

Climate, host and landscape determinants of bovine babesiosis in Great Britain: analysis of Imidocarb treatment notifications, 2016–2024

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Abstract

Background Bovine babesiosis is a clinically important tick-borne disease of cattle in Great Britain, yet its spatial distribution and key geographical risk factors remain poorly characterised due to limited routine surveillance. Imidocarb dipropionate (Imizol), the only licensed treatment for bovine babesiosis, must be notified to the Animal and Plant Health Agency whenever it is prescribed or administered to cattle. These compulsory notifications therefore provide a proxy dataset for examining spatial patterns in clinically recognised bovine babesiosis.

Methods Imizol notification records from 2016 to 2024 were used as a proxy for disease occurrence to model the spatial suitability for bovine babesiosis in Great Britain. Presence was defined at a 2 km grid resolution and modelled using machine learning. Predictor variables captured seasonal climate, vegetation greenness, livestock densities and predicted habitat suitability for red, roe and fallow deer as key risk factors. Models were trained using southwest England data from 2016 to 2022, temporally validated using southwest England data from 2023 to 2024, and externally evaluated using independent data from outside the training region.

Results Models showed high performance in internal cross-validation (mean AUC = 0.81; mean correlation = 0.55) and temporal validation (continuous Boyce Index = 0.81), and external validation outside southwest England indicated moderate transferability (Boyce Index = 0.58). Climatic predictors accounted for the greatest relative influence in the models, particularly autumn cooling (mean relative influence = 37.3%) and atmospheric moisture (8.5%), consistent with seasonal climatic constraints on tick activity. Among non-climatic predictors, roe deer habitat suitability and sheep density contributed moderate influence, while vegetation greenness had a smaller effect. Proportional land-cover variables showed consistently low individual influence.

Conclusions Mandatory veterinary medicines notification data can be used as a proxy for disease occurrence to model spatial suitability of bovine babesiosis at national scale. Seasonal climatic constraints on tick activity and host-associated factors were the strongest determinants of predicted disease patterns. Resulting risk maps may help anticipate areas of elevated risk and guide disease surveillance at regional scales, including highlighting locations where environmental conditions appear suitable for disease occurrence but treated cases have not yet been reported.

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Keywords Bovine babesiosis · *Ixodes Ricinus* · Boosted regression trees · Livestock health

Background

Tick-borne diseases are an increasing concern for livestock across temperate regions as climatic warming and landscape changes reshape the distribution, abundance, and seasonal activity of vector populations [1, 2]. In northern Europe, land use policies promoting woodland regeneration alongside the recovery and expansion of wild ungulate populations have increased the suitability of many agricultural landscapes for *Ixodes* ticks, the principal and widespread vector of pathogens affecting both animals and humans [3, 4]. Concurrent transitions towards more sustainable farming systems that prioritise biodiversity and conservation objectives, and carbon sequestration for climate change mitigation [5] may further increase opportunities for contact between livestock, wildlife hosts and infected ticks.

Babesiosis, caused by the protozoan parasites of the genus *Babesia*, is considered an emerging or re-emerging infectious disease in Europe [6]. Bovine babesiosis, caused predominantly by *Babesia divergens* in northern Europe, remains one of the most clinically important tick-borne diseases of cattle. Infection can lead to acute haemolytic anaemia and rapid mortality, resulting in both animal health and production impacts on affected farms [7]. Transmission of *B. divergens* depends on the distribution and seasonal dynamics of *Ixodes ricinus*, a three-host tick dependent on humid microclimates and access to suitable vertebrate hosts. The prevalence of *B. divergens* in questing ticks is typically very low [8, 9], and the parasite is thought to be maintained through vertebrate reservoirs, particularly cattle with persistent or subclinical infections [7]. Recent evidence also indicates that wild deer can carry the parasite, although their role in transmission to livestock remains uncertain [10]. Clinical expression of bovine babesiosis is also influenced by host age and patterns of exposure. Young calves are susceptible to *B. divergens* infection but generally exhibit resistance to severe clinical disease, although the mechanisms underlying this age-related resistance remain incompletely understood [7, 11]. It has been proposed that, in endemic areas, cattle are more likely to become infected at a young age while still relatively resistant to clinical disease, after which they may develop protective immunity, potentially resulting in relatively few clinical cases despite ongoing parasite transmission [11]. Conversely, where transmission is sporadic or newly established, cattle may first be exposed later in life and may therefore be at greater risk of developing clinical disease.

Despite the considerable animal health and production impacts associated with bovine babesiosis, surveillance in the UK remains extremely limited. The disease is not statutorily notifiable, and national laboratory-based scanning surveillance captures only a small proportion of cases [12–14]. A notable exception arises from veterinary medicines legislation; Imidocarb dipropionate (Imizol), the only licensed treatment for *B. divergens* infection in cattle, must be notified to the national animal health authority (the Animal and Plant Health Agency) every time it is prescribed or administered to food-producing animals. This requirement reflects regulatory controls associated with its prolonged meat and milk withdrawal periods [13, 15, 16]. Imizol is licensed solely for the treatment and prevention of *B. divergens* infection in cattle and no alternative treatments are available; therefore, these mandatory notifications provide a nationally collected dataset that can be used as a proxy for clinically recognised disease requiring treatment.

In the absence of comprehensive surveillance, treatment-based datasets provide a practical alternative, and the use of prescribing or dispensing data as a proxy for disease occurrence is well established in human medicine [17, 18]. This approach enables meaningful inferences about disease patterns even when case reporting is incomplete. In this study, Imizol treatment notifications are interpreted as a proxy for the spatial distribution of clinically recognised cases of bovine babesiosis requiring treatment. While not all *B. divergens* infections result in treatment and some degree of under-ascertainment is inevitable, the mandatory nature of Imizol notification, its exclusive licensing for bovine babesiosis, and the absence of alternative licensed treatments together provide a national indicator of a clinically significant disease occurring at the farm level and the underlying environmental conditions that support transmission from ticks to livestock. However, treatment may sometimes be administered

on the basis of clinical suspicion without laboratory confirmation, and surveillance analyses have shown that a substantial proportion of samples submitted for suspected bovine babesiosis are negative on diagnostic testing [14]. These notifications therefore reflect the combined influence of ecological conditions, cattle exposure, veterinary recognition, treatment-seeking behaviour, diagnostic practices and regulatory reporting, rather than underlying transmission processes alone.

Using eight years (2016–2024) of Imizol notification data from 479 farm premises, we characterised the environmental, climatic, and host-related correlates of treated clinical bovine babesiosis across Great Britain, with particular emphasis on southwest England, a region recognised as endemic for bovine babesiosis in the UK [19]. Using machine learning boosted regression tree approaches, we then identified the key geographical risk factors associated with patterns in treatment-requiring cases of bovine babesiosis, and generated spatial predictions of suitability for treated clinical babesiosis occurrence across Great Britain.

Methods

Disease presence data

This study used 2,931 Imizol use notifications received by the Animal and Plant Health Agency from veterinary practices across Great Britain between 2016 and 2024. Each notification corresponded to an individual cattle prescription or treatment, and multiple notifications could originate from the same farm. Of all notifications, 2,870 (97.9%) included a farm address and 2,782 (96.9%) included a dispensing date. Notifications were aggregated to unique farm addresses, resulting in 479 farms with at least one Imizol use notification during the study period. The number of notifications per farm ranged from 1 to 133 (median = 2; mean = 6) and annual totals ranged from 31 notifications in 2016 to 623 in 2019, affecting 26–129 unique farms per year. Imizol notifications were highly clustered geographically; of the 479 notified farms, 446 (93%) were located within the southwest region of England and 33 (7%) elsewhere in Great Britain (Fig. 1).

Imizol notifications were interpreted as a proxy for clinically recognised, treatment-requiring bovine babesiosis, rather than total infection incidence. Throughout this study, model outputs are therefore interpreted as relative suitability for treated clinical babesiosis occurrence rather than absolute disease risk. To ensure that environmental relationships were estimated under conditions of sustained disease occurrence rather than sporadic reporting, the primary analysis dataset was restricted to farms within the southwest region of England. This approach reduces ambiguity in absence interpretation and allows relationships inferred under endemic conditions to be independently evaluated elsewhere. Notifications from outside this region were reserved for independent external evaluation. The southwest accounts for approximately 33% of the national cattle herd, with a greater proportion of dairy than beef cattle, and 20% of the national sheep flock [20]. The region has an established presence of *I. ricinus* and tick-borne disease in cattle [14, 19, 21–23]. Land use is predominantly rural, characterised by agricultural land, woodland, heathland, and coastal habitats that support a mixture of livestock farming systems [20, 24]. The southwest region comprised the following upper-tier local authority (UTLA) areas: Cornwall, Devon, Plymouth, Torbay, Somerset, Dorset, Hampshire, Wiltshire, North Somerset, Bath and North East Somerset, Gloucestershire, Bristol, South Gloucestershire and Swindon.

Environmental, climatic and host-related variables

Predictors were selected to represent key ecological mechanisms known to influence *I. ricinus* survival, activity and host distribution on agricultural landscapes, and therefore the likelihood of cattle exposure to *B. divergens* (Table 1). Full details of data sources and processing steps for all predictors are provided in Supplementary Methods S1.

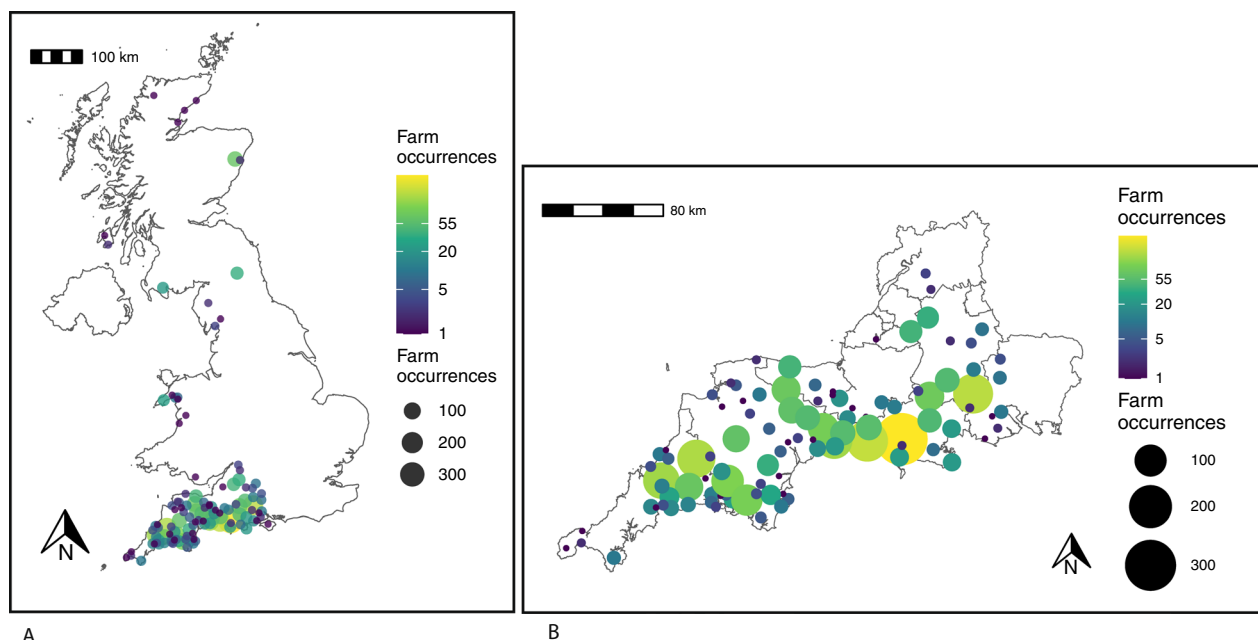


Fig. 1 Spatial distribution of Imizol-treated bovine babesiosis notifications in Great Britain between 2016 and 2024. **A** Distribution of all notified farms across Great Britain. **B** Enlarged view of the southwest England training region, overlaid on upper-tier local authority (UTLA) boundaries used to define the model training area. Points represent farms with at least one Imizol notification; point colour and size indicate the number of notifications recorded at each farm

Table 1 Environmental, climatic and host-related predictors used in the spatial analysis of Imizol-treated bovine babesiosis in southwest England

Category	Predictor name	Description/units	Mean $\pm$ SD	Range
Environment	Area of Broadleaved Woodland	Percentage area of Broadleaved Woodland per cell	9.01 $\pm$ 12.02	0–96
	Area of Coniferous Woodland	Percentage area of Coniferous Woodland per cell	2.07 $\pm$ 7.74	0–99
	Area of Arable and Horticulture	Percentage area of Arable and Horticulture per cell	22.93 $\pm$ 25.60	0–100
	Area of Improved Grassland	Percentage area of Improved Grassland per cell	50.01 $\pm$ 28.36	0–100
	Normalised Difference Vegetation Index (NDVI)	Median growing-season NDVI (unitless ratio, –1 to +1) per cell	0.73 $\pm$ 0.06	0.23–0.85
Climate	Soil moisture	Mean m ³ water per m ³ soil volume per cell	0.42 $\pm$ 0.05	0.27–0.67
	Spring warming	Mean daily rate of increase in maximum temperature (°C day ⁻¹) between February and April, estimated per cell	0.003 $\pm$ 0.003	–0.02 to 0.02
	Autumn cooling	Mean daily rate of decrease in minimum temperature (°C day ⁻¹) between September and November, estimated per cell	–0.13 $\pm$ –0.01	–0.15 to –0.08
	Saturation deficit	Mean April–August saturation deficit (kPa) averaged across 2016–2024 per cell	0.35 $\pm$ 0.05	0.23–0.48
Host	Cattle population density	Cattle population density per km ² per cell	59.45 $\pm$ 35.0	0–167.58
	Sheep population density	Sheep population density per km ² per cell	56.88 $\pm$ 41.93	0–243.38
	Predicted red deer suitability	Continuous habitat suitability index derived from presence-only species distribution models for British red deer	0.04 $\pm$ 0.10	0–1.40
	Predicted roe deer suitability	Continuous habitat suitability index derived from presence-only species distribution models for British roe deer	0.65 $\pm$ 0.53	0–3.72
	Predicted fallow deer suitability	Continuous habitat suitability index derived from presence-only species distribution models for British fallow deer	0.31 $\pm$ 1.01	0–20.40

Summary statistics (mean $\pm$ SD and range) across 2 km grid cells

Land-cover variables were included to represent broad-scale landscape composition, which is well established as an important determinant of spatial variation in tick abundance and infection prevalence in agricultural landscapes [19, 25, 26]. These associations likely reflect landscape-level variation in host availability, grazing systems and environmental conditions influencing off-host tick survival and activity. Accordingly, proportional cover of broadleaved woodland, coniferous woodland, arable and horticultural land, and improved grassland was obtained from the UKCEH Land Cover Map 2023 [27]. Vegetation greenness was included as an indicator of habitat structure and microclimatic suitability for tick questing and survival, with Normalised Difference Vegetation Index (NDVI) derived metrics previously linked to spatial variation in *I. ricinus* abundance and activity [28] and to *B. divergens* seroprevalence in dairy cattle [29–31]. Growing-season NDVI was calculated for April–August, to coincide with the peak in reported tick activity in the UK and to follow previous species distribution modelling practice of excluding winter NDVI when vegetation greenness is minimal [32], and was derived from MODIS MOD13A2 [33]. Soil moisture was included as a predictor of off-host tick abundance based on field evidence demonstrating strong associations between soil-related moisture conditions and *I. ricinus* nymph density in endemic landscapes [34]. Volumetric soil moisture was derived from the COSMOS-UK gridded dataset for the period 2016–2023, which represents the full temporal coverage currently available for this product [35].

Temperature is a primary determinant of development, survival and activity levels in *I. ricinus* [36]. Indices of spring warming (February–April) and autumn cooling (September–November) were included to capture seasonal thermal dynamics affecting tick phenology and seasonal activity patterns, following approaches used in recent vector risk modelling [37]. These variables were derived from HadUK-Grid daily temperature data (2016–2024) [38]. Atmospheric moisture was represented using saturation deficit for April–August to coincide with the period of highest tick activity and livestock exposure. Saturation deficit, derived from air temperature and relative humidity, quantifies desiccation stress and is strongly associated with reduced *I. ricinus* questing and nymph abundance under dry conditions [39, 40]. Saturation deficit was calculated from HadUK-Grid daily temperature and relative humidity [38].

Large mammalian hosts are essential for maintaining *I. ricinus* populations, with deer presence consistently showing strong positive associations with environmental tick abundance across Europe. While some studies report increasing tick abundance with higher deer densities, others indicate that deer presence alone, rather than abundance, is sufficient to elevate tick populations [41–43]. Wild deer in the United Kingdom have also been shown to carry *B. divergens*, indicating a potential role in parasite maintenance in enzootic systems in addition to sustaining tick populations [10]. Predicted habitat suitability surfaces for red deer (*Cervus elaphus*), roe deer (*Capreolus capreolus*) and fallow deer (*Dama dama*) were therefore included to represent spatial variation in availability of key wild deer hosts. Deer suitability layers were derived from published species distribution models developed for British deer [44]. While sheep are competent hosts for *I. ricinus*, grazing has been associated with reduced questing tick densities [45]. Cattle are also used as hosts by *I. ricinus* and are the primary livestock species affected by *B. divergens* [7]. Cattle density therefore represented both host availability and the presence of susceptible hosts required for clinical babesiosis occurrence. Sheep and cattle population density were obtained from national livestock census data [46].

Spatial analysis

Disease presence was represented as a binary outcome at a 2 km grid resolution and modelled using Boosted Regression Trees (BRTs). BRTs were selected because they effectively model complex, non-linear relationships and interactions among ecological, climatic, and host-related predictors, and are widely applied in ecological epidemiology and vector-borne disease modelling, where multiple environmental factors shape disease risk [47, 48]. All analyses were conducted in R version 4.4.1 [49] using the packages *dismo* [50], *gbm* [51], *terra* [52], *ecospat* [53] and *spdep* [54].

Imizol use notifications were aggregated to farm level then grouped into three datasets for model training and validation: (i) a model-fitting dataset comprising farms within the southwest England analysis region reported between 2016 and 2022 ($n = 363$), (ii) a temporal validation dataset comprising farms within the southwest England analysis region reported during 2023–2024 ($n = 167$; including 87 newly reported and 80 recurrent farms) and (iii) an external validation dataset comprising farms outside the southwest England analysis region reported between 2016 and 2024 ($n = 33$). Restricting model fitting to the endemic southwest region allowed environmental–host relationships to be estimated under conditions of sustained disease occurrence, while the latter two datasets were used to assess temporal and spatial transferability.

All environmental, climatic and host-related raster predictors were processed within a common spatial framework based on a 2 km grid in the British National Grid projection (EPSG:27700). Because Imizol treatment notifications were aggregated across multiple years, predictors were parameterised to represent typical conditions rather than interannual variability, with climatic, vegetation, and soil moisture variables summarised as multi-year period means or medians. Continuous predictors were spatially aggregated to the 2 km grid and categorical land-cover variables expressed as proportional cover.

Farm postcodes were georeferenced, projected to the 2 km baseline grid and assigned to corresponding grid cells. Presence was defined as any 2 km grid cell containing at least one farm with reported Imizol-treated bovine babesiosis. The 363 southwest analysis farms occupied 323 grid cells (range: 1–4 farms per cell), while temporal and external validation farms occupied 162 and 32 cells, respectively. To assess the influence of spatial clustering in presence locations, models were fitted using both unthinned datasets (all presence cells retained) and spatially thinned datasets. Spatial thinning was performed using a 5 km grid, in which a maximum of one presence location was retained per 5 km grid cell. Spatial thinning was applied to reduce the influence of geographically clustered sampling, which can inflate model complexity and bias estimates of predictive performance in species distribution models [55, 56]. Farms were assigned to 5 km grid cells derived from their projected coordinates and one presence was randomly selected per occupied cell. The resulting spatially thinned dataset was subsequently analysed using the original 2 km grid.

Presence cells were matched with an equal number of randomly selected pseudo-absence grid cells, since equal presence:absence ratios maximise the performance of BRTs [57]. Pseudo-absences were sampled from 2 km grid cells with no reported Imizol use during 2016–2022, and with cattle density ≥ 5.6 cattle/km². This threshold corresponds to the 25th percentile of cattle density in the study region and was used as a pragmatic cut-off to ensure that pseudo-absences represented areas where cattle were present and exposure to ticks was ecologically plausible, while avoiding unstocked areas where treated clinical babesiosis notifications could not occur. To assess sensitivity to the choice of cattle density threshold used for pseudo-absence selection, additional BRTs were fitted using alternative thresholds of ≥ 1 cattle/km² and ≥ 10 cattle/km². As notifications represent the absence of reported Imizol use rather than confirmed disease absence, pseudo-absences were interpreted as locations without recorded treated clinical cases during the study period.

BRTs were fitted using a learning.rate of 0.002, tree.complexity of 4 and a bag.fraction of 0.6, chosen to ensure that the optimal number of trees always exceeded 1000 [47]. To account for uncertainty associated with both spatial thinning of presence locations and pseudo-absence selection, models were fitted 100 times, each run using a newly thinned presence dataset (for the thinned models) and a resampled set of pseudo-absences. Predictor values were extracted for each grid cell, and only cells with complete data across all predictors were retained. Model performance metrics and relative influence values were summarised across the ensemble of fitted models. Relative influence is reported as the percentage contribution of each predictor to the fitted boosted regression tree model and reflects both the frequency with which a variable is selected for tree splits and its contribution to improving model fit [47].

Pairwise Pearson correlations were calculated across non-missing raster cells of the full predictor stack to assess collinearity among climatic, environmental and host-related variables. Most predictor pairs showed weak to moderate correlation ($|r| < 0.6$); however, autumn cooling and saturation deficit were strongly negatively correlated

($r = -0.88$). While collinearity generally has limited impact on predictive performance in tree-based machine learning models, it can affect estimates of variable importance because the model may distribute influence across correlated predictors or assign high importance to variables that are correlated with a true driver. To evaluate robustness to this collinearity, additional BRT ensembles were fitted excluding saturation deficit and excluding autumn cooling in turn, and internal performance and relative influence were compared with the full model. Predictive transferability was additionally evaluated for the full model and the saturation-deficit-excluded model using independent validation datasets.

The relationships between Imizol-treated babesiosis suitability and individual predictor variables were examined using marginal response curves generated by the models. For each predictor, response curves were averaged across the 100 BRT submodels by calculating mean and standard deviation of the marginal predicted probabilities within ~40 bins of the predictor values [58].

Residual spatial autocorrelation in model residuals was assessed using Moran's I, calculated from a 4-nearest-neighbour spatial weights matrix derived from grid cell centroids. Residuals were defined as the observed presence-absence value minus the ensemble-mean predicted probability for each training cell. The median distance to the fourth nearest neighbour was 6.3 km (5–95% range: 2.8–14.0 km). Spatial autocorrelation was assessed separately for thinned and unthinned models.

Temporal transferability was evaluated using farms with reported Imizol-treated clinical babesiosis in southwest England during 2023–2024, while spatial transferability was assessed by evaluating predictions at farms reported outside the southwest region (2016–2024, Fig. 1a). Predictive performance was quantified using the continuous Boyce Index. For the temporal validation dataset of newly affected southwest England locations (2023–2024), we quantified the proportion of presence locations correctly classified using the cross-validated probability threshold from the fitted BRT models.

The final model was projected across Great Britain at 2 km resolution to generate a continuous surface of predicted suitability for Imizol-treated bovine babesiosis. Predictions were averaged across the ensemble of 100 replicate models to produce a final suitability map. Predicted values represent relative climate, environment and host-related suitability for treated clinical babesiosis occurrence, rather than infection incidence or absolute risk.

Results

Results are presented for the primary unthinned BRT model due to its higher performance in validation with independent data (see below). Results from spatially thinned models and sensitivity analyses are reported in the Supplementary information.

Model performance

The unthinned BRT model showed strong internal predictive performance (Table 2). The median number of trees fitted across the 100 replicate models was 2050 (mean = 2106), mean cross-validation correlation was 0.55 (SD = 0.03) and mean cross-validation AUC was 0.81 (SD = 0.02), demonstrating good discrimination between presence and pseudo-absence locations. Training AUC values showed no evidence of over-fitting (mean = 0.81).

Relative influence of predictors

Relative influence (RI) estimates from the unthinned BRT model were highly consistent across the 100 replicate models (Table 3). Autumn cooling accounted for the largest proportion of model influence (mean RI = 37.33%). The remaining influence was distributed across a set of climatic, host-related and vegetation predictors with broadly comparable contributions. Roe deer suitability ranked second overall (mean RI = 8.57%), closely followed by saturation deficit (mean RI = 8.45%) and sheep population density (mean RI = 7.46%). Additional host-related

Table 2 Accuracy metrics for the unthinned BRT model

Metric	Median	Mean	SD
Number of trees	2050	2106	401
Total deviance	1.39	1.39	0.00
Residual deviance	0.81	0.81	0.05
Cross-validation deviance (mean)	1.06	1.06	0.03
Cross-validation deviance (SE)	0.04	0.04	0.01
Cross-validation correlation	0.55	0.55	0.03
Cross-validation correlation (SE)	0.03	0.03	0.01
Training set AUC	0.81	0.81	0.02
Cross-validation AUC	0.81	0.81	0.02
Cross-validation AUC (SE)	0.02	0.02	0.00

Table 3 Relative influence (RI, %) and modal rank of predictors in the BRT model of values across 100 model runs (*SD* standard deviation)

Rank	Predictor	Mean RI	Median RI	SD RI
1	Autumn cooling	37.3	36.9	4.6
2	Predicted roe deer suitability	8.6	8.4	1.7
3	Saturation deficit	8.5	8.4	2.5
4	Sheep population density	7.5	7.1	1.8
5	Predicted red deer suitability	6.3	6.3	1.6
6	NDVI	6.1	6.0	1.9
7	Cattle population density	4.7	4.8	1.5
8	Predicted fallow deer suitability	4.6	4.3	1.4
9	Spring warming	4.2	4.2	1.2
10	Area of Improved Grassland	3.8	3.8	1.4
11	Soil moisture	3.0	2.8	1.0
12	Area of Arable and Horticulture	2.1	2.0	1.0
13	Area of Broadleaved Woodland	1.8	1.6	0.8
14	Area of Coniferous Woodland	1.7	1.5	1.0

Relative influence is expressed as the percentage contribution of each predictor to the fitted boosted regression tree model; values across all predictors sum to 100%

and environmental predictors, including red deer suitability, NDVI and cattle population density, contributed moderate influence (mean RI $\approx$ 4–6%). Proportional land-cover variables and soil moisture had relatively low individual influence (mean RI $<$ 4%), indicating limited explanatory power at the 2 km spatial resolution used in this analysis.

Marginal response curves from the unthinned BRT model revealed non-linear associations between Imizol-treated babesiosis suitability and the top-ranked predictors (Fig. 2). Predicted suitability for occurrence of Imizol-treated babesiosis increased sharply in areas with slower autumn cooling (values closer to zero) indicating climates where temperatures decline more gradually during autumn. Predicted suitability declined with increasing saturation deficit. For host-related predictors, predicted suitability increased with increasing roe deer suitability and was higher at lower sheep densities.

Residual spatial autocorrelation

BRT residuals showed weak but statistically significant positive spatial autocorrelation: Moran's $I=0.057$; $z=2.18$; $p=0.015$, indicating that neighbouring grid cells remained slightly more similar than expected after

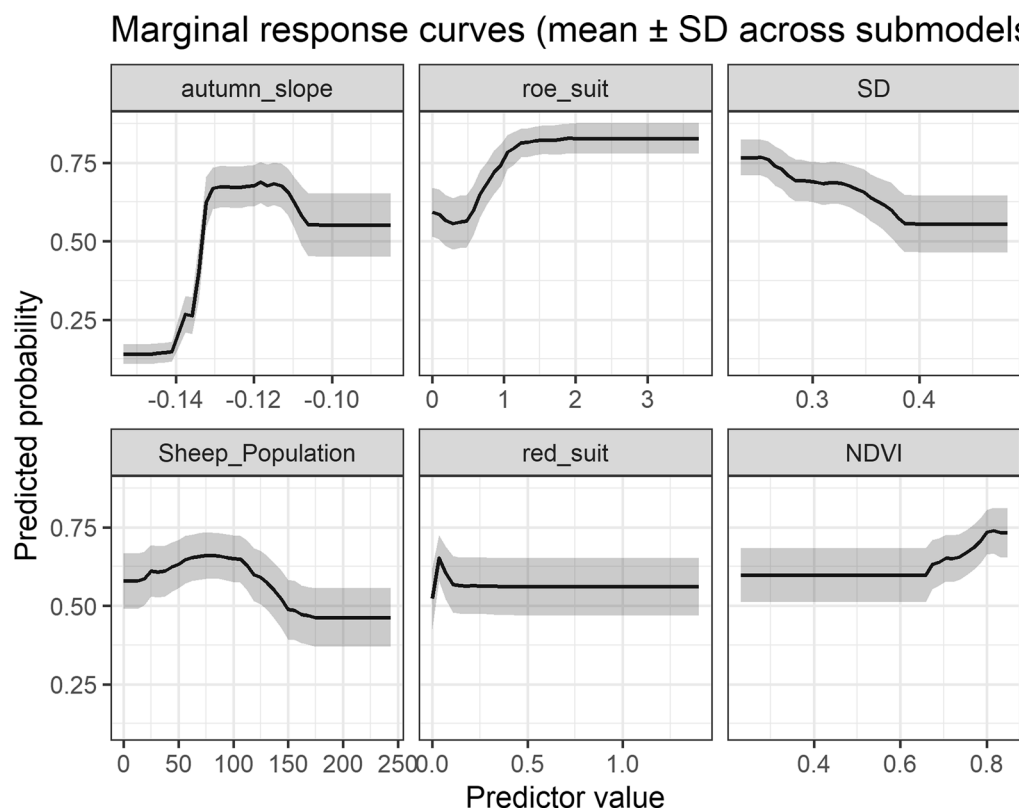


Fig. 2 Marginal response curves for the six most influential predictors of Imizol-treated bovine babesiosis. Solid lines show the mean predicted probability across the 100 BRT submodels; grey ribbons show ± 1 standard deviation across submodels at each predictor value, with other predictors held at their mean values. Predictor abbreviations: *SD* saturation deficit; *roe_suit* and *red_suit* predicted habitat suitability for roe and red deer

accounting for environmental predictors. The small effect size suggests limited residual spatial structuring after accounting for environmental predictors, despite statistical significance driven by the large number of locations.

Validation of predictive models

The unthinned model demonstrated strong temporal predictive performance when validated against southwest farms reported in 2023–2024. When validation was restricted to newly affected grid cells only ($n=87$ farms), the continuous Boyce Index was 0.805, indicating strong discrimination capacity. When all southwest 2023–2024 farms were included ($n=167$), predictive performance remained equally high (Boyce Index = 0.805). Using the training-derived probability threshold, 67.4% (SD 3.2%) of newly affected southwest England locations reported in 2023–2024 were correctly classified as suitable. When extrapolated across Great Britain, model performance outside the southwest was lower but remained positive (Boyce Index = 0.583), indicating moderate transferability beyond the core endemic region. Predicted suitability was highest across southwest England, consistent with the region used for model training, with additional spatially localised areas of elevated suitability identified elsewhere in Wales, northwest England and parts of Scotland (Fig. 3).

Spatial thinning and sensitivity analyses

Spatial thinning resulted in consistently lower internal and temporal predictive performance compared with the unthinned model (Supplementary information Tables S1 and S2).

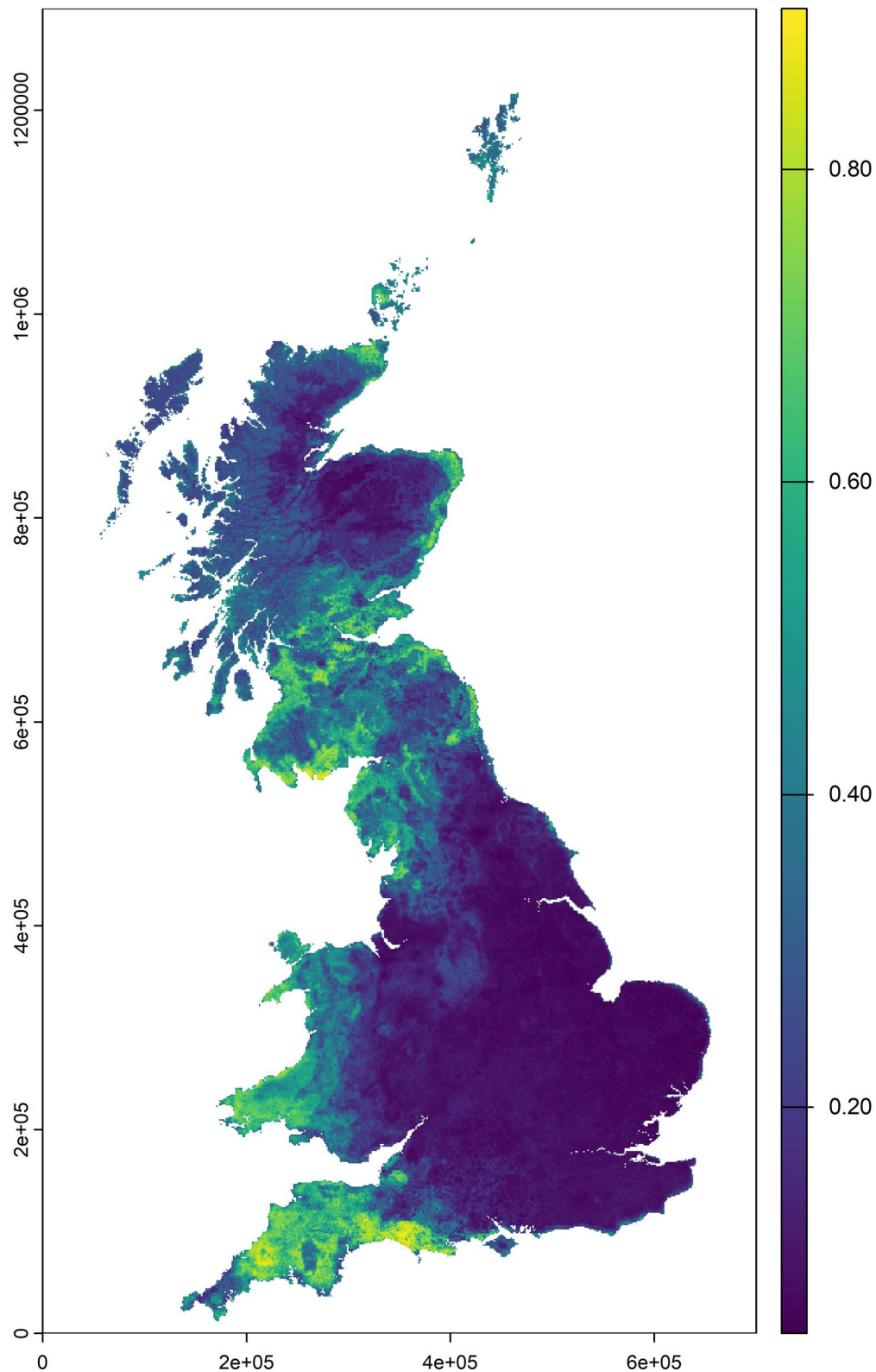


Fig. 3 Predicted spatial suitability for Imizol-treated bovine babesiosis across Great Britain from BRT models. Colours represent the mean predicted probability of occurrence across 100 model runs, with higher values indicating greater predicted suitability for treated clinical babesiosis

Exclusion of saturation deficit produced only marginal differences in internal cross-validation performance relative to the unthinned model including all predictors (Supplementary information Table S3); however, validation against independent datasets showed consistently lower Boyce Index values for the saturation-deficit-excluded model (Supplementary information Table S4). Exclusion of autumn cooling reduced internal performance metrics relative to the unthinned model including all predictors (Supplementary information Table S3). Relative influence rankings were broadly preserved across sensitivity analyses excluding correlated climatic predictors (Supplementary information Table S6). When autumn cooling was excluded from the model, saturation deficit became the highest-ranked predictor, whereas exclusion of saturation deficit increased the relative influence of autumn cooling. This pattern indicates that the two variables capture overlapping aspects of seasonal climatic constraints on tick activity, rather than representing independent drivers. Consequently, their individual relative influence values should be interpreted cautiously because correlated predictors may distribute model importance between them or substitute for one another in the fitted trees. Both correlated climatic predictors were retained in the final model to optimise predictive performance and transferability.

Model performance was robust to variation in the cattle density threshold used for pseudo-absence selection. Sensitivity analyses using alternative thresholds of ≥ 1 and ≥ 10 cattle/km² produced cross-validated AUC, correlation and deviance values that were effectively identical to those of the primary model (Supplementary information Table S5), indicating that overall predictive performance was not sensitive to inclusion of lightly or more intensively stocked cattle systems in the background sample. Relative influence patterns were also stable across cattle density threshold sensitivity analyses (Supplementary information Table S7). In both alternative threshold models, autumn cooling remained the dominant predictor, accounting for over one third of total model influence, while saturation deficit, deer suitability indices and livestock density contributed moderate influence.

Discussion

This study provides the first national-scale analysis of climate, environment and host correlates of treated clinical bovine babesiosis in Great Britain using compulsory Imizol notification data as a proxy for disease occurrence. In a context where bovine babesiosis is not statutorily notifiable and laboratory-based surveillance captures only a small proportion of clinical cases [6], this approach offers a rare opportunity to quantify broad-scale determinants of disease patterns and to identify areas where treated clinical babesiosis may plausibly emerge.

Climatic predictors dominated model performance, consistent with extensive evidence that *I. ricinus* development and host-seeking activity are primarily constrained by temperature and atmospheric moisture [36, 59]. Slower autumn cooling and lower saturation deficit were strongly associated with increased suitability for treated clinical babesiosis, capturing overlapping aspects of a late-season climate regime that permits prolonged tick questing and sustained livestock exposure. These findings align with field and experimental studies demonstrating that mild autumn conditions can extend tick activity or generate secondary autumn activity peaks [60, 61], while elevated saturation deficit suppresses questing even under otherwise favourable temperatures [39, 40, 43]. The comparatively low influence of spring warming likely reflects its limited spatial variability within the southwest England study region, as indicated by the small mean and standard deviation of this metric (Table 1), rather than a lack of biological relevance for tick phenology. Our modelling results are consistent with UK government evidence reviews suggesting that climatic warming in the UK may extend periods of tick questing activity, with implications for livestock exposure and the geographic distribution of risk [62]. The results are also consistent with recent spatial analyses of other *I. ricinus* borne pathogens in Great Britain, including tick-borne encephalitis virus, which similarly identify seasonal temperature and moisture constraints as key determinants of pathogen emergence and geographic risk patterns [37].

Host-related predictors contributed meaningfully to model performance, with deer suitability and sheep density ranking among the most influential non-climatic variables. Deer are essential hosts for adult *I. ricinus* and are consistently associated with increased tick abundance and distribution expansion across Europe [32, 41, 63].

Their importance is epidemiologically plausible for babesiosis both through vector population amplification and potential involvement in *B. divergens* maintenance, as wild deer in the UK have been shown to carry *B. divergens* or closely related parasites [10, 64] and to play a role in feeding adult ticks [63]. The association between sheep density and predicted suitability highlights the complex role of mixed grazing systems in shaping tick hazard for cattle. Sheep are competent hosts for *I. ricinus* but are not known to develop or maintain *B. divergens* infection, and therefore influence babesiosis risk indirectly through effects on tick population dynamics rather than pathogen transmission. Depending on grazing intensity and landscape context, sheep may act as maintenance hosts for ticks or reduce questing tick abundance through grazing-mediated habitat modification, thereby modifying cattle exposure in mixed systems [45, 65]. By reducing the density of questing ticks in the environment, sheep may indirectly reduce exposure of cattle to tick bites, although the extent to which this translates into reduced disease risk remains uncertain. Cattle population density showed relatively low influence compared with climatic and wildlife-associated predictors, suggesting that spatial patterns in occurrence of treated clinical babesiosis is more strongly shaped by environmental suitability for tick activity than by cattle density alone at the spatial scale considered.

Proportional land-cover variables contributed relatively little to model performance at the 2 km resolution used in this analysis. This likely reflects scale limitations rather than a lack of ecological relevance. Tick abundance and host–vector contact are often driven by fine-scale habitat features such as pasture–woodland edges, hedgerows, and ecotonal structures that are not well captured by coarse compositional land-cover metrics aggregated over large grid cells [66–68]. In national-scale analyses, such features may be diluted within broad land-cover proportions, particularly where key ecological processes are already partly represented by explicit host predictors such as deer suitability and livestock density [69]. This does not imply that landscape management is unimportant; rather, it suggests that the spatial scale of available covariates and disease data may be too coarse to detect well-established field-scale mechanisms.

Weak but significant residual spatial autocorrelation indicates that fine-scale processes operate in addition to the broad-scale environmental suitability captured by the BRT models. In vector-borne disease systems, such residual clustering is commonly attributed to processes acting at finer spatial scales, including local host movement, fine-scale vector dispersal and heterogeneity in habitat structure or management that is not fully captured by coarse climatic or landscape predictors [70]. In the context of bovine babesiosis, this may reflect movement of deer across neighbouring grazing areas, local redistribution of ticks between adjacent farms or unmeasured variation in farm-level exposure or management practices. Farm-level management practices may also influence observed patterns of treated clinical babesiosis but were not captured in the predictors used in this analysis. Although the magnitude of spatial autocorrelation was low, these findings highlight scope for incorporating finer-resolution habitat metrics or explicitly spatial modelling approaches to further improve inference and predictive transferability.

A key contribution of this study is the demonstration that routinely collected veterinary medicines notification data can be leveraged to develop spatially transferable models of suitability for clinically important tick-borne disease in livestock. The resulting suitability maps should be interpreted as complementing existing passive laboratory surveillance for bovine babesiosis rather than reproducing the distribution of laboratory-confirmed cases. Whereas laboratory surveillance identifies where disease has been confirmed, the present models quantify the climatic, environmental and host-related conditions associated with treated clinical bovine babesiosis and use these relationships to predict spatial suitability across Great Britain to identify areas with similar underlying suitability. The predicted suitability surface therefore represents longer-term suitability for treated clinical disease, rather than observed case counts or year-specific outbreak dynamics. Because the suitability surface is derived from relationships between treated clinical disease occurrence and underlying climatic, environmental and host-related predictors, it provides a basis for assessing how changes in these conditions may influence future spatial suitability.

Areas of high predicted suitability without reported Imizol notifications therefore highlight locations where ecological conditions appear permissive for disease occurrence, even if treated clinical cases were not detected during the study period. These areas may represent locations where disease has not occurred, where cases have not required treatment, or where treated cases have not been reported. Consistent with this interpretation, when evaluated against independent data the model correctly classified approximately 67% of newly affected farms (87 locations) reported in southwest England during 2023–2024 as suitable, despite being trained exclusively on earlier data. This supports the interpretation that the suitability surface captures underlying conditions associated with disease occurrence rather than patterns of past case reporting alone.

Although predictive performance outside the southwest endemic region should be interpreted cautiously, reflecting the limited number of reported farms in non-endemic areas and model training under conditions of sustained disease occurrence, these areas remain epidemiologically relevant. Given these data limitations, predicted suitability surfaces are likely to be most informative for surveillance when trained and interpreted at a regional, sub-national scale. From a surveillance and policy perspective, they highlight locations where treated clinical babesiosis could plausibly occur under similar conditions, supporting targeted veterinary awareness, diagnostic investigation and field investigations in regions outside the traditional southwest endemic focus.

Several limitations inherent to the use of treatment notification data should be acknowledged. Imizol notifications represent treated, clinically recognised cases of bovine babesiosis rather than total infection incidence and therefore reflect veterinary recognition, treatment-seeking behaviour, prescribing practices and regulatory compliance in addition to underlying transmission processes. Furthermore, because clinical disease is influenced by host immunity (and treatment and disease reporting effort by farmers and vets can be uneven across the landscape or between farmer and vet groups), areas supporting sustained parasite transmission may not necessarily experience the highest incidence of clinically recognised disease. Subclinical or untreated infections are not captured in this study and farm address coordinates may not precisely represent grazing locations, particularly in extensive systems. Because predictors were summarised across multiple years, the models characterise typical environmental and host-related conditions associated with treated clinical babesiosis, rather than year-specific outbreak patterns. Predicted values should therefore be interpreted as indicating where conditions are generally suitable for treated clinical babesiosis to occur, rather than as estimates of absolute disease risk or infection prevalence.

As notification datasets continue to accumulate, future work integrating finer-resolution habitat metrics, independent data on tick abundance or pathogen prevalence (including in deer as wildlife sentinels) and prospective validation could further strengthen the use of treatment-based data as tools for surveillance, risk assessment and preparedness for livestock tick-borne diseases under environmental change.

Conclusion

Using compulsory Imizol notification data as a proxy for treated clinical disease, this study identifies key climatic, host and environmental correlates of bovine babesiosis across Great Britain. Seasonal climatic constraints on tick activity dominated model performance, with additional contributions from deer suitability and sheep density. Mandatory veterinary medicines notification data provide a valuable complementary surveillance resource for identifying areas where clinically significant babesiosis may plausibly occur and for supporting targeted veterinary awareness and surveillance under ongoing climatic and environmental change. Resulting spatial suitability maps are likely to be most informative for anticipating areas of elevated risk and guiding disease surveillance when developed and interpreted at a regional, sub-national scale.

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Data availability Imidocarb (Imizol®) treatment notification data are held by the UK Animal and Plant Health Agency and are subject to data governance and confidentiality restrictions; these data are not publicly available.

Declarations

Ethics approval and consent to participate Not applicable.

Consent for publication Not applicable.

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