Latent class growth analysis of the effect of individually tailored biosecurity advice on the presence of endemic pathogens in British beef suckler herds

Mastin, A., Beauvais, W., Van Winden, S., Fishwick, J., Cardwell, J. and Pfeiffer, D., The Royal Veterinary College, United Kingdom; amastin@rvc.ac.uk

Farm biosecurity is considered integral to the avoidance of pathogen incursion, yet the effect of biosecurity measures is rarely studied. This study investigated the effect of individually tailored biosecurity advice on the presence of bovine viral diarrhoea virus (BVDV), bovine herpesvirus 1 (BHV1), *Leptospira interrogans hardjo* (L.hardjo), and *Mycobacterium avium paratuberculosis* (Map) in English and Welsh beef suckler herds. 116 farms were randomly assigned to ‘intervention’ and ‘control’ groups. Vets visited these farms annually for three years to blood sample 50 cattle and assign a numerical ‘risk score’ for each pathogen. At least three pieces of biosecurity advice were given to intervention farms and advice was given to control farms if requested. Bayesian methodology was used to identify seropositive farms (amongst youngstock for BVDV, BHV1 or L.hardjo; and adults for Map), and latent class growth analysis (LCGA) was used to identify classification of farms according to patterns of pathogen experience and risk score over time. The effect of intervention status on pathogen presence and risk score within these groups was then studied. Three risk score groups (low, medium and high) and two pathogen presence groups (low and high odds) were identified for each pathogen. Medium risk score groups showed a gradual decrease over time, with other groups remaining static. A decrease in odds of BVDV presence was observed amongst farms with low initial odds of presence, but pathogen presence was otherwise static. Intervention farms with medium risk scores had lower BHV1, L.hardjo, and Map scores than control farms, but pathogen experience remained similar to controls. Farms in high risk score groups were more likely to be in high pathogen presence groups for all pathogens except Map, where the opposite was observed. Based on these results, LCGA may provide a useful tool for capturing complex heterogeneity in longitudinal data.