

POLICY BRIEF: NETWORK REPRESENTATION OF DEER IN GREAT BRITAIN TO INFORM SURVEILLANCE AND CONTROL OF INFECTIOUS DISEASE

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1. KEY MESSAGE

We constructed contact network representations for the national populations of the six most common species of deer found in Great Britain. Spatial clusters identified in these networks would be useful for planning disease surveillance and control strategies for infectious diseases of cervids.

2. MAJOR FINDINGS

Some clustering is evident in simulated deer contact networks. Disease spread within the identified clusters is more likely than spread between the clusters. The areas occupied by the six deer species in Great Britain overlap in ways which might allow jumps of disease pathogens across the country in ways which would not otherwise occur.

3. OBJECTIVES

Study the spatial distribution of six deer species (Chinese water, Chinese muntjac, fallow, red, roe, and sika) in Great Britain, in order to inform strategies for:

- a) Surveillance for infectious disease;
- b) Control of infectious disease in the event of incursion.

4. POLICY IMPLICATIONS

The connected clusters identified in the simulated deer networks could be used to plan surveillance strategies: surveillance activities should aim to cover all areas/clusters in the networks. Disease control strategies in the event of disease incursion might be most effective if targeted at spatial corridors separating the identified network clusters. Additional man-made barriers to restrict deer movement could help to further fragment the tightly linked red deer cluster in Scotland.

5. IMPORTANT ASSUMPTIONS AND LIMITATIONS

Data: Used deer density estimates for 2015, based on presence absence data for 2005-2015 and habitat suitability factors. Limited GPS tracking data (1998-2000, 2003-2004) for a small number of red deer from five herds in the Cairngorms National Park area were used to estimate herd home range sizes.

Methods: Deer herd locations were simulated based on the density estimates. Contact networks of links between deer herds were constructed, based on distance between herds (as proxy for contact probability between herds and environmental pathogen contamination). We identified connected clusters in these networks, within which spread of infectious disease is more likely to occur.

Limitations: Assumed herd sizes are constant and of equal size. Ignored seasonal changes in deer activity (e.g. ruts) due to lack of data. Did not take into account natural/man-made barriers to movement. Tracking data available only for small number of red deer. Analyses were performed separately for the six deer species, as no data on interspecies transmission were available.

6. FIGURE

Example figure indicating clusters in the simulated red deer network is shown below. Similar figures for other five deer species are available in the full project report.



7. LINKS TO EXISTING PUBLICATIONS OR REPORTS

Report on Smartsheet: EPIC 3 Topic 2, Milestone 2.2.1.4

8. POLICY COMMENTS/RESPONSE

None to date.