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First report of the within-farm prevalence of bovine digital dermatitis in Chinese Holstein dairy cows in Jiangsu, China: A Bayesian modelling approach

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ABSTRACT

Digital dermatitis is one of the most important causes of lameness in dairy cattle, particularly in housed, intensively-managed cattle. The number of modern intensive dairy farms in China has increased markedly in recent years; however, we lack research on digital dermatitis in Chinese dairy cattle. This preliminary study aimed to estimate the prevalence of digital dermatitis on three conveniently selected farms in Jiangsu, China. The washed hind feet of all lactating cows on all three farms were examined during milking with the aid of a mobile phone light source. True prevalence was then estimated from the apparent prevalence using a Bayesian super-population approach to account for the imperfect nature of identifying digital dermatitis in cows during milking. Despite none of the farms having thought it necessary to implement routine digital dermatitis monitoring or control, the disease was found on all three sampled farms. All lesions observed were either chronic M4 or M4.1 type-lesions, with no M2 lesions (i.e. acute ulcerated lesions) observed. The estimated true prevalences on the farms were 7.3% (95% credible interval [CrI]: 5.4%–9.6%), 8.3% (95%CrI: 6.3%–10.8%), and 29.8% (95%CrI: 22.9%–37.2%).

1. Introduction

Bovine digital dermatitis (DD) is an important infectious cause of lameness in dairy cows (Corlevic and Beggs, 2022) and in many studies has been found to be one of the most prevalent hoof lesions observed on dairy farms (Browne et al., 2022; Sadiq et al., 2017; Solano et al., 2016). Lesions of DD are most commonly observed on the hind feet (Laven and Proven, 2000) and display a variety of morphological stages which are commonly described using either the M-system (Berry et al., 2012; Döpfer et al., 1997) or the Iowa DD scoring system (Krull et al., 2014). Both scoring systems are designed to capture the pathophysiology of DD lesion stages, rather than the impact on the animal, as all types of DD lesions can be painful, although some stages may be more severe than others (Thomas et al., 2022).

Since it was first identified, DD has been reported in almost all areas of the world, with the highest herd-level prevalences being recorded in intensive housed systems (Pirkkalainen et al., 2021; Salem et al., 2023; Weber et al., 2023). However, as far as the authors are aware, the prevalence of DD on dairy farms in China has not been well documented in peer-reviewed articles, although large, intensive dairy farms are common (Du et al., 2023). Digital dermatitis may be being overlooked because of the relatively short history of intensive dairy farming in China (Guo et al., 2022), but the nature of intensive dairy farming, with many cows housed together as well as the requirement to handle large volumes of slurry (De Jong et al., 2021) and the need to use outside staff to do prophylactic and/or therapeutic hoof trimming (Yang et al., 2018), means that DD is highly likely to develop and become establish on Chinese dairy farms. In order to increase the awareness of DD in China and, if necessary, to develop targeted control programmes, we need more baseline data on the prevalence of DD on Chinese dairy farms, so that we can identify the need for intervention on such farms.

Estimating within-farm prevalence of DD requires foot inspection. Inspection of feet lifted in a trimming crush is currently considered to be the best method of DD detection, with results obtained during such inspection being commonly used to validate other DD detection methods (Cramer et al., 2018; Solano et al., 2017). However, foot inspection in a trimming crush is a time and labour-intensive approach that is not feasible on many Chinese dairy farms. This is particularly so in Jiangsu

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Province, as dairy farms in Jiangsu do not usually have hoof trimming facilities. Inspection using a trimming crush is thus possible only when outside hoof trimmers are present on farm. A quicker, simpler alternative is to screen for DD in the milking parlour (Solano et al., 2017; Yang et al., 2017b). However, although this method has a high specificity (point estimate 0.84 to 0.999) (Yang et al., 2019) it has a low sensitivity (~0.6) (Cramer et al., 2018; Yang et al., 2017a).

While estimating DD prevalence via observation in the milking parlour, whole herd screening is more accurate than random sampling and takes the same amount of time, as the observer has to be present for the whole of milking whichever method is used (Yang et al., 2019). Nevertheless, even when whole herd screening is used, the imperfect diagnostic performance of parlour screening needs to be accounted for in estimating true DD prevalence on a farm. This is best done using a Bayesian superpopulation approach (Jones and Johnson, 2016). The aim of this preliminary study was therefore to estimate the true prevalence of DD on dairy farms in Jiangsu Province, China, using whole herd screening and a Bayesian superpopulation approach.

2. Materials and methods

2.1. Study area and farm recruitment

The study was conducted in Jiangsu province in Eastern China, an area of China where there are few dairy farms (comprising 1.2% of Chinese dairy cows; China Dairy Data Report 2023). Nine farms owned by leading Chinese dairy groups were contacted to ask whether they would be willing to participate in a pilot study of DD in Jiangsu. Of the nine farms, six expressed concerns regarding visits to the properties by external people. The three remaining farms were included in the study. All three farms kept their cows permanently indoors in cubicle (free stall) barns with concrete walkways and no exercise areas.

Farms 1 and 3 had ~1000 milking cows while farm 2 had ~200. All cows kept on the three farms were Holstein cows. All farms fed their cows principally via a total mixed ration. All farms had herringbone milking parlours with cows being milked three times a day at the time of our visit. The average reported milk yield was ~40 kg/cow day, ~ 28 kg/cow day and ~ 35 kg/cow day for Farms 1, 2 and 3, respectively. Farms 1 and 3 used sand as the bedding material in the cubicles, while on Farm 2 no bedding was observed. At the time of the study, none of the three farms had implemented routine DD monitoring or control.

2.2. DD lesion training and assessment

Before the first on-site clinical examination, the first author (XM) familiarised themselves with the appearance and characteristics of DD lesions in dairy cows by reviewing the literature and examining digital images depicting different DD lesion stages on the interdigital skin of the hind feet. Their ability to identify DD M-stages was then assessed using 100 digital images of DD; success was defined as >90% agreement between XM and the fourth author (DAY), i.e. the two authors identified the same M-stage of DD in >90 of the 100 pictures.

For the first farm visit (Farm 1), DAY demonstrated the examination process: once the milking unit was in place, the hind feet of the cows were cleaned using cleaning water from a hose (at moderate pressure to prevent udder contamination). The hind feet were then examined for DD lesions, aided by the use of a mobile phone light source. The two authors then independently examined a subset of 216 cows (six rows) and recorded their examination results separately. The two results were then compared to ensure that there was still >90% agreement, i.e. the two authors agreed on whether DD was present or absent in over 90% of the 216 examined cows. Once this was confirmed, XM completed the examination of the remaining cows on Farm 1. For the remaining two farms, XM independently screened all the cows on their own.

2.3. Statistical analysis

Data were analysed using a Bayesian superpopulation approach, as per Yang et al. (2019), except that as none of the farms had an apparent prevalence of 0%, there was no zero-inflation to model and, for within-farm prevalence, we modelled the farm effect using fixed effects rather than using a logit-normal random effect. The full model is given as below:

$$X_i \sim Bin(n_i, p_i),$$

$$p_i = \pi_i\theta + (1-\pi_i)(1-\eta),$$

$$Y_i^+ \sim Bin(x_i, \gamma_i),$$

$$\gamma_i = \frac{\theta\pi_i}{p_i},$$

$$Y_i^- \sim Bin(n_i - x_i, 1-\delta_i),$$

$$\delta_i = \frac{\eta(1-\pi_i)}{1-p_i},$$

$$\theta \sim beta(a_\theta, b_\theta),$$

$$\eta \sim beta(a_\eta, b_\eta),$$

$$\pi_i \sim beta(a_i, b_i),$$

where X_i denotes the cases observed during the inspection in the milking parlour and p_i and π_i are the apparent and true prevalences of the i^{th} farm and the i^{th} superpopulation. Sensitivity and specificity are denoted by θ and η, respectively, while Y_i^+ is the number of the true positives (DD observed and truly present); and Y_i^- is the number of false negatives (DD not observed but truly present). Both Y_i^+ and Y_i^- are random variables that follow binomial distributions with their probability parameters being positive predictive value (γ_i) and 1 – negative predictive value (δ_i), respectively.

Beta distributed priors were used for sensitivity, specificity, and the prevalence of DD of each superpopulation. The priors for sensitivity and specificity were based on those used by Yang et al. (2017a). For sensitivity, we used the same mode of 0.65 as Yang et al. (2017a) but reduced the spread of likely values. We estimated that at 95% certainty, true sensitivity was <0.8, producing beta (12.711,7.306). For specificity, we specified a stronger prior than used by Yang et al. (2019); i.e. beta (1500,10). This is based on a mode of ~0.995 with a very small spread (standard deviation = 0.002), reflecting our increased certainty around the specificity of DD lesion identification. The priors for the true prevalences of each superpopulation were derived from estimates provided by either farm manager or the on-farm veterinarian. The best estimate for π_1 was at 5% (mode), with 95% certainty that it was <15%, which corresponds to beta (2.879,36.701); the modal value for π_2 was 15% with a 95% certainty that it was <30%, which corresponds to beta (5.042,23.905). The prior information for π_3 was the same as that for π_1.

Since our model was not identifiable (Johnson et al., 2019), it was particularly important to perform a sensitivity analysis to assess whether changing our priors would have an obvious impact on our posterior inferences. For this analysis, two additional different priors were specified for sensitivity: 1) beta (45.258, 24.831) with a mode at 0.65 and 5th percentile at 0.55, and 2) beta (2.784, 1.961) with a mode at 0.65 and 95th percentile at 0.9. For specificity, we also specified two additional priors: 1) beta (100,2) similar to the main prior for specificity but with a wider spread (standard deviation = 0.01), and 2) beta (34.166,1.335) which is a more diffuse and conservative prior with the mode at 0.99 and 5th percentile at 0.9 (used by Yang et al. (2019)). For the priors for the true prevalences of each of the three superpopulations (i.e. π_1 , π_2 and π_3), we produced three modifications: 1) keeping the original modal value but increasing the 95th percentile to 20%; 2) as for 1) but increasing the 95th percentile to 40%; and 3) changing the mode to 7% but keeping the 95th percentile constant. For each sensitivity analysis scenario, only one prior was changed (all other priors remained the same as in the main analysis). Thus there were seven sensitivity scenarios.

For parameter estimation, the Markov Chain Monte Carlo (MCMC) method was employed using JAGS (Plummer, 2003), with three Markov chains initialised with different values. After discarding the first 10,000 iterations, the next 20,000 iterations were retained, model convergence was assessed using the trace plots and autocorrelation plots.

Table 1
The posterior distributions of model parameters, including posterior mean, standard deviation (SD) and 95% credible intervals (95%CrI).

Parameters	Posterior mean	SD	95%CrI
Sensitivity	70.9%	0.078	55.9%–85.5%
Specificity	99.3%	0.002	98.9%–99.7%
π_1	7.3%	0.013	4.8%–10.1%
π_2	28.3%	0.045	20.4%–37.9%
π_3	8.4%	0.013	6.1%–11.3%

π_i, the true prevalence of the superpopulation i, for $i = 1, 2, 3$.

3. Results

Across all three farms, 2534 cows were examined in the milking parlour, with 56 lesions being identified from 969 cows on farm 1, 42 lesions being identified from 188 cows on farm 2 and 90 lesions being identified from 1377 cows on farm 3. Most lesions (175/188) observed were M4, with 13 M4.1 lesions observed (two on Farm 1, six on Farm 2 and five on Farm 3, respectively). No M2 lesions were observed on any farm. The typical DD lesions detected on the three farms are shown in Fig. 1. Almost all lesions were observed in the typical site for DD, i.e. between the heel bulbs (see Fig. 1 A to D), but DD lesions were also seen on the dew claws on two cows (see Fig. 1 E and F). As only M4 and M4.1 lesions were observed across all three farms and accurately distinguishing between those two lesion types during milking is difficult (Solano et al., 2017), for further analysis the data were amalgamated into DD lesion observed or not observed.

The posterior distributions including posterior mean and 95% credible intervals (95%CrI) of the model parameters are summarised in Table 1. Fig. 2 compares the prior distributions of the five parameters to their posterior distributions. For sensitivity, we observed a small shift of the posterior distribution to the right; for specificity, as expected, the very strong prior resulted in no change between prior and posterior distribution. In contrast to the limited/no changes in sensitivity and specificity, we observed clear differences between the priors and the posteriors for DD prevalence. Our estimated true prevalences of DD at the cow level were 7.3% (95% credible interval [CrI]: 5.4%–9.6%), 29.8% (95%CrI: 22.9%–37.2%), and 8.3% (95%CrI: 6.3%–10.8%), on Farms 1, 2 and 3, respectively. These estimates are compared with the individual farm's apparent prevalence in Fig. 3.

The sensitivity analyses suggested our estimated within-superpopulation prevalences were robust to alterations in the estimates of prior prevalence (Table 2). As expected, small increases in prevalences were observed for all three superpopulations with decreased sensitivity (and vice-versa). However, clear differences were seen when the prior for the specificity was changed. Both sensitivity analyses used a prior with increased uncertainty around our specificity, and thus increased our uncertainty around the prevalences of our superpopulations (see standard deviations in Table 2). In addition, both sensitivity analyses resulted in reduced estimated within-superpopulation prevalences. The effect was most marked in Farms 1 and 3, with little impact on the prevalence estimate for Farm 2, which had an apparent prevalence >3 times higher than the other farms. The same was also true for the CrI, with little impact of altering prior

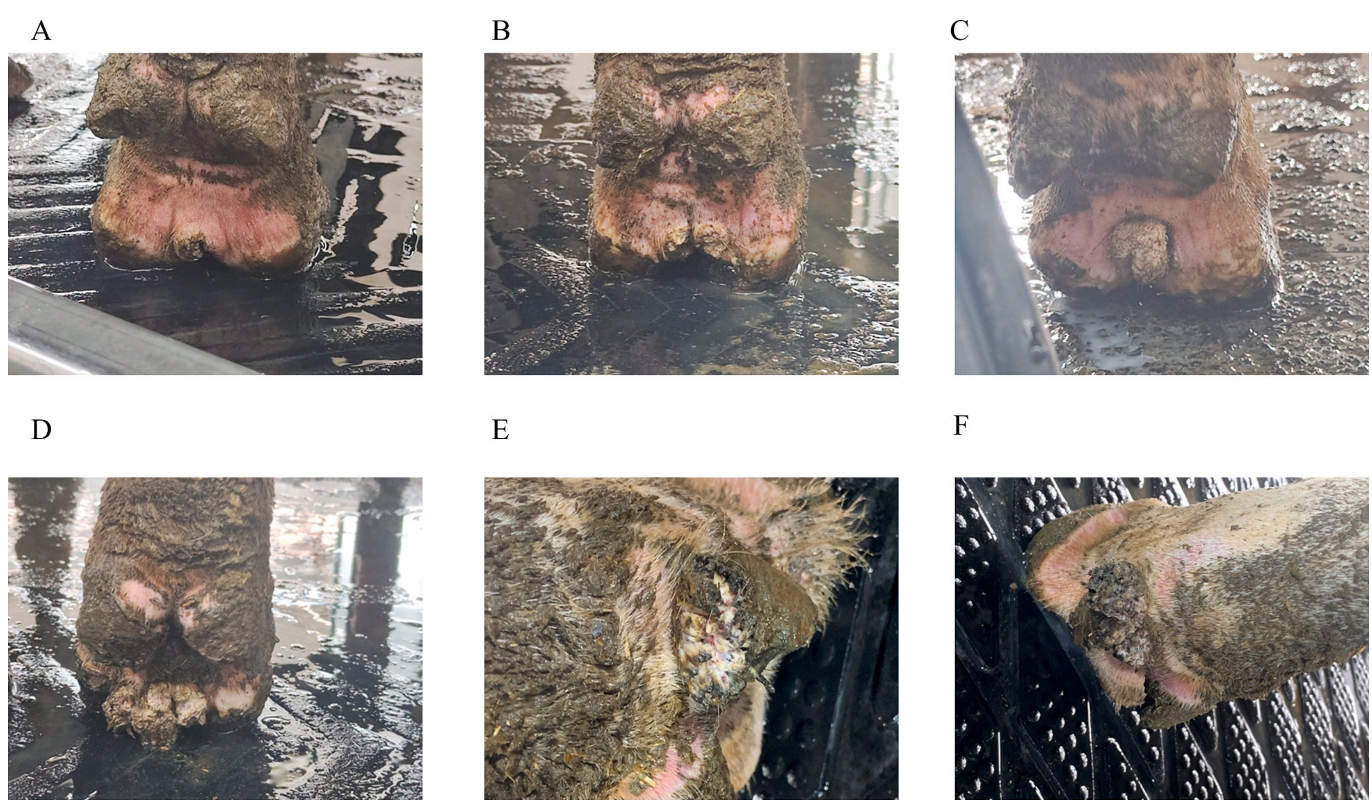

Fig. 1. Typical digital dermatitis lesions observed on dairy farms in Jiangsu, China. A-D are lesions in the typical site between the bulbs of the heel, while E and F are lesions observed on the dew claws of the hind feet.

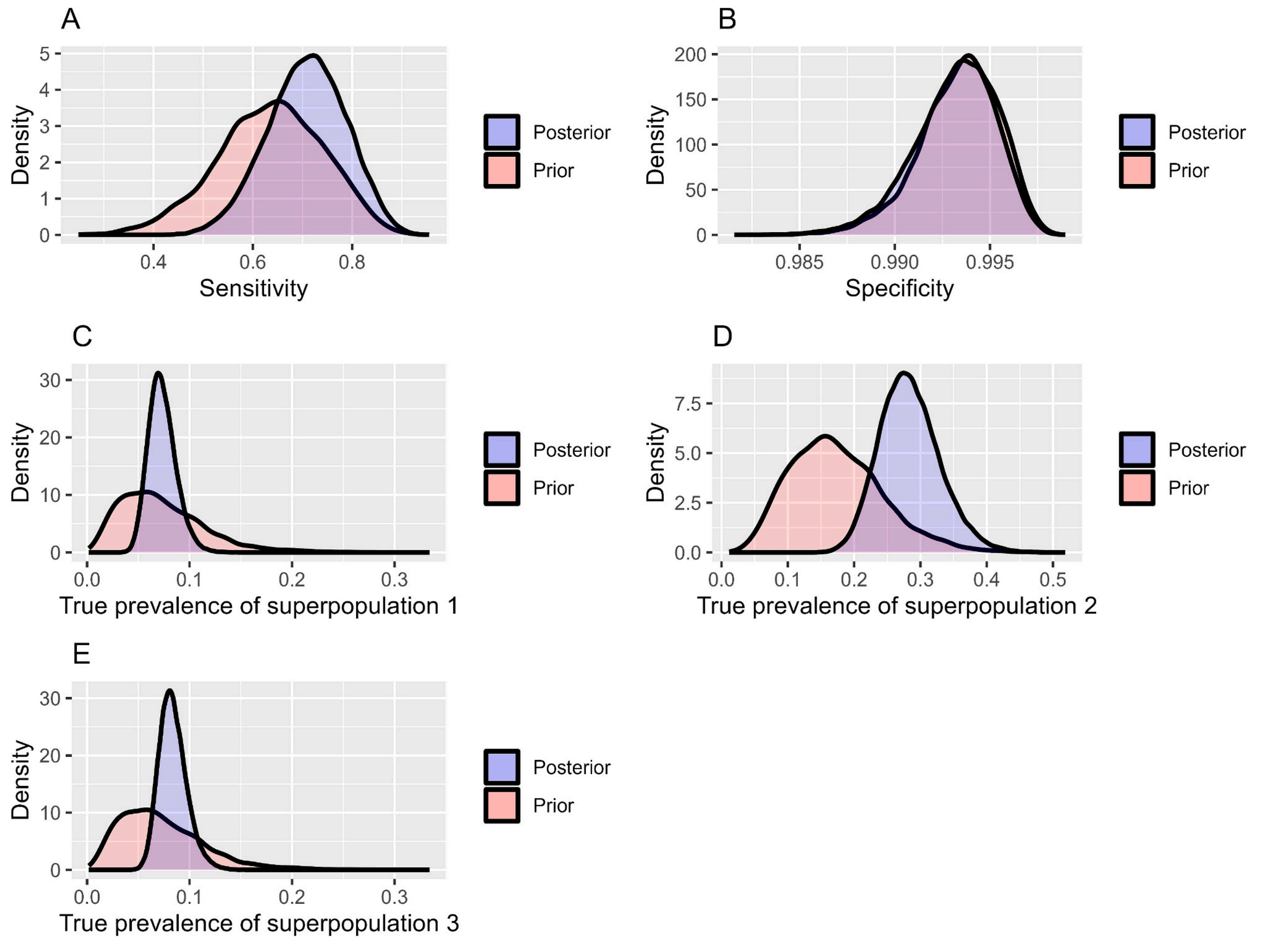

Fig. 2. Comparison of posterior and prior distributions for five model parameters, namely sensitivity, specificity, and the true prevalence of three superpopulations.

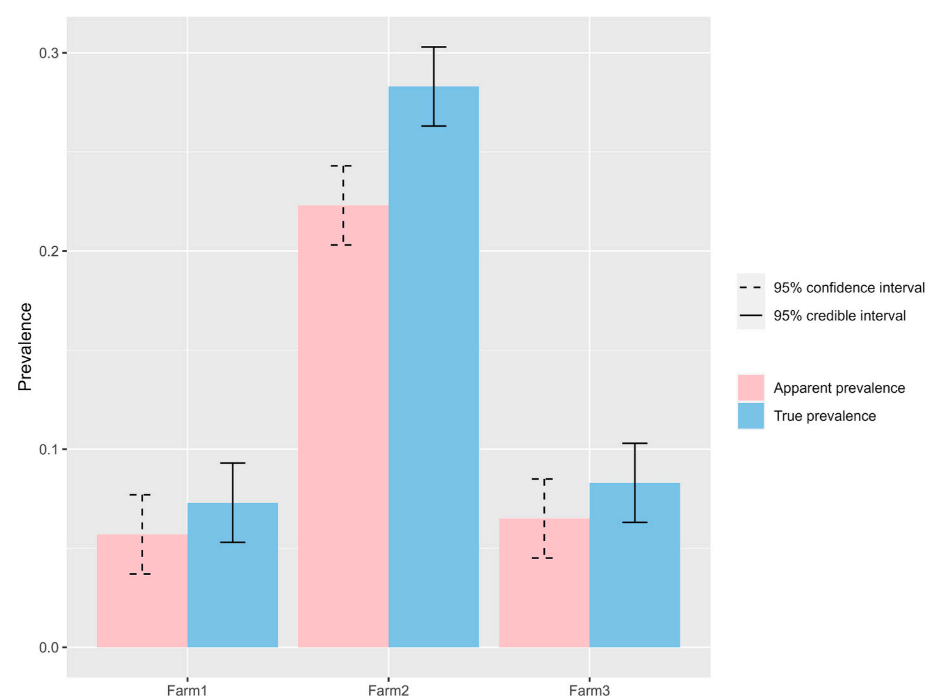

Fig. 3. The comparison between the true prevalence and apparent prevalence of each dairy farm in Jiangsu, China.

Table 2
The results of seven scenarios in the sensitivity analysis. The posterior distributions of the parameters are summarised using the posterior mean, standard deviation (SD) and 95% credible intervals (95%CrI). For each sensitivity analysis scenario, we change one prior at time while keeping the others constant.

Parameters	Posterior mean	SD	95%CrI
Using beta (45.258,24.831) for the sensitivity			
Sensitivity	67.1%	0.051	56.9%–76.7%
Specificity	99.3%	0.002	98.8%–99.7%
π_1	7.7%	0.013	5.4%–10.3%
π_2	29.4%	0.043	21.7%–38.3%
π_3	8.5%	0.012	6.6%–11.3%
Using beta (2.784,1.961) for the sensitivity			
Sensitivity	78.4%	0.106	56.1%–96.2%
Specificity	99.3%	0.002	98.8%–99.7%
π_1	6.7%	0.014	4.5%–9.9%
π_2	26.3%	0.046	18.5%–36.7%
π_3	7.7%	0.014	5.4%–10.9%
Using beta (100,2) for the specificity			
Sensitivity	68.6%	0.085	51.6%–84.3%
Specificity	97.8%	0.011	95.5%–96.6%
π_1	5.6%	0.018	2.1%–9.2%
π_2	27.7%	0.048	19.2%–38.0%
π_3	6.6%	0.019	3.0%–10.3%
Using beta (34.166,1.335) for the specificity			
Sensitivity	67.7%	0.087	50.1%–83.9%
Specificity	97.3%	0.013	94.8%–99.6%
π_1	4.9%	0.019	1.5%–8.9%
π_2	27.5%	0.049	18.8%–37.9%
π_3	5.9%	0.020	2.2%–10.0%
Changing prior for π_1 with a mode 5% and the 95th percentile being increased to 20%			
Sensitivity	70.4%	0.081	54.2%–85.3%
Specificity	99.3%	0.002	98.8%–99.7%
π_1	7.4%	0.014	5.0%–10.6%
π_2	28.5%	0.046	20.4%–38.5%
π_3	8.4%	0.014	6.1%–11.5%
Changing prior for $\pi_2$with a mode 5% and the 95th percentile being increased to 40%			
Sensitivity	70.5%	0.080	54.4%–85.2%
Specificity	99.3%	0.002	98.8%–99.7%
π_1	7.4%	0.014	5.0%–10.5%
π_2	28.5%	0.046	20.5%–38.3%
π_3	8.4%	0.014	6.1%–11.5%
Changing prior for π_3 by increasing a mode to 7% while holding the 95th percentile at 15%			
Sensitivity	70.4%	0.078	55.1%–85.1%
Specificity	99.3%	0.002	98.9%–99.7%
π_1	7.3%	0.014	5.0%–10.3%
π_2	28.5%	0.045	20.5%–38.2%
π_3	8.5%	0.013	6.1%–11.4%

π_i, the true prevalence of the superpopulation i, for $i = 1, 2, 3$

specificity on the CrI for Farm 2, while on Farms 1 and 3 the upper and lower limit of the CrI were both reduced (although, on both farms, the reduction in the upper limit was much smaller than the reduction in the lower limit [compare Table 1 and Table 2]).

4. Discussion

This is the first study to estimate the DD prevalence in dairy cows kept permanently indoors in Jiangsu, China. The reluctance of local farmers to be involved in the study, combined with a general lack of concern about DD (8/9 farms approached stated that they were not interested in knowing their DD prevalence), meant that the scope of our investigation was limited. Nevertheless, we believe that the information from this study can offer valuable perspectives to the broader lameness research community worldwide.

Firstly, our study estimated the true prevalence of DD for each individual farm using a Bayesian superpopulation approach that accounted for the imperfect examination process in the milking parlour. This is important because the reference standard method for identifying DD lesions involves inspecting the lifted foot in the trimming crush. However, many farms around the world lack suitable facilities for this time-consuming method. For example, a high proportion of farms in China, New Zealand, Tanzania and Sri Lanka (authors personal observations) lack such facilities. In contrast, observing DD in the standing cow during milking is feasible on almost all dairy farms with either herringbone or rotary milking parlours. Nevertheless, we know that monitoring DD in this way is less accurate than observing the lifted foot, so we need to be able to take account of that reduced accuracy. The Bayesian superpopulation approach is a robust but computationally achievable approach to doing so (Yang et al., 2019). However, as our analysis shows, its accuracy (especially in herds with a relatively low prevalence of DD) is dependent on having robust estimates of specificity and sensitivity. This process is dependent on the publication of studies such as this one, where prior and posterior estimates are presented, tested and modified. Furthermore, having more data on DD improves the accuracy of estimates of its prevalence. For example, in this study our wide prior distribution of within-farm prevalence was replaced by a much narrower posterior distribution (Fig. 2).

The priors we used for sensitivity and specificity were derived from our previous research in New Zealand (Yang et al., 2017a; Yang et al., 2019; Yang and Laven, 2019). Although there are substantial differences between New Zealand and Chinese dairy farming systems, we consider that between observer differences are likely to be the most significant source of subjectivity when examining cows for DD during milking (Vanhoudt et al., 2019). The major change compared to our previous priors was the concentration of the prior distribution for the specificity around 0.995, reflecting our belief that false positives are extremely unlikely when lesions with a typical appearance are observed (see Fig. 1). However, the Bayesian latent class model assumes that the specificity is constant for all animals in all populations (Kostoulas et al., 2017), and thus any lesion has a finite probability of being considered as a false positive. To deal with this issue, we need an analytical model that relaxes the assumption of constant test performance across a population. For example, Jones et al. (2023) proposed a method that allowed sensitivity to vary between populations by treating sensitivity as a function of the within-herd prevalence. For our DD setting, it would be useful to develop a method that allows specificity to be 1 for animals that are observed to have typical DD lesions on inspection while being milked, whereas allowing the specificity of less definitive lesions to be determined at the animal level. Until such a method is developed, fixing specificity at ~1 is probably the best alternative, although this is likely to moderately overestimate DD prevalence, especially where atypical hoof skin lesions are common.

The limited number of farms enrolled in our study means that we can only provide limited information about DD in dairy herds in Jiangsu province. However, if we presume the two larger herds are representative of many similar herds in Jiangsu, the relatively low prevalence we observed might explain why dairy farmers in Jiangsu are generally not concerned about DD. However, lack of farmer awareness of a disease is not evidence that a disease is not important (Ritter et al., 2017). We need further data on within-farm prevalence of DD, especially in Jiangsu, but also in wider China. One potential difference between DD on our study farms and those in Europe or North America was the presentation of the disease. We observed no M2 lesions (i.e. ulcerative lesions ≥2 cm in diameter with a red-grey surface) in any of the 2534 cows included in our study; in contrast in Europe and North America M2 lesions are commonly observed, irrespective of where cows are examined (Cramer et al., 2018; Vanhoudt et al., 2023). One hypothesis which may explain the difference in lesion presentation between this study and European/

North American studies is that the lack of that regular DD monitoring and treatment on our study farms means that DD lesions have been progressing and regressing naturally. This is similar to what we observed in New Zealand where M4 lesions predominated and only one M2 lesion was observed across multiple studies (Yang et al., 2017b; Yang et al., 2019; Yang et al., 2020). However, even in Europe, not all farms affected by DD have M2 lesions. For example, in Finland, Pirkkalainen et al. (2021) reported that 80/81 farms had detectable lesions of DD, but M2 lesions were identified on only 10 of those farms (and M1 lesions on only 2). This low proportion of herds with M2 lesions was not associated with a low cow level prevalence of DD as it is in New Zealand (Yang et al., 2020), as Pirkkalainen et al. (2021) estimated the true cow-level prevalence of DD was 40.6%.

The lack of variation in the morphological presentation of DD on our study farms, means we lack information on the key transitions between DD lesions on Jiangsu farms. We need more data from more farms to identify whether the absence of M1 and M2-stage lesions reported here is typical of dairy farms in Jiangsu or wider China, and, if this is the case, what this absence means in regard to the modes of transmission of DD in Chinese dairy farms. Although we observed no M2 lesions, we did observe a small number of active M4.1 lesions (~7% of lesions, seen on ~0.5% of cows). It is likely that this is an underestimate of such lesions as they are difficult to detect in the standing cow (Solano et al., 2017). Treatment of M4.1 lesions is recommended from both an animal welfare and an economic perspective. According to Solano et al. (2017), a prompt treatment for M4.1 lesions could prevent aggravation into M2 lesions. However, despite no treatment on any of the three farms, M4.1 lesions seem to be the only active lesions present on those farms. This needs further confirmation, and, particularly if this conclusion is correct, we need more information on the impact of treatment on the presentation of DD on dairy farms in Jiangsu.

5. Conclusions

This preliminary study provides the very first data of DD on dairy farms in Jiangsu, China. It has clearly identified that we need more DD and lameness research in Chinese dairy cows, and to develop our understanding of DD from a veterinary and a statistical perspective. Based on the difficulties we encountered of obtaining on-farm data, relating to DD, we evidently need more education of the farming and veterinary community to raise awareness of this potentially, highly significant infectious disease on dairy farms in China.

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CRediT authorship contribution statement

X. Ma: Writing – original draft, Software, Investigation, Formal analysis, Data curation. **R.A. Laven:** Writing - review & editing, Supervision, Validation. **P. Jiang:** Supervision, Validation, Writing – review & editing. **D.A. Yang:** Writing – review & editing, Writing – original draft, Supervision, Methodology, Funding acquisition, Conceptualization.

Declaration of competing interest

None of the authors has a financial or personal relationship with other people or organisations that could inappropriately influence or bias the content of this paper.

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