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Coxiella burnetii (Q fever) infection in dairy cattle and associated risk factors in Latvia

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SUMMARY

The purpose of this study was to describe prevalence and spatial distribution of *Coxiella burnetii* infections in dairy cow sheds in Latvia and to investigate risk factors contributing to *C. burnetii* infections. Blood serum samples from abortion cases from 1010 sheds have been tested by ELISA for the presence of *C. burnetii* antibodies and bulk tank milk (BTM) samples from 252 sheds have been tested by real time polymerase chain reaction and ELISA for the presence of *C. burnetii* DNA and antibodies. Prevalence of *C. burnetii* antibody-positive sheds in cases of abortion was 13·4%. A total of 10·7% and 13·2% of dairy cow sheds tested positive for the presence of *C. burnetii* DNA and antibodies in BTM, respectively. Two distinct areas of clustering of test-positive dairy cattle sheds were identified by spatial scan statistics of abortion cases and randomly sampled BTM samples. Three factors were identified as significantly contributing to the risk of *C. burnetii* DNA presence in BTM – number of cattle in shed (>200 animals/shed) (OR 3·93), location of the shed within risk area in Northern Latvia (OR 8·29) and for the first time, purchasing cattle from abroad has been shown to significantly increase risk (OR 2·68) of *C. burnetii* infection in dairy cows in Latvia.

Key words: ELISA, Q fever, risk assessment, serology, zoonoses.

INTRODUCTION

Coxiella burnetii – a gram-negative intracellular bacterial pathogen is the causative agent of Q fever – a widespread zoonotic disease. Although the number of acute human infections in the majority of European countries remains confined to <100 cases/year [1], local outbreaks are not uncommon in western, central and southern Europe. Domestic ruminants have been the main source of human infections during latest outbreaks of Q fever [2–4], therefore surveillance of *C. burnetii* infections in domestic animals can also serve as a precautionary measure for prevention of Q fever outbreaks in humans.

The majority of reported outbreaks of Q fever in humans in Germany, UK and The Netherlands have been associated with ovine and goat abortion waves and high prevalence of infections in small domestic ruminants [2, 4, 5]. Although large outbreaks have rarely been associated with cattle farming (except for Poland [6]), molecular genotyping data does not exclude cattle as a possible reservoir of *C. burnetii* strains infectious to humans [7]. Studies of seroprevalence in persons

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occupationally associated with cattle farming have revealed a significant proportion of seropositive individuals, suggesting that cattle–human contact can be a common route of infection [8, 9].

Animal birth products either from abortions or normal deliveries pose the highest risk for animal and human infections due to a high load of *C. burnetii* in placental tissues [10]. Aerosols containing airborne particles from ruminant farms, especially animal birthing places and farms with high ruminant abortion rates are considered to pose the highest risk for human infection [11, 12]. Increased risk of *C. burnetii* infections in animals has previously been associated with local agricultural practice related factors – such as regional herd density [13], herd size [14–16], animal housing system [15, 17], animal movements [13, 18], *C. burnetii* prevalence in goats [3] and sheep [7], hygiene practice [18, 19] as well as climatic and geographical characteristics of the region, for example wind [13, 20, 21]. Thus, factors primarily associated with increased risk of Q fever infections are locally and regionally specific, imposing a need for regional assessments of Q fever spread and associated factors.

Probably due to a low incidence rate of *C. burnetii* infection in humans, information regarding Q fever epidemiology in domestic animals in north-eastern Europe is scarce and confined to seroprevalence data included in national and EU reports. Dairy cattle farming is a predominant branch of animal husbandry in Latvia with 25 000 cattle sheds reported in 2015 [22]. Surveillance based on ELISA of *C. burnetii* prevalence in cattle in Latvia has identified 14·6% and 10·3% seropositive cattle abortion cases in 2012 and 2013, respectively [23]. In the time period from 2008 till 2012 there have been five officially registered cases of Q- fever in humans in Latvia [23]. Although seroprevalence data from cattle abortion cases suggests that a certain part of the Latvian dairy cattle population is infected by *C. burnetii*, spatial epidemiology, overall prevalence at herd level or associated risk factors have not been assessed previously. The present study analyses abortion-related and overall prevalence of *C. burnetii* infections in dairy cattle in Latvia based on three diagnostic parameters: presence of *C. burnetii* DNA in bulk tank milk (BTM), immunological response to *C. burnetii* in BTM and immunological response in blood serum. In addition, factors associated with increased risk of *C. burnetii* infections in cattle in Latvia are assessed. To the best of our knowledge, this is the first study reporting *C. burnetii* prevalence in dairy cattle and associated risk factors in any of the Baltic countries.

MATERIALS AND METHODS

Sample collection

In total 2088 dairy cow blood samples representing 1010 dairy cattle sheds were sampled during 4 year period of 2012–2015 (Table 1). All samples were collected from cases of cattle abortions under the national dairy cattle abortion surveillance program. Dairy cattle shed were used as the unit of analysis for herd level prevalence assessment and a given shed was considered seropositive if at least one blood serum sample originating from the shed tested positive. The term 'shed' is used in official statistics by the Agricultural Data Center of Latvia. The term 'herd' is used to describe the total number of cattle owned by a single owner. However, animals belonging to the same herd can be kept in different sheds sometimes distantly located. Thus, the term 'herd' is more related to ownership of animals rather than the functional unit therefore, it was considered that 'shed' is a more appropriate unit of analysis rather than 'herd'. Data from cow sheds that were represented by more than five independent abortion cases during sampling period (68 sheds in total) was used for within-herd seroprevalence assessment.

A total of 346 BTM samples from 252 dairy cattle sheds initially submitted under the national programme of bovine leucosis virus and *Brucella* sp. surveillance during the 6 month period of July–December 2015 were included in the analysis (Table 2). There are significant differences in total number of animals held by different sheds included in the study. Although the guidelines of BTM sample collection did not specify number of animals per sample or number of samples per shed, in general veterinary practitioners have collected more samples from sheds with larger total number of animals and only one or few samples from small sheds (total number of animals and number of BTM samples collected have strong correlation – Pearsons's linear coefficient $R^2 = 0{\cdot}855$, $P < 0{\cdot}05$ (data not shown)).

Analysed samples represent 5% of all Latvian dairy cattle sheds.

Assays for *C. burnetii* infection and seropositivity

Presence of *C. burnetii* DNA in BTM samples was determined by quantitative polymerase chain reaction

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Table 1. *Number of cows (blood samples) tested in each dairy cattle shed*

Year	2012		2013		2014		2015	
Number of samples from one shed	Number of sheds	Total number of samples	Number of sheds	Total number of samples	Number of sheds	Total number of samples	Number of sheds	Total number of samples
1	117	117	206	206	227	227	157	157
2	30	60	48	96	42	84	31	62
3	6	18	15	45	18	54	9	27
4	8	32	7	28	4	16	5	20
5	3	15	3	15	5	25	6	30
6	3	18	3	18	5	30	2	12
7	1	7	2	14	3	21	2	14
8	0	0	2	16	4	32	5	40
9	0	0	1	9	2	18	2	18
10	2	20	3	30	0	0	1	10
11	0	0	0	0	2	22	5	55
12	0	0	1	12	0	0	2	24
14	1	14	0	0	0	0	0	0
15	0	0	0	0	0	0	1	15
16	0	0	0	0	0	0	1	16
20	0	0	1	20	2	40	0	0
26	0	0	0	0	0	0	1	26
32	0	0	0	0	1	32	0	0
55	0	0	0	0	0	0	1	55
96	0	0	0	0	0	0	1	96
Total	171	301	292	509	315	601	232	677

Table 2. *Number of bulk tank milk samples tested in each dairy cattle shed*

Number of samples from one shed	Number of sheds	Total number of samples
1	214	214
2	20	40
3	7	21
4	4	16
6	1	6
7	3	21
9	2	18
10	1	10
Total	252	346

(qPCR). For this purpose, the Rotor-gene Q 5plex real-time PCR instrument (Qiagen, Germany) and the Adiavet Cox Realtime qPCR kit (Adiagene, France) that targets the *IS1111* DNA sequence were used according to manufacturers' instructions. DNA for qPCR was extracted manually with the QIAamp DNA Mini kit (Qiagen, Germany) according to the protocol supplied with Cox Realtime qPCR kit.

All blood samples and BTM samples were screened for the presence of anti-*C. burnetii* antibodies by enzyme-linked immunosorbent assay (ELISA) using the ID screen Q fever indirect multi-species kit (IDvet, France). The results for each bulk milk and blood sample were interpreted according to the manual provided by the manufacturer.

Spatial clustering analysis

Data of *C. burnetii* DNA and antibody presence in BTM samples was used to identify regions of increased risk of *C. burnetii* infection. Data of *C. burnetii* antibody presence in blood serum samples were used to detect spatial clusters of *C. burnetii* related abortion cases. A cattle shed from which the analysed BTM or blood serum sample had originated was considered a unit of analysis for a spatial scan statistics analysis. Geographical location data for cattle sheds were derived from the Agricultural Data Centre of the Republic of Latvia. Detection of spatial clustering of test-positive cattle sheds in each year was performed using SaTScan v.9.3. software [24] using Bernoulli probability model scanning for high and low-rate *C. burnetii* agent and antibody occurrence circular clusters [25]. The maximal cluster size was

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set to 15% of population at risk according to an average herd level *C. burnetii* infection prevalence of the analysed dairy cattle population. Hypothesis testing of *P* values for randomised *vs*. real cluster formation were based on the standard Monte Carlo method with 999 permutations.

Results of spatial clustering and spatial distribution of *C. burnetii* infections were visualised using software QGIS 2·12·2. [26].

Risk factor analysis

For risk factor analysis, '*C. burnetii* positive/negative shed' was used as a dependent variable. *C. burnetii* DNA presence was assessed in BTM samples analysed with qPCR and the shed was considered as *C. burnetii* positive if *C. burnetii* DNA was detected in at least one BTM sample from the shed. The risk for a shed to be identified as *C. burnetii* positive in association with 13 risk factors was analysed using univariable logistic regression calculation with software MedCalc 16·8·4. [27]. The following risk factors were included in the univariable analysis: (1) sample size representing number of animals included in the sample, (2) number of cattle in the shed from which BTM was collected, (3) number of sheep in the shed from which BTM was collected, (4) indegree – number of cattle sheds from which the analysed shed has received animals during the 2 year period (2013–2015) prior to the analysis, (5) cattle from abroad represents number of animals purchased from abroad during the 2 year period prior to the analysis (country representation in cases of cattle purchase from abroad is indicated in Table 3), (6) shed density represents average number of cattle sheds/km^2 of local municipality (in total there are 110 local municipalities in Latvia with average area of 580 km^2) as on 1 January 2015, (7) cattle density representing number of cattle/km^2 of local municipality, (8) heifer and cow density (number of heifers and cows/km^2), (9) cow density (number of cows/km^2), (10) sheep density (number of sheep/km^2), (11) goat density (number of goats/km^2), (12) average wind speed m/s – represents average wind speed of the driest month of 1 year period prior to the analysis at the meteorological station closest to the analysed cattle shed, (13) localisation of the sample with regard to the region of increased risk determined by SaTScan analysis (Northern Latvia). Data of animal numbers, shed numbers and animal movements was retrieved from the Agricultural Data Centre of the Republic of Latvia, data of wind speed and precipitation was derived from Latvian Environment, Geology and Meteorology Centre open access data [28]. Variables representing animal and shed density and average wind speed were entered in the analysis in form of continuous data. For the purposes of analysis numerical variable 'sample size' was catgorised based on quartiles using MedCalc 16·8·4. [27]. Variables 'number of cattle in the shed' and 'indegree' were categorised into biologically meaningful categories. Principal component analysis (PCA) including all variables of $P < 0{\cdot}2$ from the univariable logistic regression was performed using FactoMineR package [29] of R software version 3.2.3. [30] to elucidate colinearity of predictor variables. Classification of variables 'Sample size', 'number of cattle in the shed' used in the univariable logistic regression was not maintained for PCA, variables have been included in PCA as numerical variables. The PCA including nine variables of $P < 0{\cdot}2$ from the univariable logistic regression identified two groups of collinear variables: (1) cattle density, cow density and heifer plus cow density, (2) cattle in the shed and sample size (Fig. 1). From pairs of collinear variables predictors with the highest correlation with corresponding principal component were chosen for a final multivariable model. Variable 'localisation of the sample' was included in the multivariate model without testing by PCA since it was a variable of a particular interest for authors. Multivariable logistic regression model building was performed using backward selection procedure with MedCalc 16·8·4. [27] including significant (univariable logistic regression $P < 0{\cdot}2$) non-collinear variables. Variables were entered in the model if $P < 0{\cdot}05$ and removed from the model if $P > 0{\cdot}1$. Variables 'cow plus heifer density', 'shed density' and 'wind speed' did not satisfy settings of multivariable

Table 3. *Countries of origin of cattle purchased from abroad in Latvian dairy cattle sheds included in the analysis of bulk tank milk for presence of* Coxiella burnetii *DNA*

Country of origin of cattle purchased from abroad	Number of sheds introducing cattle from abroad
Germany	11
The Netherlands	5
Denmark	2
Estonia	3
Finland	1
Sweden	1
Lithuania	1
Czech Republic	1

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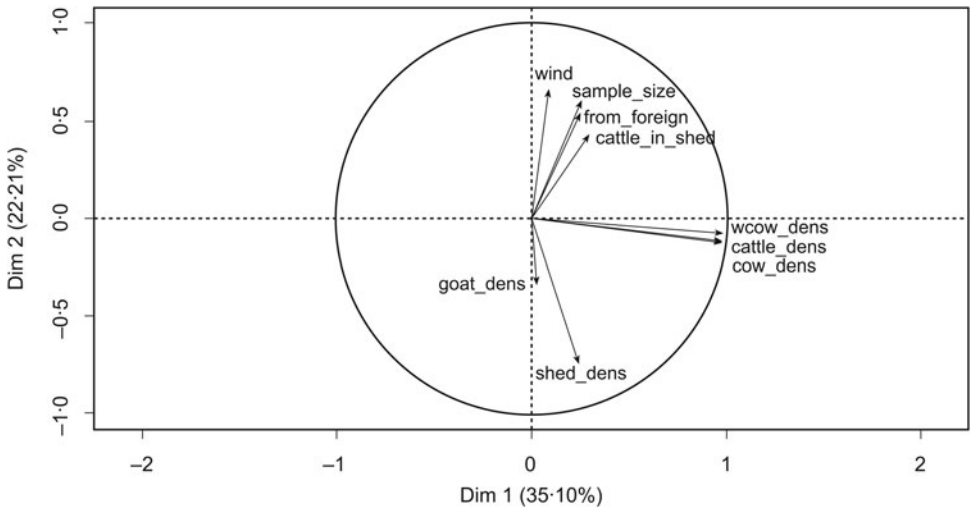

Fig. 1. Principal component analysis including predictor variables identified in univariable logistic regression analysis as significantly (Wald's $P < 0{\cdot}05$) associated with increased risk of *Coxiella burnetii* DNA presence in bulk tank milk (BTM).

logistic regression model backward selection procedure and were excluded. Validity of a multivariable logistic regression model was assessed by the likelihood ratio test, the Hosmer–Lemeshow test for global goodness of fit (GOF) and receiver operating characteristic curve using MedCalc 16·8·4. [27].

RESULTS

Prevalence of Q fever in dairy cows

A total of 13·4% (95% confidence interval (CI) 9·9–16·9) of cow sheds included in the national abortion surveillance programme tested positive for the presence of *C. burnetii* antibodies in blood serum of dairy cows sampled in cases of abortion. At the individual level, on average 27·0% (95% CI 19·8–33·2) of tested animals contained *C. burnetii* antibodies in blood serum after abortion.

In 10·7% (95% CI 7·2–14·2%) of cow sheds at least one BTM sample tested positive for *C. burnetii* DNA and 13·2% (95% CI 7·9–18·5%) of sheds tested positive for presence of antibodies to *C. burnetii* in milk. For 91% of BTM samples tested the result was identical for both indicators – *C. burnetii* DNA and *C. burnetii* antibodies, suggesting high diagnostic agreement between both analyses (Table 4).

Table 4. *Prevalence of* Coxiella burnetii *antibodies and* C. burnetii *DNA in Latvian dairy cow BTM samples (n = 346) tested by ELISA and real time PCR*

		Number of samples analysed by ELISA		
		Positive	Negative	Total
Number of samples analysed by real time PCR	Positive	46	5	51
	Negative	23	272	295
	Total	69	277	346

BTM, bulk tank milk; PCR, polymerase chain reaction.

Spatial distribution of dairy cow sheds with *C. burnetii* infected animals

Based on data of *C. burnetii* antibody presence in blood serum samples from abortion cases spatial epidemiology scan statistics identified increased risk clusters of *C. burnetii* infected dairy cow sheds in the South-Central part of Latvia (Fig. 2). A single high risk cluster was detected for each year of the study 2012–2015 (maximum likelihood ratio test P values $P = 0{\cdot}007$, $0{\cdot}001$, $0{\cdot}005$ for years 2012, 2014 and 2015, respectively), except for 2013. Circular areas of all identified clusters were partially overlapping.

High rate clusters of *C. burnetii* infected dairy cow sheds were also detected based on presence of *C. burnetii* DNA ($P = 0{\cdot}002$) and *C. burnetii* antibodies ($P = 0{\cdot}001$) in BTM samples (Fig. 3). Identified clusters had overlapping areas and were located in the Northern part of Latvia.

Risk factor analysis

From 13 variables analysed, 10 were identified by a univariable logistic regression as significantly associated ($P < 0{\cdot}2$) with presence of *C. burnetii* DNA in BTM (Table 5). Seven of 10 significant variables

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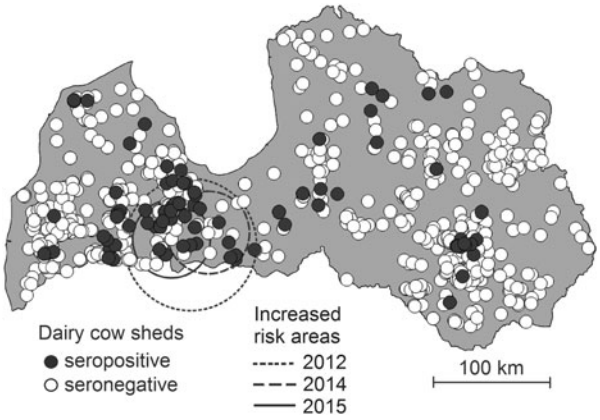

Fig. 2. Spatial distribution of dairy cow sheds sampled during 2012–2015 under the national programme of cow abortion surveillance for *Coxiella burnetii* antibodies in blood serum of dairy cows after abortions. Areas of increased risk to detect *C. burnetii* antibodies in blood serum samples are indicated.

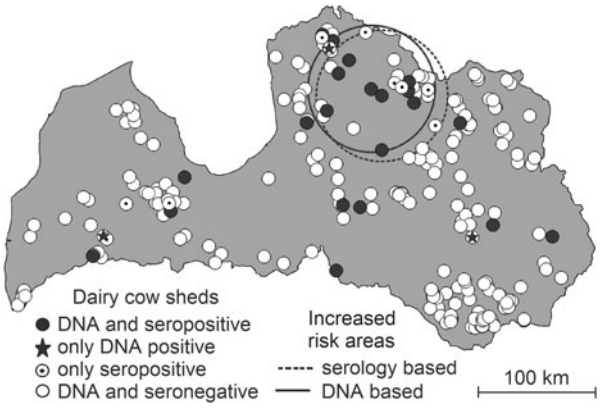

Fig. 3. Dairy cow sheds analysed for *Coxiella burnetii* DNA and *C. burnetii* antibody presence in bulk tank milk (BTM) samples in 2015. Areas of increased risk to detect *C. burnetii* DNA or *C. burnetii* antibodies in BTM are indicated.

from univariable regression were used for multivariable logistic regression model building.

Multivariable logistic regression using backward selection procedure included four from seven tested variables in the final multivariable model (Table 6). Three from four variables included in the final model showed significant positive association with *C. burnetii* DNA presence in BTM samples – cattle number in the shed, purchasing animals from abroad and localisation within the area of increased risk as determined by SaTScan analysis (Table 6). Large dairy cattle sheds (with more than 200 cows) holding cattle purchased from abroad and located in increased risk region of Northern Latvia are at significantly higher risk of acquiring *C. burnetii* infection. The final multivariable logistic regression model of four variables satisfied statistical requirements – likelihood ratio test confirmed overall significance of the model ($P < 0{\cdot}0001$), the model fitted the data (Hosmer and Lemeshow GOF test did not allow for rejection of the model, $P = 0{\cdot}5198$) and had good predictive ability as assessed by ROC curve (area under the curve = 0·820, 95% CI 76·6–86·5%).

DISCUSSION

To the best of our knowledge, this is the first study assessing prevalence and spatial spread of Q fever in dairy cows in any of Baltic countries and analysing underlying risk factors.

In the present study a total of 13·2% (95% CI 7·9–18·5%) of tested Latvian dairy cattle sheds hold cows of either present or recent *C. burnetii* infection as estimated by presence of *C. burnetii* antibodies in BTM samples. Estimated *C. burnetii* prevalence in samples from abortion cases was almost identical to prevalence in randomly sampled BTM samples suggesting that significant contribution of *C. burnetii* infections to cattle abortions in the analysed cattle population is unlikely. Diagnosis via PCR for the presence of *C. burnetii* DNA in BTM estimated slightly lower prevalence of 10·7% (95% CI 7·2–14·2%), which may suggest the immunological response is more enduring than the shedding of the causative agent into milk and shedding can be intermittent in cattle [31].

The estimated prevalence of Q fever in Latvian dairy cows is close to the 8% herd level prevalence reported for Sweden [32] and considerably lower than the herd level prevalence reported in countries of western Europe (82% in The Netherlands [18], 79% in Denmark [16], 72% in Germany [33] or 70% in Spain [34]) or central Europe (40% in Poland [35]). Other countries of northern Europe have reported even lower levels of prevalence in dairy cattle herds – 0% in Norway [36] and 0·24% in Finland [37] suggesting that in northern Europe *C. burnetii* infections of dairy cattle are significantly less common as opposed to western and central Europe. Unfortunately there are no data available regarding dairy cattle Q fever herd level prevalence in the two other Baltic countries – Estonia and Lithuania, however comparatively low *C. burnetii* prevalence in Latvian dairy cow population might indicate that North European region of low prevalence in dairy cattle extends to Baltic countries.

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Table 5. *Univariable logistic regression analysis of risk factors associated with prevalence of* Coxiella burnetii *DNA in dairy cow BTM samples*

Variable	No. of BTM samples tested	No. positive (%)	OR (95% CI)	Wald's test *P* value
Sample size				<0·0001*
<10	79	2 (3)	Ref	
10–13	47	1 (2)	0·84 (0·07–9·49)	0·8858
14–27	61	6 (10)	4·20 (0·82–21·59)	0·0005*
>27	63	18 (29)	14·54 (3·21–65·88)	<0·0001
Number of cattle in shed				<0·0001*
<200	227	18 (8)	Ref	
⩾200	23	9 (39)	7·46 (2·84–19·61)	<0·0001*
Number of sheep in shed				0·4193
Absent	232	26 (11)	Ref	
Present	18	1 (6)	0·47 (0·06–3·45)	0·47
In-degree (2013–2015)				0·5490
0	110	11 (10)	Ref	
1–2	95	9 (10)	0·94 (0·37–2·38)	0·8992
⩾3	45	7 (16)	1·66 (0·59–4·59)	0·3308
Number of cattle from foreign	250		4·09 (1·95–8·58)	0·0002*
Shed density (sheds/km^{2a})	250		0·11 (0·02–0·80)	0·0295*
Cattle density (cattle/km^2)	250		1·12 (1·01–1·25)	0·0304*
Cow density (cows/km^2)	250		1·29 (1·03–1·60)	0·0246*
Cow and heifer density (number/km^2)	250		1·15 (1·03–1·29)	0·0158*
Sheep density (sheep/km^2)	250		0·94 (0·61–1·46)	0·7852
Goat density (goats/km^2)	250		0·09 (0·003–3·34)	0·1962
Wind speed (m/s^b)	250		1·71 (0·95–3·08)	0·0764
Location regarding increased risk area[c]				<0·0001*
Samples outside the region	218	15 (7)	Ref	
Samples within the region	32	12 (38)	8·12 (3·34–19·72)	<0·0001*

BTM, bulk tank milk; CI, confidence interval; OR, odds ratio.
[a] All density related variables have been based on variable values of the corresponding municipality.
[b] Average wind speed m/s in the month with lowest overall precipitation.
[c] Increased risk region located in Northern part of Latvia determined by SaTScan analysis.
*Statistically significant.

Table 6. *Multivariable logistic regression analysis of risk factors associated with prevalence of* Coxiella burnetii *DNA in dairy cow BTM samples*

Variable	Category	OR (95% CI)	Wald's test *P* value
Number of cattle in shed			
	<200	Ref	–
	⩾200	3·93 (1·12–13·81)	0·0329*
Number of cattle from foreign		2·68 (1·08–6·69)	0·0345*
Goat density (number per km^2)		0·02 (0·0002–1·02)	0·0511
Location regarding increased risk area[a]			
	Outside	Ref	
	Inside	8·29 (3·09–22·24)	<0·0001*

BTM, bulk tank milk; CI, confidence interval; OR, odds ratio.
[a] Increased risk region located in Northern part of Latvia determined by SaTScan analysis.
*Statistically significant.

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Spatial scan statistics analysis of *C. burnetii* infection prevalence in cases of dairy cow abortions identified regions of higher *C. burnetii* infection risk in south-central Latvia. This region is characterised by intensive dairy farming with farms holding comparatively larger numbers of dairy cattle and routinely introducing dairy cattle from abroad. Increased risk for Q fever spread in regions of intensified dairy cattle husbandry have previously been observed in Ireland [14], Denmark [16] and Sweden [20] and vaccination has been suggested as the most appropriate preventive measure restricting spread of Q fever in high-risk areas [20]. Interestingly, clustering of antibody-positive BTM samples and seropositive abortion cases occurred in two distinct regions. Such differences might be explained by a dissimilar role of *C. burnetii* in triggering cow abortions in both regions (probably caused by presence of different *C. burnetii* strains). However, further studies are required to confirm this hypothesis.

Multivariable regression analysis identified large cattle numbers in shed and localisation in North Latvia increased risk region as factors significantly contributing to increased risk of *C. burnetii* infection. Association between herd size, animal density and increased risk of *C. burnetii* infection is well known [14, 16, 18, 20]. However estimated herd size (>200 animals) significantly increasing risk of infection in the Latvian dairy cow population considerably differed from the high risk herd size (>80 animals) reported for the Danish dairy cattle population [16], which is likely attributable to the higher overall prevalence of Q fever in Denmark. Significant country-to-country differences in border values of the identified risk factors suggest that local guidelines and preventive measures to restrict spread of *C. burnetii* infections can only partially be based on estimates from another region. Assessment of risk factors needs to be performed for each country individually to ensure correct identification of farms and areas subjected to the increased risk of *C. burnetii* infections.

Univariable logistic regression identified animal purchasing from abroad as significantly increasing risk of BTM to be *C. burnetii* DNA positive. Multivariable regression analysis confirmed animal purchasing from abroad as a factor significantly increasing risk of *C. burnetii* infection in Latvian dairy cattle. The majority of animals acquired from abroad in analysed dairy cattle farms have originated from heavily infected dairy cattle populations of Germany, Denmark and the Netherlands (Table 3). Animal movements have previously been identified as a factor significantly contributing to spread of dairy cattle *C. burnetii* infections in Sweden and Netherlands [13, 18]. Previously published studies of risk factors contributing to *C. burnetii* dairy cattle infections have analysed animal movements within countries. However, results of the current study indicate that cases of animal movement between countries, especially between regions of significantly different *C. burnetii* prevalence, need to be subjected to additional control to restrict spread of *C. burnetii* infections in low prevalence regions. Risk factor analysis of *C. burnetii* antibody-positivity of Danish dairy cattle herds showed that quarantine of purchased animals can significantly reduce risk of introduction of *C. burnetii* infection [15]. Control measures including quarantine and *C. burnetii* infection diagnosis of cattle purchased from abroad could limit spread of *C. burnetii* infections and preserve low prevalence of *C. burnetii* infections in the Latvian dairy cattle herds.

CONCLUSIONS

Estimated prevalence of *C. burnetii* antibody and *C. burnetii* DNA positive herds in Latvia is comparatively low (<15%). These results position Latvia among north-eastern European countries (as Sweden, Norway and Finland) with previously described low *C. burnetii* infection prevalence in dairy cattle. However, low prevalence status can be jeopardised by the practice of purchasing cattle from abroad, especially from heavily infected dairy cattle populations of Western Europe. Therefore, precautionary measures including quarantine and *C. burnetii* infection status identification need to be realised before introducing newly purchased cattle into herd.

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DECLARATION OF INTEREST

None.

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