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Using pathogen strain-typing to inform transmission dynamics in social networks of livestock movements

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**Purpose:**

The movement of infected stock is thought to be the primary factor for introducing *Mycobacterium avium* subsp. *paratuberculosis* (MAP) to properties, although documented evidence of farm-to-farm transmission of MAP is scarce. The objective of this study was to combine molecular pathogen typing with animal movement data to infer the possible extent of transmission of MAP between farms.

**Methods:**

The data for this study were provided by Landcorp Farming Limited (LC), farming deer, sheep, beef and dairy cattle on 119 properties throughout New Zealand. Data of livestock movement between LC properties were available from 2006 to 2010. All farms were screened for evidence of MAP infection in a subset of 20 animals per farm and species in 2010. MAP isolates from positive pooled fecal cultures on each farm were typed, resulting in 11 VNTR/SSR strains. We analyzed the probability of two in-contact farms sharing the same strain, depending on different measures of connectedness between farms in the contact network.

**Results:**

Our analysis supports that farms sharing the same MAP strain were significantly more closely connected ( $p < 0.05$ ) in the livestock movement network than farms harboring different strain types.

**Conclusions:**

Social links between farms are of dyadic nature, in other words the outcome for analysis was at the level of a pair of objects. The purpose was thus to correlate adjacency matrices representing relations between farms. A major obstacle for analyzing dyadic data is the lack of independence between observations, making classical significance tests often inappropriate. However there is a lack of consensus for alternative methods, especially in the case of multivariate analysis.

**Relevance:**

We show the short-comings of classical significance tests for dyadic observations and present results based on Multiple Regression Quadratic Assignment Procedure, an alternative based on permutation tests for making inferences in social network data and how it applies to our epidemiological data.