

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

Background



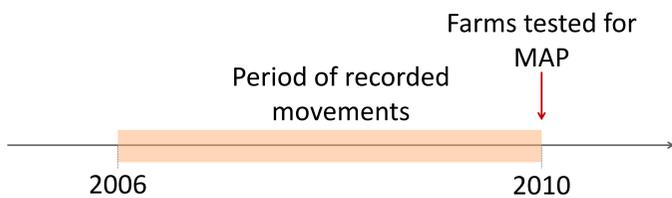
- Infection of livestock with *Mycobacterium avium paratuberculosis* (MAP) causes paratuberculosis (PTB).
- MAP infection is endemic in New Zealand farms.
- PTB may cause economic losses in some properties.
- No national control program in New Zealand, livestock trade supposedly the main source of introduction of MAP on farm.

In this endemic context, is livestock trade an important means of transmission of PTB between farms?

Data

Source: Landcorp Farming Corporation (LC), national farming enterprise

- systematic records of **livestock movements** (Beef, Sheep, Deer, Dairy) from 2006 to 2010.
- **screening for paratuberculosis** in June/July 2010:
 - 102 LC farms tested for presence of MAP,
 - Pooled faecal culture at the mob level (species within farm, 162 mobs),
 - MAP positive pools were typed (VNTR-SSR genotyping).



Results:

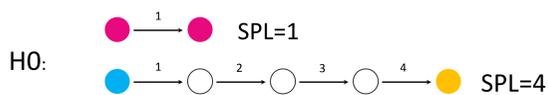
- **3531 movements**, 1.15 millions animals moved from 01/07/2006 to 30/06/2010,
- **54 MAP isolates** from positive pools were typed, originating 33 LC properties (1 to 3 different strains of isolates/farm),
- 7 VNTR-SSR loci → **11 distinct MAP strain types**.

Methods

Research question:

Are 2 farms **closely connected via livestock movements** more likely (than distant farms) **to share the same strains of MAP?**

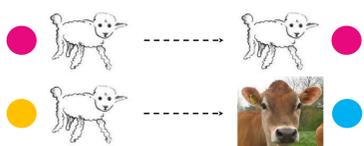
- **Outcome** = are 2 infected farms harbouring the **same MAP strain** (0/1)? (measure of clustering in the **distribution of MAP strains** on farm)
- **Main explanatory variable** = the **shortest path length** (SPL) between the 2 farms, following livestock movements. (measure of clustering in the **livestock movement network**)



Circles = farms, arrows = livestock movement between farms, colors = particular strains of MAP on farm

- Possible **confounding** for the observed distribution of MAP strains on farm:

Species effect



Farms hosting the same livestock species = likely to harbour the same strains of MAP? (MAP relative species specificity)

Island effect



Farms on the same island = likely to harbour the same strains of MAP? (geographical/ecological/evolutionary clustering of MAP strains)

Principle of the analysis

- Pair-wise relationships between farms are called dyadic observations :
 - pairs are not independent,
 - “traditional” hypothesis testing not valid.
- Dyadic observations are represented as socio-matrices, in this case:
 - “proximity” of farms in the livestock movement network (shortest path length between farms = main explanatory variable),
 - other shared attributes at the pair level :
 - same MAP strain on farm? (outcome, binary),
 - on the same island? same livestock species on farm? (confounders).

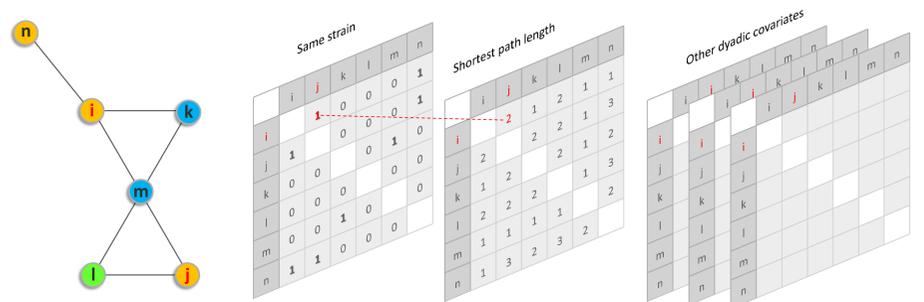


Fig. 1: theoretical network of 6 farms infected with MAP, connected by livestock movements (black lines). Colors represent particular MAP strains. Dyadic relationships are represented in socio-matrices.

- This is a problem of **correlation between matrices**.
- We used **Quadratic Assignment Procedure (QAP)** for multiple logistic regression on matrices (robust inferences for correlated observations).

Main results

- a.** 33 LC farms from which MAP isolates were typed plotted according to their geographical coordinates manually arranged to avoid farms overlapping. Colors represent MAP VNTR-SSR type
- b.** subset of LC network representing farms (circles) linked via livestock movements (arrows) projected in the Fruchterman-Reingold layout (irrespective of their geographical coordinates). Colors represent MAP VNTR-SSR type (white=farm not tested or negative, other=same color code as b). Only the 33 positive farms and farms that were along the shortest path between them were kept to simplify the display. As an illustration, the red arrows display all shortest path linking farms harbouring the “green” strain of MAP.

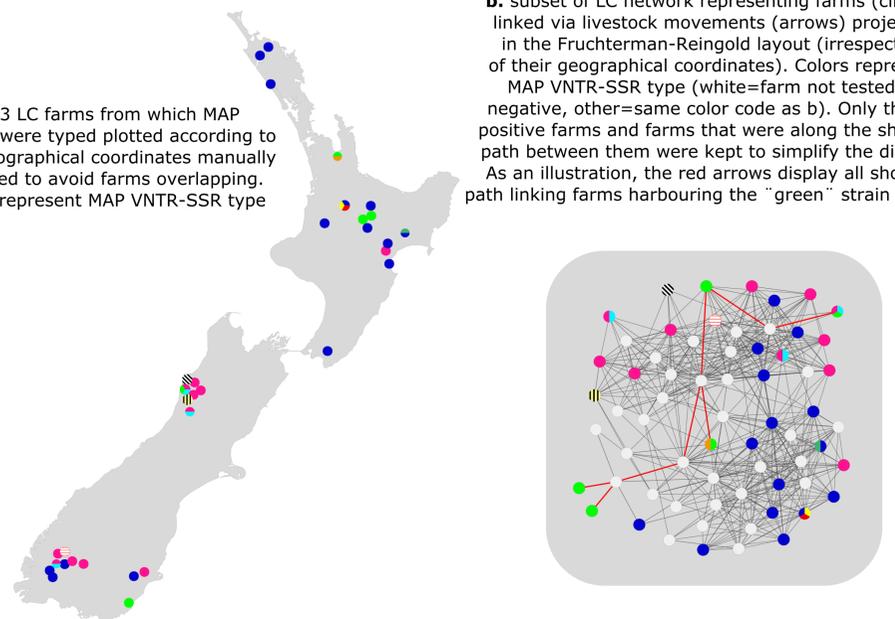


Fig.2: visualisation of the clustering in the distribution of MAP strains a. geographically and b. in the livestock movement network

- Over and above the island and species effect, movement pattern (SPL) was significantly associated with MAP strain on farm ($p < 0.05$).
- Interaction between SPL and species: the effect of SPL was stronger when two farms hosted different species and strongly significant only in this strata.
- Farms directly connected via livestock movement were most at risk of sharing the same strain of MAP. Each step further along the network path decreased the odds that 2 farms infected with MAP shared the same strain by 60%, for pairs of farms not hosting the same species.

Conclusion : these results support the role of livestock movements in the transmission of PTB between farms in New Zealand.