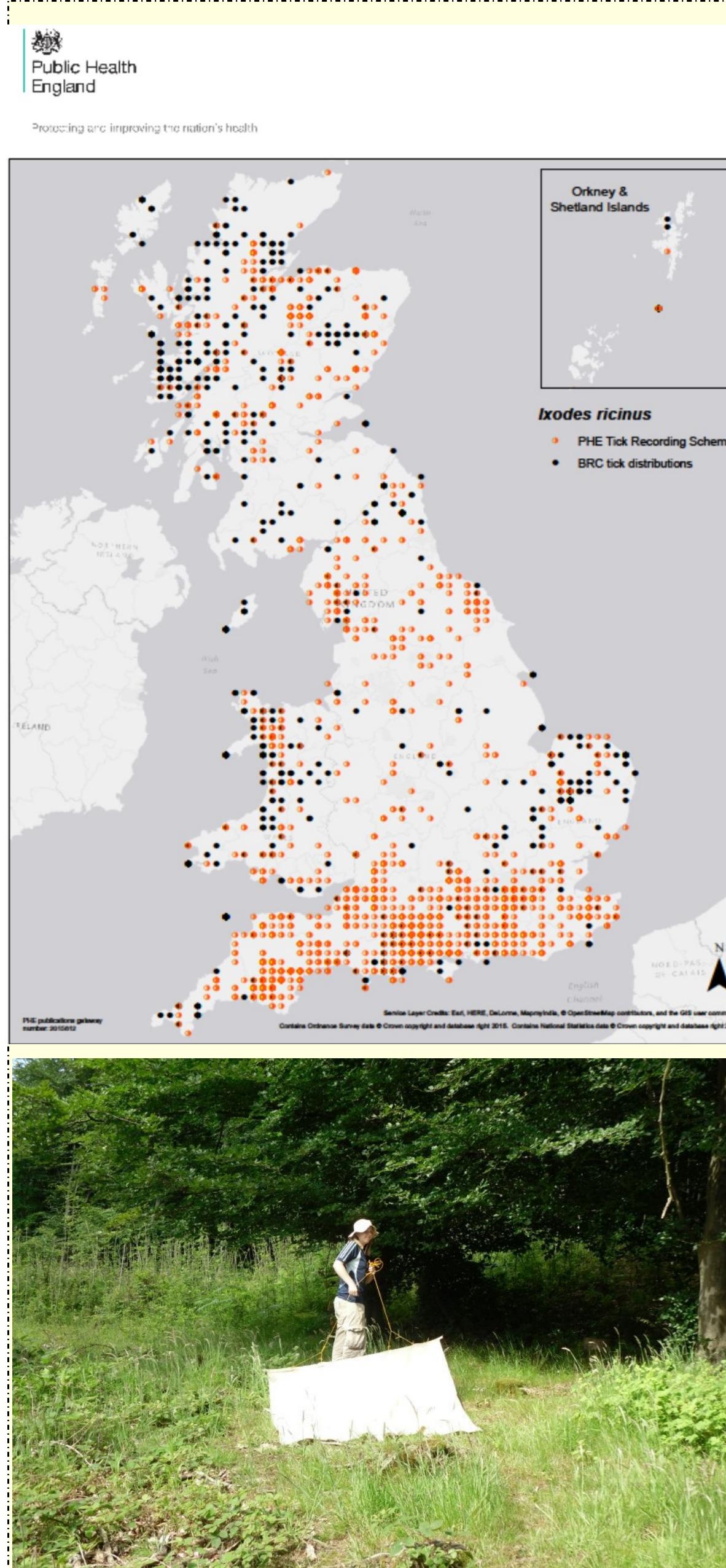


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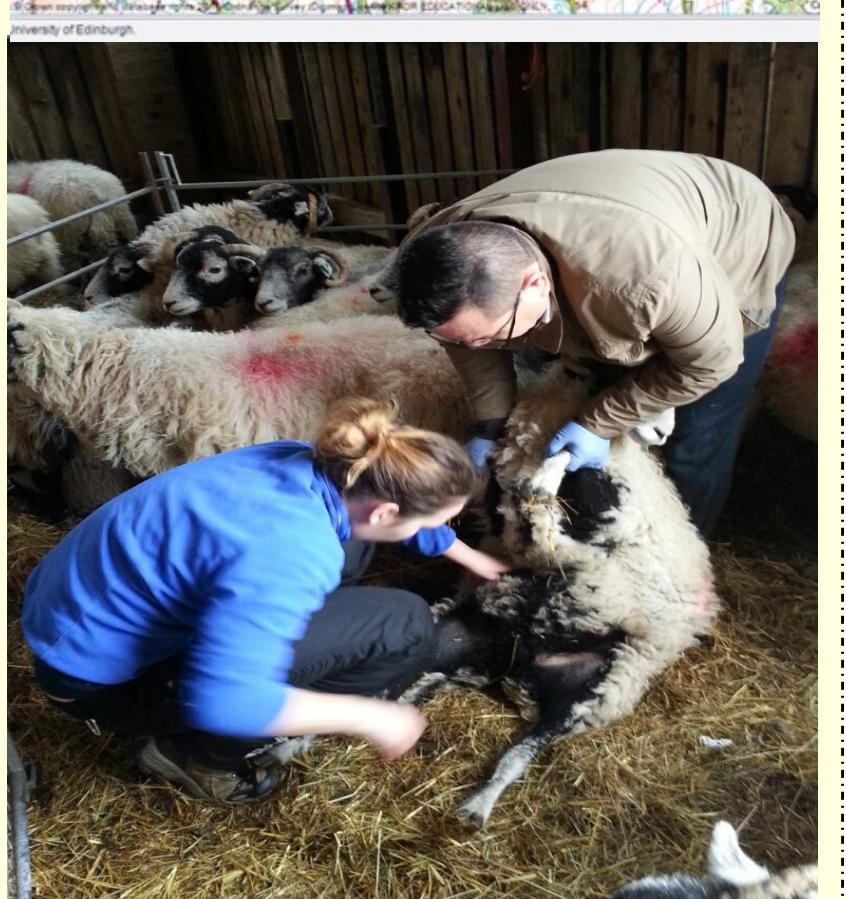
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Introduction & Aims

Changes to farm production subsidies have had a significant impact on livestock farming in the British uplands, provoking the maintenance of far less stock. The resulting decrease in grazing pressure potentially alters upland ecology in many ways, one of which is a shifting of the 'infectious disease landscape'; in which pathogens with transmission cycles favoured by a changing upland ecology will become of greater veterinary importance. Tick-borne pathogens are not only a case in point, but their threat is now augmented by increasing tick abundance, changing climate, and the extraordinary nationwide increase in the abundance of deer (that serve as a key host species).

The project planned to simultaneously explore the three tick-borne diseases (TBD's) that pose the greatest threat to livestock in the UK uplands: (i) red water fever, caused by *Babesia divergens*, (ii) louping ill caused by the louping ill virus, and (iii) tick-borne fever, caused by *Anaplasma phagocytophilum*. All three are transmitted by the catholic-feeding tick *Ixodes ricinus*, and have established wildlife reservoirs. Due to lack of funds and time, many of these diseases go unreported, but anecdotal evidence suggests that they remain a well-recognised threat to livestock.



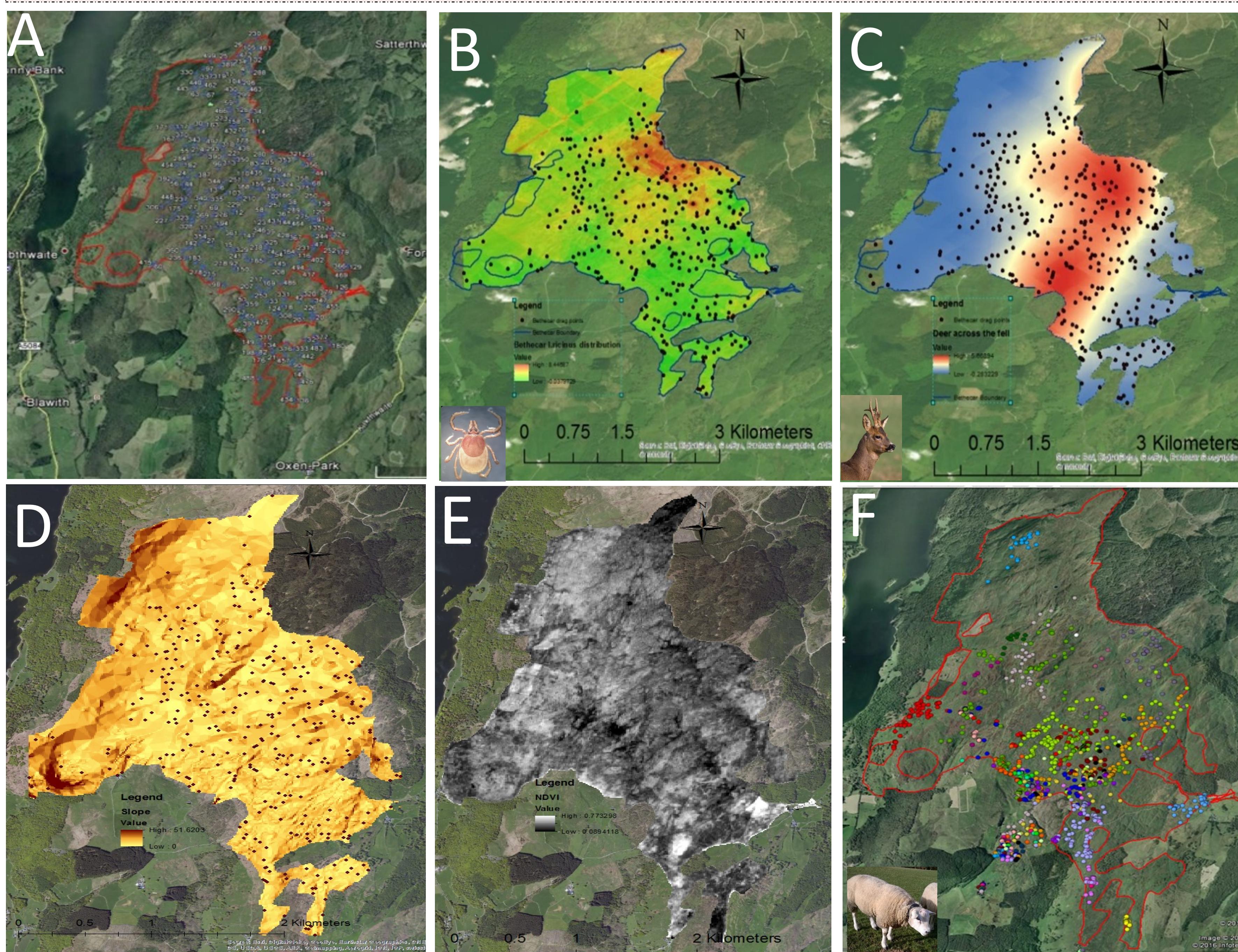
Research was concentrated on common grazing land in Cumbria, objectives aimed to investigate the idea that:

Risk = Environmental Hazard x Exposure Rate

- By taking a holistic view to assess environmental hazard & quantify exposure rates on grazed common moorland
 - Identifying the ecological drivers behind the questing tick population
 - Determining whether questing ticks evenly distributed across the Moor
 - Understanding if exposure rates shaped by individual sheep movement on the Moor
 - Assessing if tick and TBD burden is equal for all sheep
- Does tick/TBD burden on sheep correlate with the environmental risk posed by the area of the Moor on which they graze?

Results

Bethcar moor was surveyed in June 2015 & April 2016, 328 waypoints were sampled via tick dragging across the moor. A total of 390 *I. ricinus* ticks were collected and processed. All ticks were tested for *A. phagocytophilum* and *Babesia* spp, giving a prevalence of 3.33% and 0.26% respectively. Positive *Babesia* samples were found to be deer associated species *B eu1* & *B venatorum*. A total of 200 nymphs and 10 adults were tested for Louping III, none were positive.

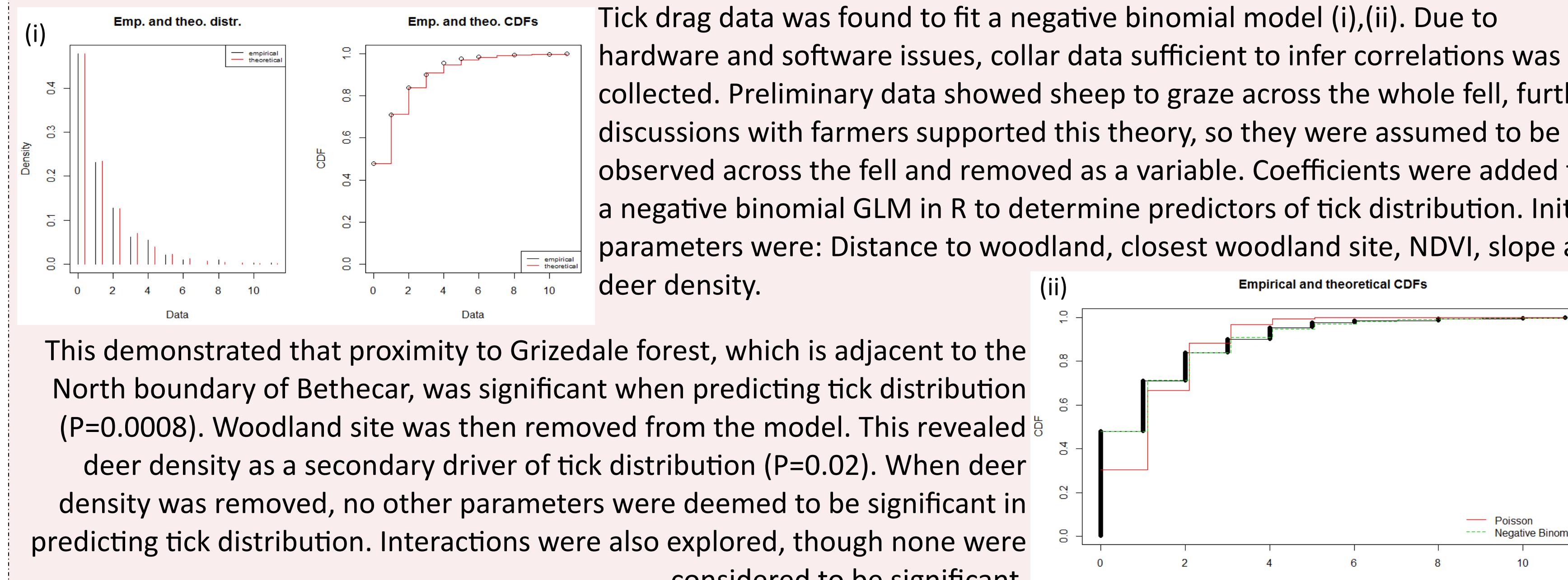


Map layers of collected data were generated in ArcMap: A) Bethcar boundary & drag points. B) Heat-map of ticks; kriging drag data. C) Deer movement across the fell. D) Slope, generated from Digital Elevation Model. E) NDVI F) Plotted sheep movement

Fitting the model

Tick drag data was found to fit a negative binomial model (i),(ii). Due to hardware and software issues, collar data sufficient to infer correlations was not collected. Preliminary data showed sheep to graze across the whole fell, further discussions with farmers supported this theory, so they were assumed to be observed across the fell and removed as a variable. Coefficients were added to a negative binomial GLM in R to determine predictors of tick distribution. Initial parameters were: Distance to woodland, closest woodland site, NDVI, slope and deer density.

This demonstrated that proximity to Grizedale forest, which is adjacent to the North boundary of Bethcar, was significant when predicting tick distribution ($P=0.0008$). Woodland site was then removed from the model. This revealed deer density as a secondary driver of tick distribution ($P=0.02$). When deer density was removed, no other parameters were deemed to be significant in predicting tick distribution. Interactions were also explored, though none were considered to be significant.



Materials & Methods

- Cross-sectional survey of 500ha of common land
 - Drag sites randomly generated
- Questing *I ricinus* ticks collected: 328 3x10m drags
- Periodic sampling of sheep for ticks
- Expert knowledge to inform wildlife movement
- Deer blood samples from the Forestry Commission
- GPS collars; individual sheep movement
- Pathogens screened for using nested & qPCR, positives sequenced
- ArcGIS & Sentinel-2 to create maps
- Use of GLM to identify drivers of tick densities

Exploring The Link

Sequence data was generated for 11 of the 13 positive *A. phagocytophilum* samples. These were compared with 118 other sequences that were obtained from ticks taken off sheep, deer bloods and other farms in the South Lakes.

Multiple sequence types were shown to be circulating Bethcar Moor, all of which clustered with other sequence types that were collected from sheep grazing the fell and sequences obtained from BLAST, which have previously been observed in sheep and ticks from sheep.

