

What is the epidemiological significance of *Mycobacterium bovis* diversity in Great Britain?

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The expanding geographical range of bovine tuberculosis high risk areas in Great Britain has resulted in escalating costs to an already expensive disease control program. The aim of this study was to investigate whether the diversity of *Mycobacterium bovis* spoligotypes could be used to predict reasons for parishes changed from low to high disease risk. While some differences in spoligotype diversity measures were detected in parishes moving from low to high risk, differences were not found to be significant. Therefore for the parishes examined, increased incidence of bovine tuberculosis could not be linked to changes in diversity. Further research is required to determine the practical epidemiological function of diversity measures in bovine tuberculosis control.

Introduction

In this study, the use of cattle *Mycobacterium bovis* spoligotype data to predict reasons for parishes changing from low to high bTB risk was examined. Ability to predict this transmission would enable tailored control measures to be applied to prevent the further expansion of these high risk areas.

Hypothesis

Spoligotype diversity of herd breakdowns is directly related to methods of transmission (fig. 1). Should establishment of high risk areas be caused by local establishment of a *M. bovis* spoligotype, then we claim that there should be an observable decrease in diversity with regards species abundance in newly emerged high risk parishes. Alternatively, if parish bTB risk change is exclusively related to the practice of buying-in cattle, similar spoligotype diversity measures should be observed. Thus, examination of *M. bovis* diversity should be able to detect the cause of incidence changes in parishes.

Methodology

Spoligotype data were attained for parishes that went from four year to one year testing between 1998 to 2008. Only including parishes with ten or more samples before and after the year of change (n=13) ensured the *M. bovis* population in the parish was sufficiently represented. Differences in sampling effort was accounted for by sub-sampling the larger dataset to the smaller dataset size for 100 repetitions (without replacement). Combined average distributions of the diversity measures Species Richness (# unique spoligotypes) and Shannon Entropy (measure of richness and abundance) for before and after testing interval change were compared.

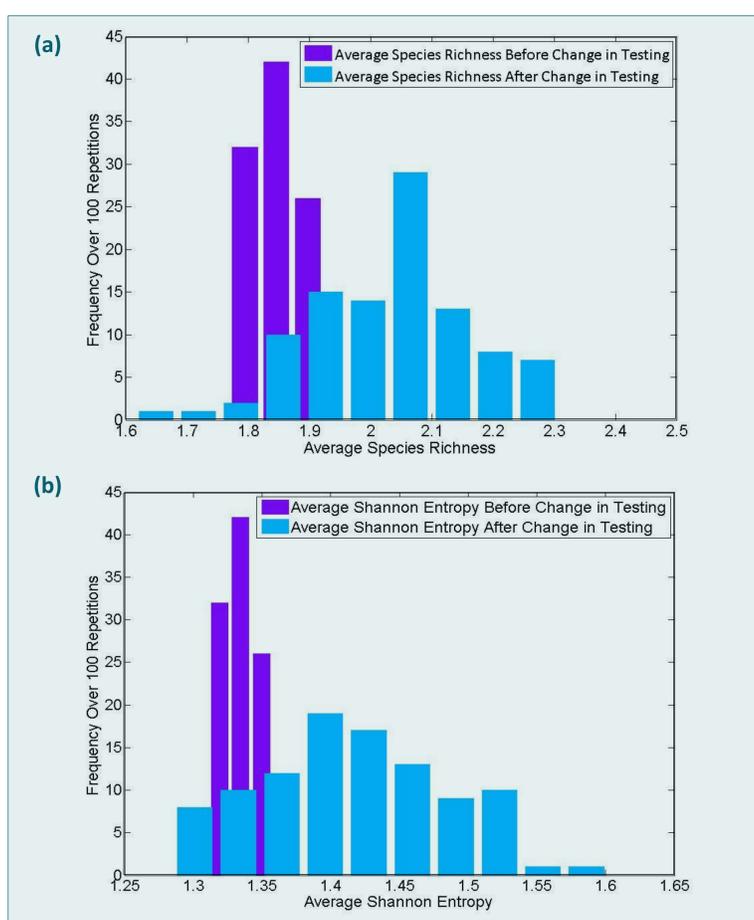


Fig. 2 Distributions of diversity measures before and after change in testing regime (a) Species Richness and (b) Shannon Entropy

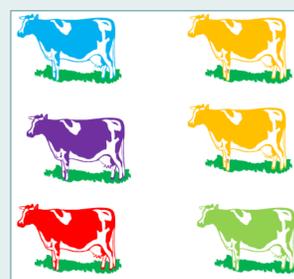
Low Risk Parish

Sporadic breakdowns caused by buying-in infected cattle

≈ SR
≈ SE

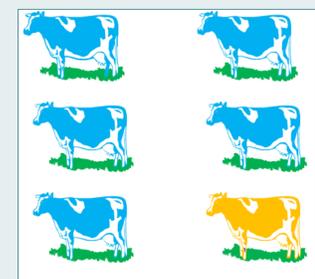
↓ SR
↓ SE

High Risk Parish



Buying-in cattle from multiple locations

High Risk Parish



Local establishment of dominant spoligotype

Fig. 1 The hypothesised cause and effect of changing bTB risk status of parishes on *M. bovis* spoligotype diversity. Each different coloured cow represents a unique spoligotype, SR = Species Richness and SE = Shannon Entropy

Results

Distributions of average spoligotype diversity measures using Species Richness and Shannon Entropy show some differences for before and after the testing interval changes (fig. 2). However, the considerable intersect of values at the lower end of the diversity scale highlight the failure to demonstrate significant differences in spoligotype diversity. Therefore for the parishes examined, changes in the epidemiology of transmission of infection could not be detected.

Conclusions

Examination of Species Richness and Shannon Entropy for parishes that went from four year to one year testing intervals showed that there were no significant differences in *M. bovis* spoligotype diversity given the amount of sampling available. The lack of variation in spoligotype diversity may indicate one of the following:

- There was no change in the transmission mechanisms in the parishes from a period of low incidence to a period of higher incidence
- Insufficient data were available to detect significant changes in spoligotype diversity
- Spoligotype diversity provided insufficient resolution to detect changes in diversity

Further research is required to determine if these assessment measures may be of benefit to monitor epidemiological changes in bTB low risk areas in GB. However, without the appropriate data, these measures are likely to be of limited use.

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