Environmental risk factors for Louping-ill virus among sheep farms in Scotland

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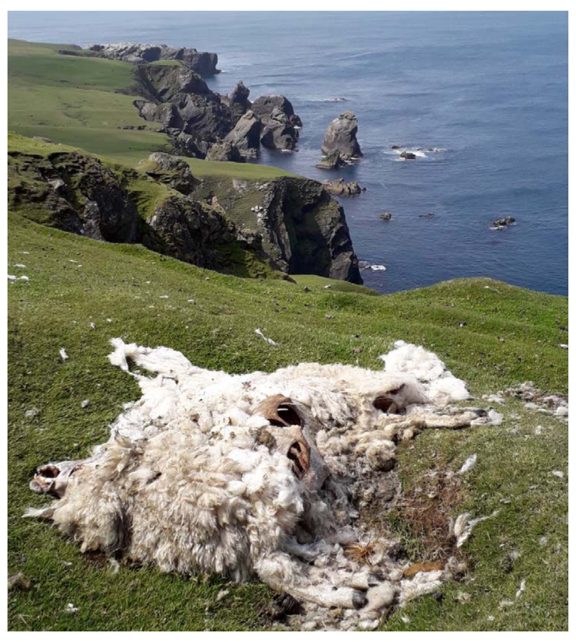
EXECUTIVE SUMMARY & KEY MESSAGES

Identifying the risk factors for disease is crucial for developing policy and strategies for controlling exposure to pathogens. Here we test for the environmental risk factors associated with Louping-ill virus - an endemic tick-borne pathogen that kills sheep. By combining seroprevalence data from 125 sheep farms across Scotland with GIS-based environmental variables, we found higher risk in upland/moorland habitats, areas with higher red deer densities, and areas with warmer climates. These results can inform policy on targeting disease mitigation and awareness in higher risk habitats and areas, and have implications for deer management policy.

BACKGROUND & AIMS

Identifying risk factors is often challenging, especially in complex disease systems, such as vector-borne diseases, that have multiple hosts and myriad potential environmental drivers.



Ixodes ricinus ticks are ubiquitous throughout most of Europe, have a complex ecology, biting most land animals, and carry many pathogens, including *Borrelia burgdorferi* that causes Lyme disease and tick-borne encephalitis virus (TBEv). The UK variant of TBEv is Louping-ill virus (LIV), which kills primarily sheep and red grouse.

Here we aim to identify the environmental risk factors for LIV among sheep farms in Scotland, to inform policy on disease mitigation strategies.

METHODS

Seroprevalence data were collected from 125 sheep farms randomly selected throughout Scotland, by blood sampling 25-29 ewes per flock between July 2006 and August 2008. Haemagglutination-inhibiting antibody (HIA) tests identified antibodies to LIV, indicating recent infection with LIV.

Environmental variables associated with each farm location were downloaded from GIS databases on habitat, climate, sheep and red deer densities.

General Linear Mixed models were conducted with % seroprevalence per flock as the response variable, environmental data as the explanatory fixed effects. A binomial model was specified and a backwards stepwise procedure conducted to eliminate non-significant factors from the model. Model selection was based on AIC.

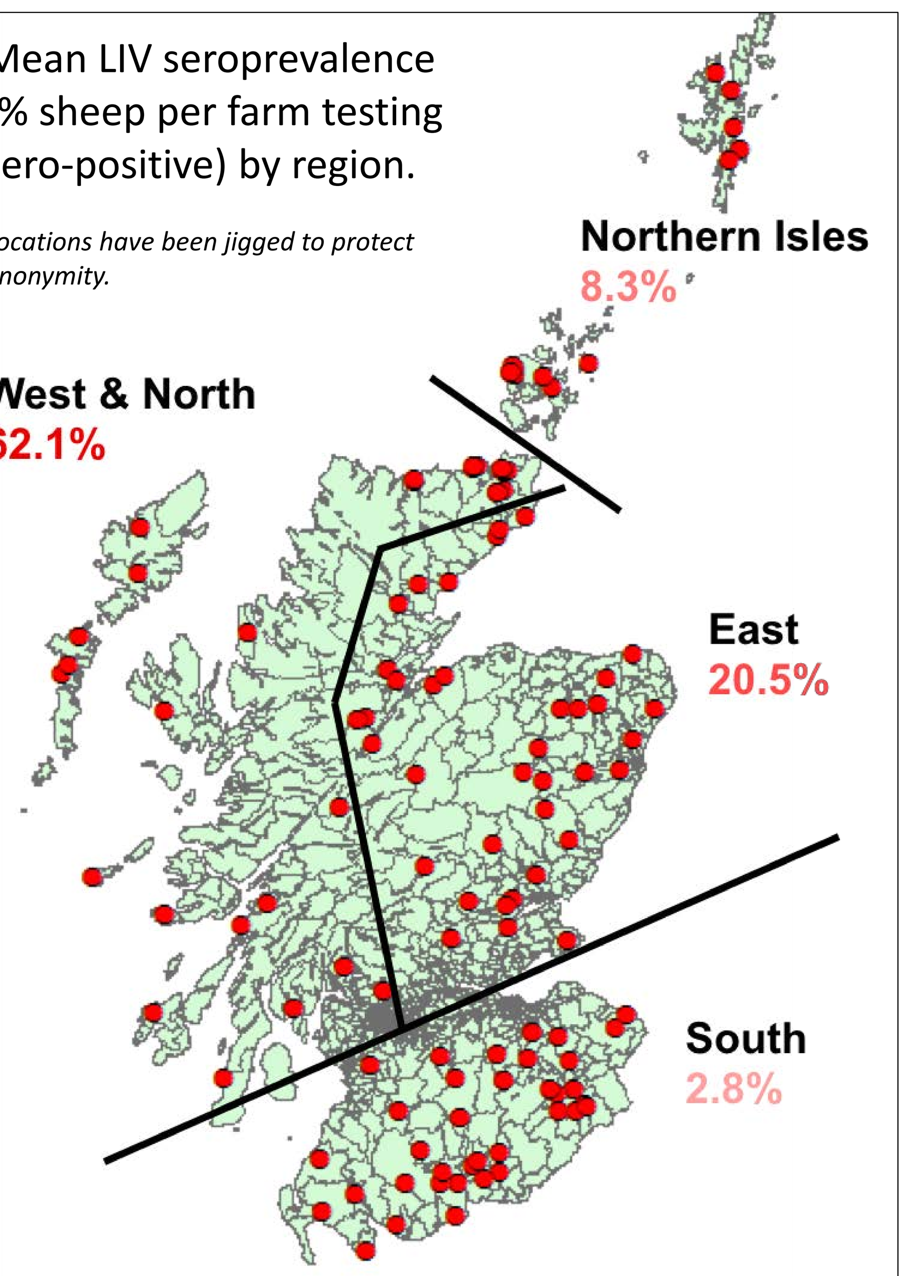
RESULTS & DISCUSSION

Of the 125 sheep farms sampled, 28 (22.4%) farms contained at least one LIV seropositive sheep. The national average seroprevalence was 6.4% (range 0-100%; median 0%). If only sero-positive farms were considered, the average seroprevalence was 28.5% (range 3.7-100%; median 25.9%).

- Lower LIV risk was associated with lowland improved grassland habitats.
- We found no effect of sheep stocking densities on LIV risk, implying that alternative tick and LIV hosts, and unmeasured factors such as on-farm management, are more important than the sheep themselves, even though sheep can carry ticks and transmit LIV.

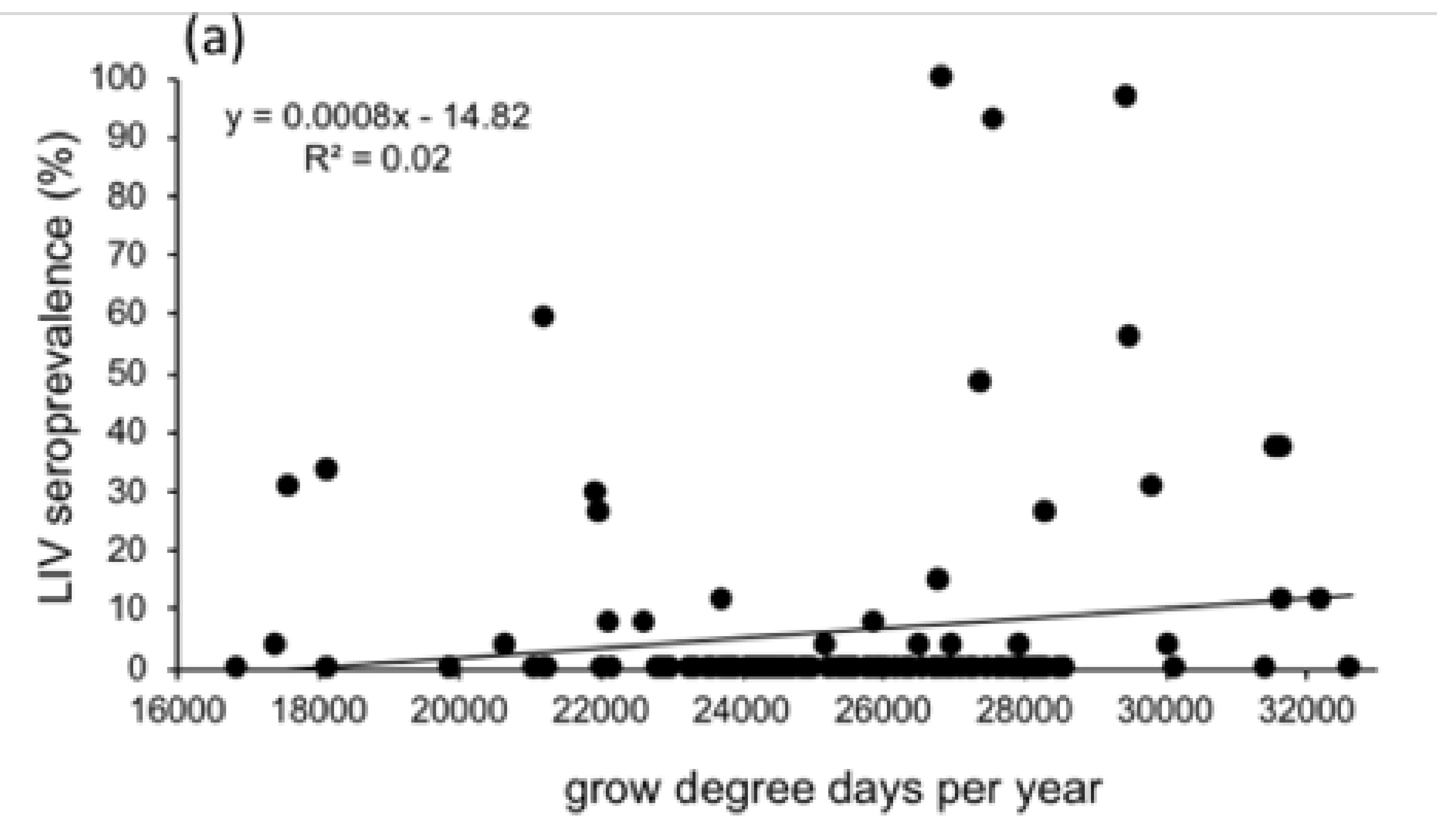
Mean LIV seroprevalence (% sheep per farm testing sero-positive) by region.

Locations have been jigged to protect anonymity.

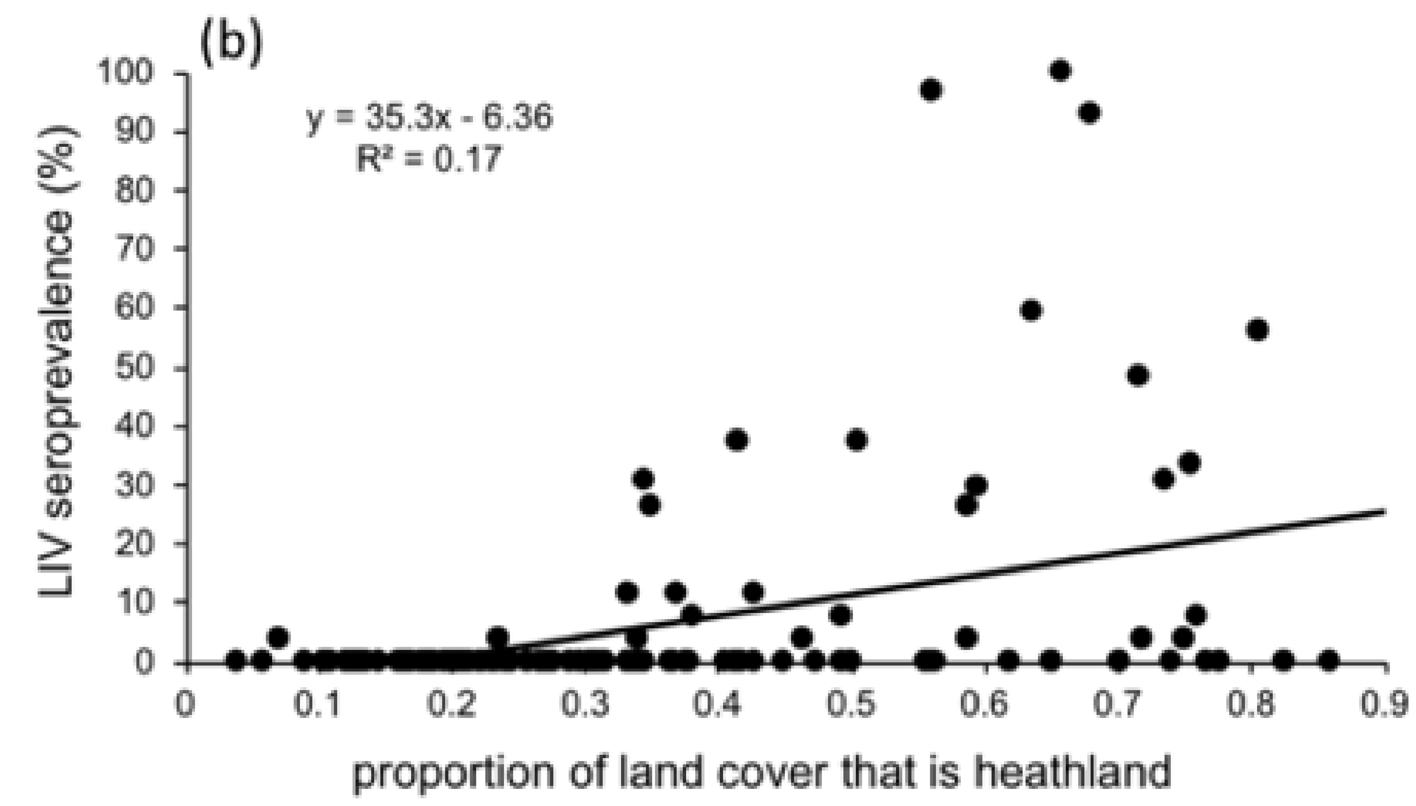


Higher seroprevalences were associated with:

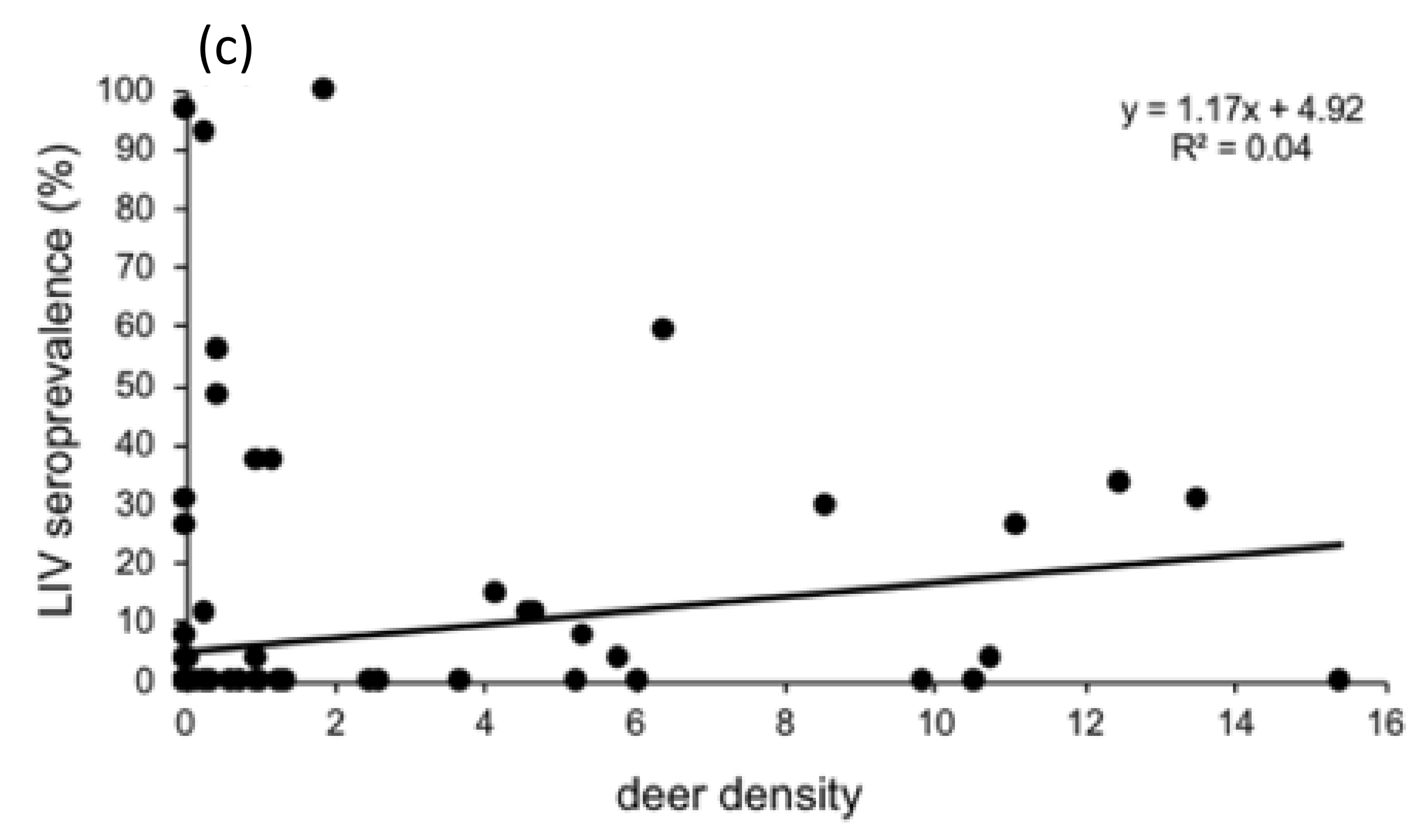
(a) Upland/moorland habitats, in accordance with the habitat preferences of alternative LIV transmission hosts (such as red grouse). Points are raw unadjusted data.



(b) Areas of higher deer density, supporting predictions from previous theoretical models, since deer are the key *Ixodes ricinus* tick hosts in this system. Points are raw unadjusted data.



(c) A warmer climate, concurring with our knowledge of how temperature affects tick activity and development rates. Points are raw unadjusted data.



CONCLUSIONS

Policy implications include targeting disease management in higher risk habitats (heathland) and warmer areas, and in the presence of alternative LIV hosts (e.g. grouse) and tick hosts (especially deer). The climate associations indicate there may be climate warming implications. These results can also inform deer management policy, especially where there may be conflict between contrasting management objectives, e.g. revenue from deer hunting vs sheep farmers.

ACKNOWLEDGEMENTS

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