as such.

5. Conclusion

There was an increasing trend in both the incidence and prevalence of S. agalactiae in the Danish dairy herd population between 2000 and 2009. We also estimated parameters that can be used to model the effectiveness of control strategies against S. agalactiae transmission.

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