A STUDY OF ANIMAL MOVEMENT IN 11 CENTRAL PROVINCES OF VIETNAM BETWEEN MARCH AND AUGUST 2014

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OUTLINE

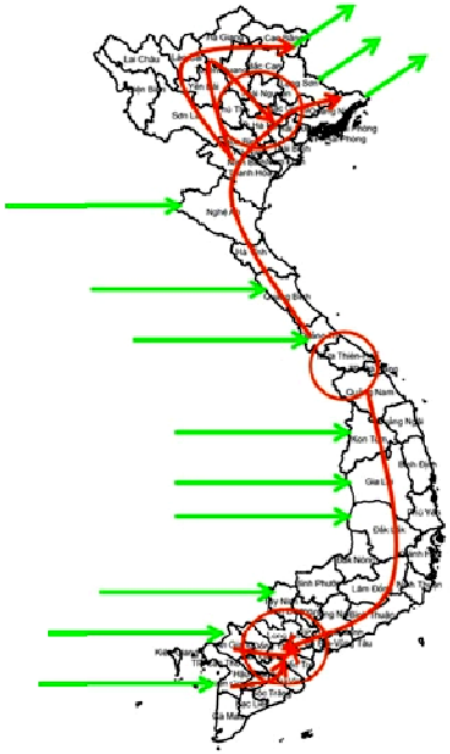
I. Background
II. Study design
III. Results and discussions
IV. Conclusions and recommendations

I. BACKGROUND

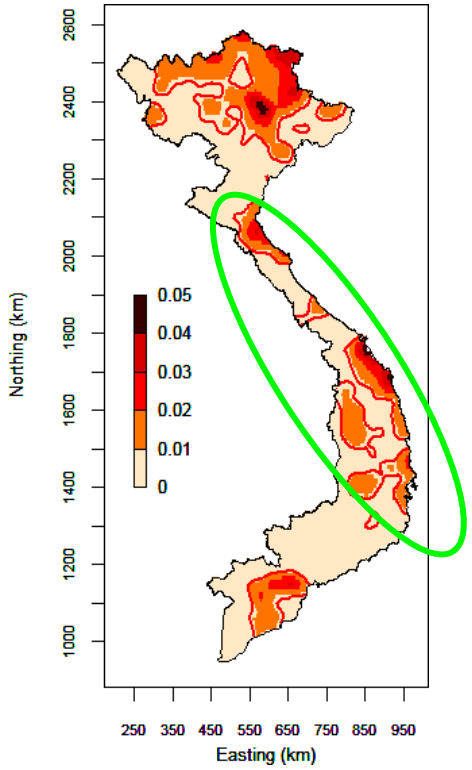
- FMDV has been in Vietnam for many years and caused serious consequences
- Animal movements within Vietnam and between countries sharing borders with Vietnam are proposed to be major factors for FMD spread
- Objectives:
  - To estimate the proportion of moved animals (cattle, buffaloes, pigs) that had prior infection with FMD virus based on antibody and virus carrier detection
  - To describe patterns of movements of FMD susceptible livestock
  - To identify some demographic risk factors that associate with FMD virus infection in moved animals

II. STUDY DESIGN

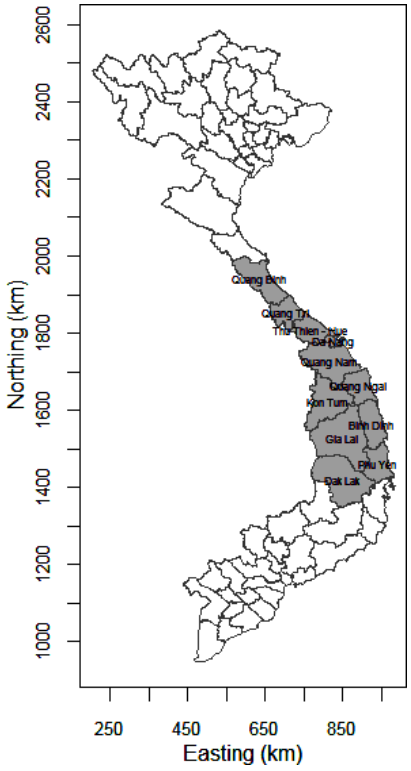
2.1. Selection of study area: 11 central provinces of Vietnam



(a) Map showing the main movement pathways of large ruminants involving Vietnam including imports, domestic movements and exports (Cocks et al., 2009)



(b) Map showing the incidence risk of FMD infected communes cumulatively estimated for the 2006 to 2012 period (Nguyễn Thu Thủy et al., 2013)



(c) Map showing the selected provinces (n = 11) for study of animal movements

II. STUDY DESIGN (cont.)

2.2. Study animal population

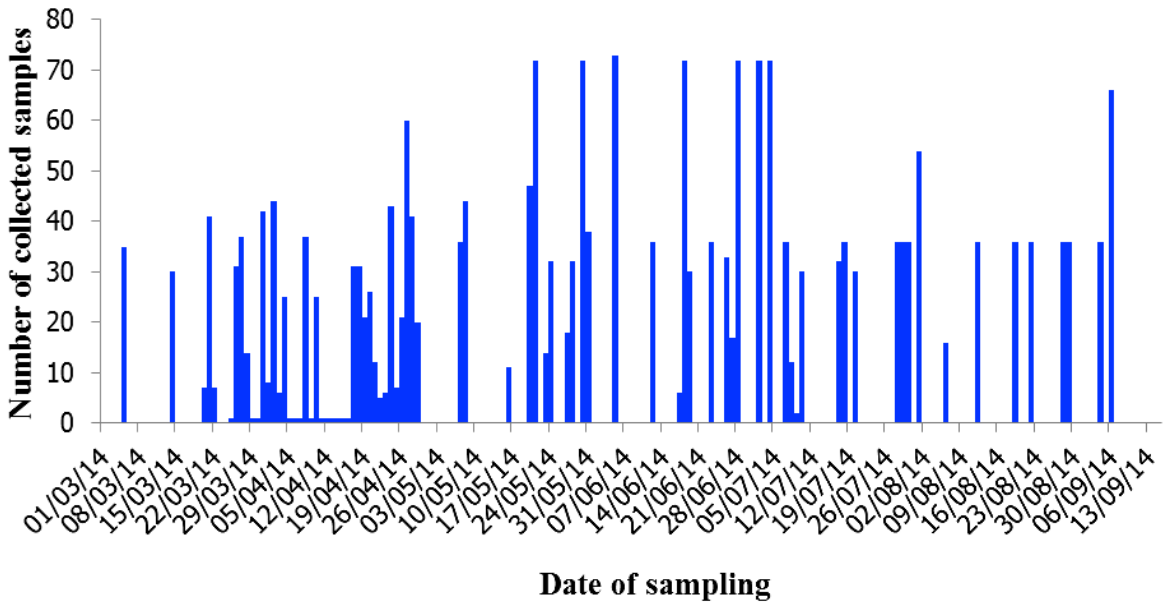
- Each study province selected 30 animals at random:
  - 24 cattle and buffaloes there were moved out of their home districts
  - 6 pigs

2.3. Sampling

- Each cattle or buffalo: Collected both serum and probang samples
- Each study pig: Collected only serum sample
- Staff of SDAH/Animal quarantine station collected samples during the first 2 weeks of the month, from March to August 2014

Field staff were trained to understand the study design and sampling

Field staff practiced taking samples



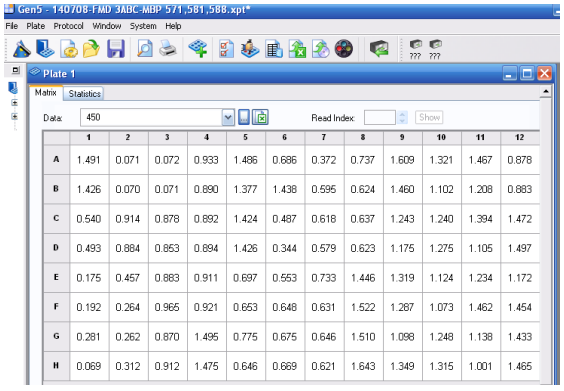
Field staff collected prbang samples

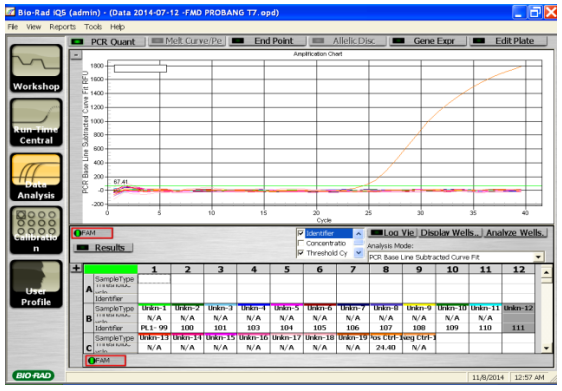
Field staff collected blood samples

II. STUDY DESIGN (cont.)

2.4. Laboratory test

- Step 1: Serum samples were tested using 3ABC ELISA
- Step 2: Only probang samples of those animals that had positive serum samples were tested using Real-time RT-PCR
- Step 3: Positive probang samples were used for virus isolation which provided virus isolates sent to RRL in Pak Chong, Thailand





II. STUDY DESIGN (cont.)

2.5. Data management

- Information about samples was recorded by field staff using a standardised form
- Information about animal movement was captured by field staff who just copied relevant information for their daily recording notebooks. These notebooks were used to record all information about animal movement
- Data of animal movement were captured from Jan to August 2014

II. STUDY DESIGN (cont.)

2.5. Data analyses

- Descriptive analysis of testing data
- Multivariable analyses were carried to identify risk factors associated with positive animals
- Social network analyses were carried out to identify fattens of animal movements

III. RESULTS AND DISCUSSIONS

3.1. FMD survey

- **Serum samples:**
  - 17.97 (95% CI 16.3 - 19.73) tested animals (**n = 1,976**) were positive
  - 68.92 (95% CI 57.1 - 79.17) buffaloes were positive
  - 20.15 (95% CI 18.15 - 22.26) cattle were positive
  - 0.25 (95% CI 0.01 - 1.39) pigs were positive
- **Probang samples:**
  - 18.36 (95% CI 14.47 - 22.80) tested animals (**n = 354**) were positive
  - 11.76 (95% CI 4.44 - 23.87) buffaloes were positive
  - 19.47 (95% CI 15.17 - 24.39) cattle were positive
- **5 FMD virus isolates were sent to RRL in Pak Chong, Thailand**

III. RESULTS AND DISCUSSIONS (cont.)

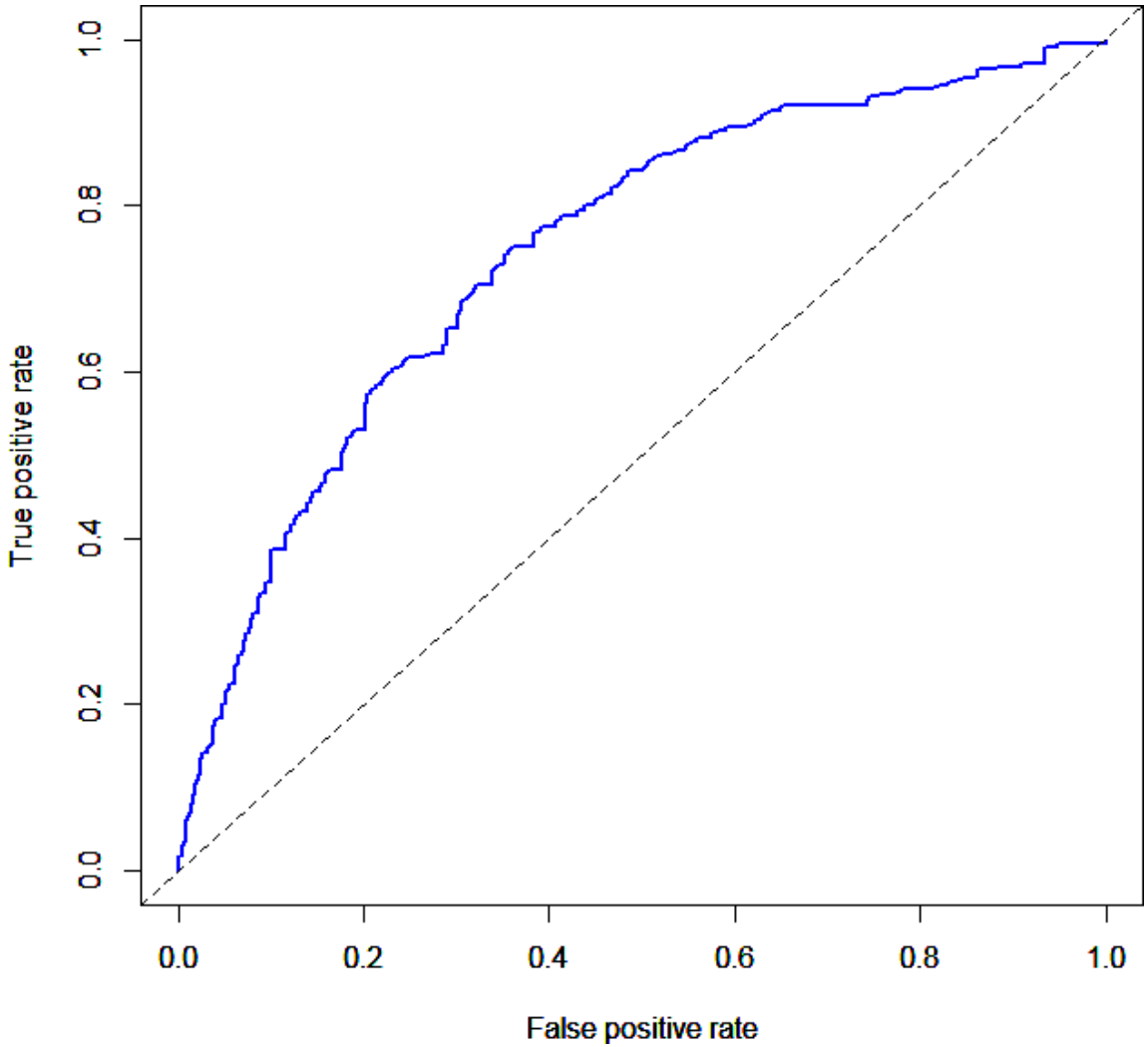
Variable	Coefficient (SE)	t-value	P-value	OR (95% CI)
Fixed effects				
Intercept	-2.85 (0.53)	-5.42	< 0.001	
1. Animals originated from				
Communes distance from the border for more than 50 km			Reference	1.00
Communes located on or near by border (distance of less for less than 50km)	**1.66 (0.44)**	**3.76**	**< 0.001**	**5.29 (3.81 – 6.32)***
2. Animals from communes that have				
Commune – to – commune road			Reference	1.00
Provincial and national roads	0.69 (0.35)	1.98	< 0.001	3.19 (2.38 – 4.62)
Commune-to-commune, provincial and national roads	0.82 (0.51)	1.60	< 0.001	2.25 (1.86 – 3.35)
3. Animals from communes that have human population of				
≤ 10.000			Reference	1.00
10.000 – 20.000	-0.0661 (0.0427)	-1.42	< 0.001	1.94 (1.18 – 2.34)
> 20.000	-0.7153 (0.0817)	2.36	< 0.001	1.73 (0.95 – 2.12)
4. Animals from communes that have number of animal raising household of				
≤ 1.000			Reference	1.00
1.000 – 2.000	-0.6941 (0.2189)	-3.173	< 0.001	2.78 (1.64 – 3.93)
> 2.000	-0.8662 (0.2093)	-4.139	< 0.001	2.93 (1.84 – 3.54)
5. Animals from communes that have animal population of				
≤ 10.000			Reference	1.00
10.000 - 50.000	-0.5873 (0.3043)	-1.930	< 0.001	2.38 (1.83 – 2.76)
> 50.000	-0.8859 (0.4128)	-2.146	< 0.001	2.11 (1.81 – 2.71)

III. RESULTS AND DISCUSSIONS (cont.)

- **Multivariable analyses:**
  - The odds of FMD virus infection of animals originated from communes located on or near by border (distance of less for less than 50km) 5.29 (95% CI 3.81 – 6.32) times the odds FMD virus infection of animals originated from communes distance from the border for more than 50 km
  - The odds of FMD virus infection of animals originated from communes that have provincial and national roads 3.19 (95% CI 2.38 – 4.62) times the odds FMD virus infection of animals originated from communes that do not have provincial and national roads

III. RESULTS AND DISCUSSIONS (cont.)

The area under the ROC curve was 0.76 indicates that the model had a good discriminatory ability to predict the animal FMD infection status.

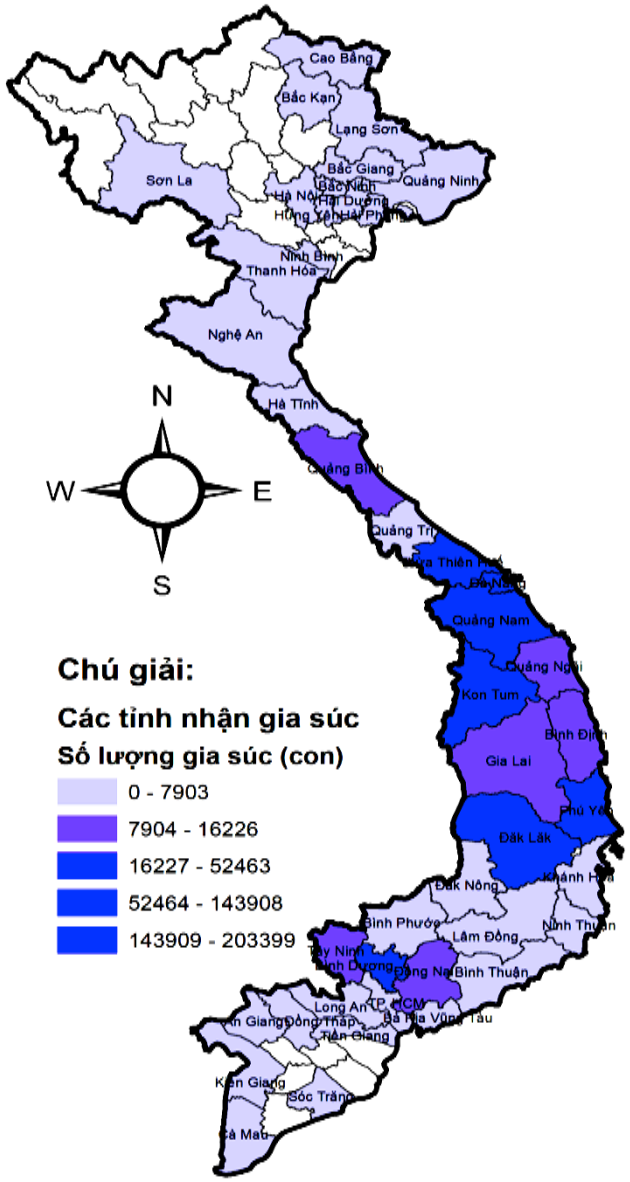


III. RESULTS AND DISCUSSIONS (cont.)

3.2. Animal movement

- A total of 29,129 animal movement events were recorded in 11 study provinces.
- A total of 1,064,365 animals:
  - 11,417 buffaloes
  - 54,573 cattle and
  - 998,375 pigs

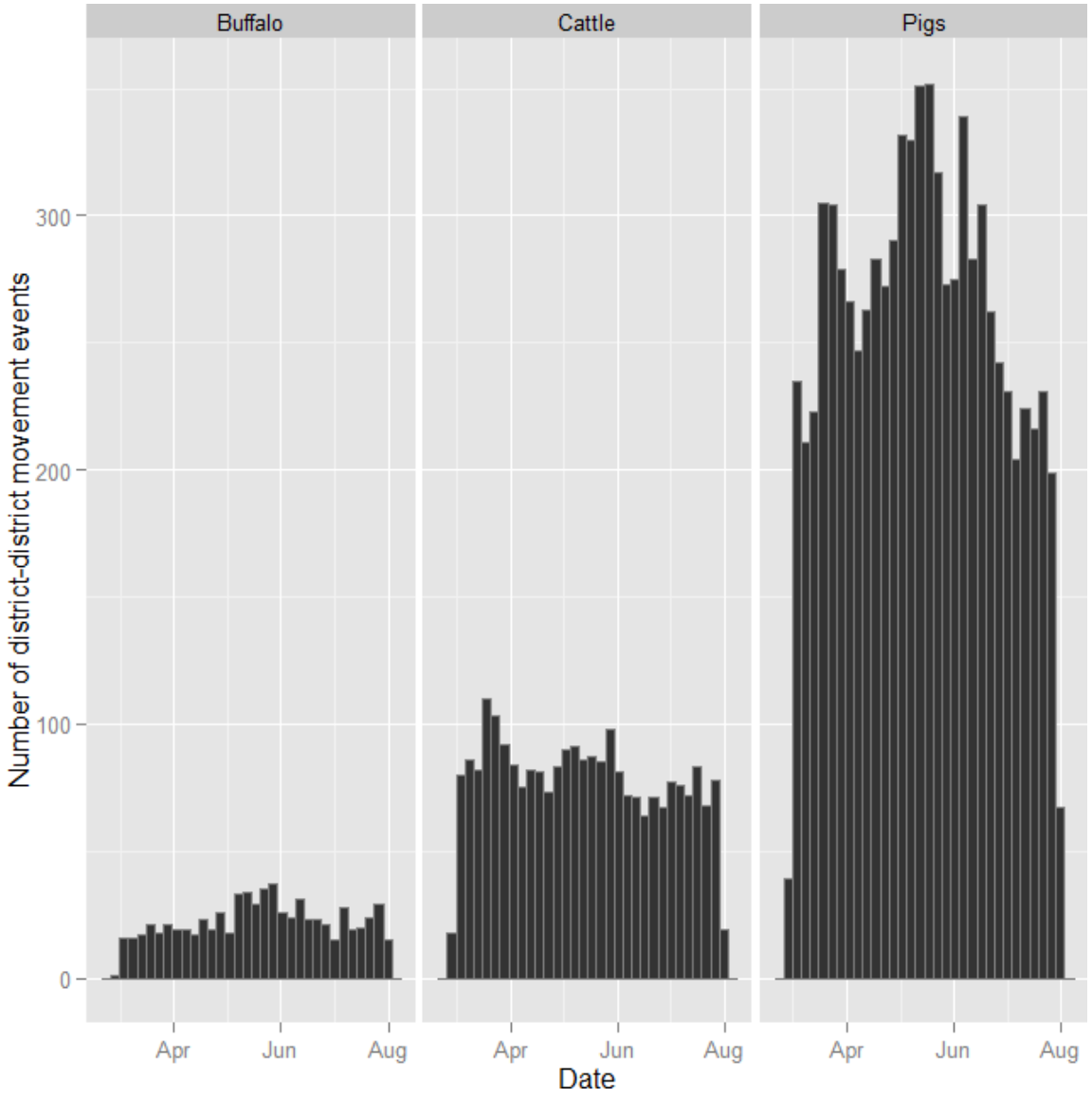
  were moved out from more than 747 communes of more than 200 districts to 45 provinces throughout Vietnam
  - Quang Ngai, Binh Dinh and Thua Thien – Hue likely had better management of animal movements as they had larger number of movement events compared with other 8 study provinces



III. RESULTS AND DISCUSSIONS (cont.)

District-to-district movements of buffalos, cattle and pigs in central Vietnam, March 2014 to July 2014. Frequency histograms showing the number of movements events per week for buffalo, cattle, and pigs

Movement events and number of each livestock specie moved was relatively constant throughout the study period



III. RESULTS AND DISCUSSIONS (cont.)

Descriptive statistics of network size, measures of centrality and cohesion for the three social networks formed by movements of buffalos, cattle, pigs, and all species combined

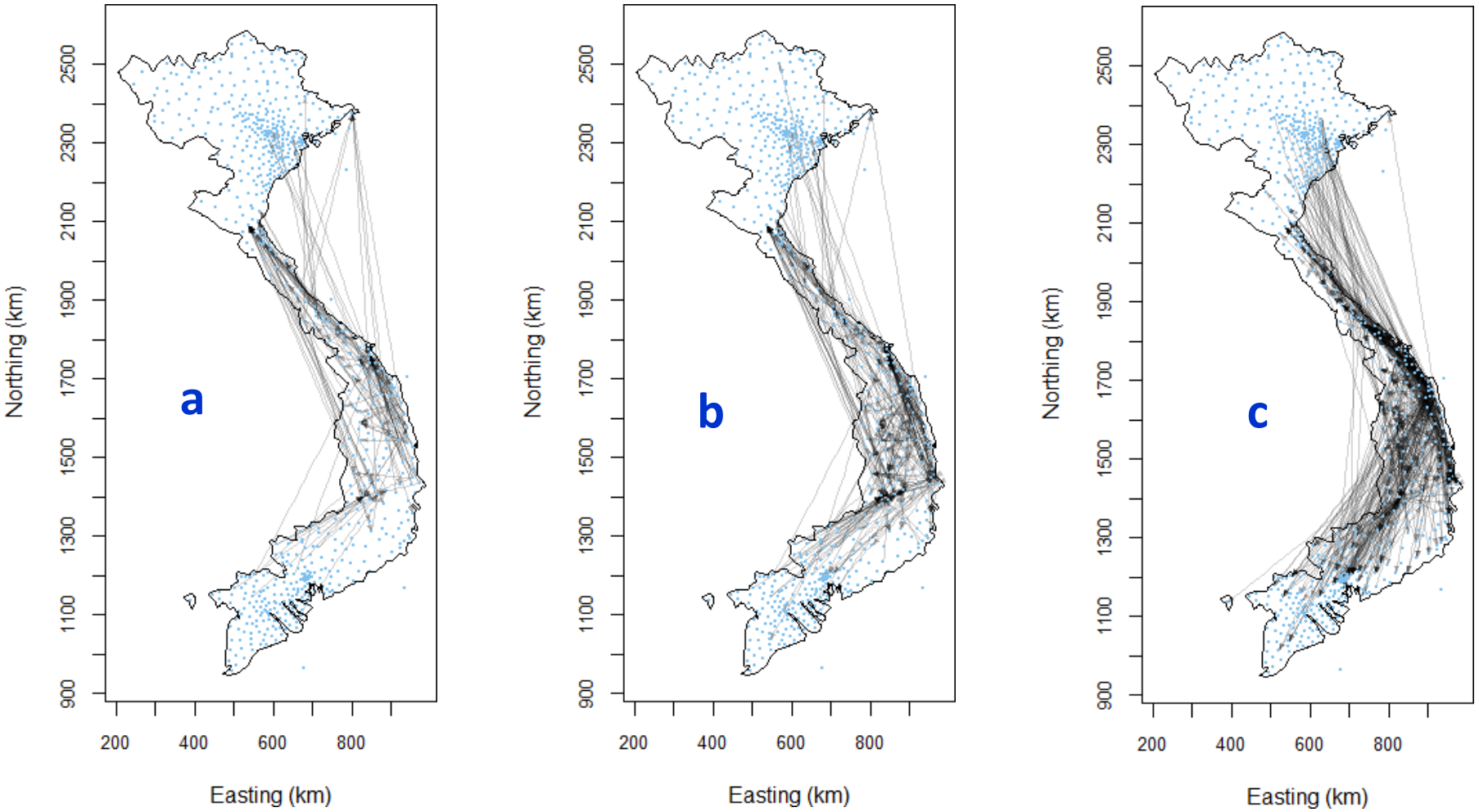
Parameter	Buffalo	Cattle	Pigs	Total
Network size:				
Number of nodes [a]	694	694	694	694
Number of directed links [b]	145	298	650	1033
Size [c]	480,942	480,942	480,942	480,942
Diameter [d]	5	8	8	10
Size of giant strong component [e]	2	9	27	99
Size of giant weak component [f]	98	145	216	274
Measures of centrality:				
Mean in-degree (range) [g]	0.21 (0–24)	0.43 (0-27)	0.94 (0-30)	1.49 (0-43)
Mean out-degree (range) [h]	0.21 (0-11)	0.43 (0-16)	0.94 (0-56)	1.49 (0-74)
In-degree centralisation [i]	0.0344	0.0384	0.0420	0.0600
Out-degree centralisation [j]	0.0156	0.0225	0.0796	0.1048
Mean betweenness (range) [k]	0.74 (0-124)	7.43 (0-874)	19 (0-2326)	120 (0-9730)
Betweenness centralisation [l]	0.1781	1.252	3.333	13.89
Measures of cohesion:				
Density (directed) [m]	0.0003	0.0006	0.0013	0.0021
Geodesic distance (mode) [n]	2.1215	3.3341	3.1954	3.7015
Clustering coefficient [o]	0.0484	0.0900	0.1044	0.1446

III. RESULTS AND DISCUSSIONS (cont.)

3.2. Animal movement

- Network size was constant for each of the three species whereas the total number of directed links varied
- **Pig:** In-degree scores were relatively small and out-degree scores for the pig network was wider **>>>** there were small numbers of districts in the central region of Vietnam that distributed to pigs to many districts
- **Buffalo and cattle networks:** the in-degree centralisation scores were greater than that of the out-degree centralisation scores indicating that there was a greater deviation in the number of in-coming contacts to a district compared with the deviation of the number of out-going contacts

III. RESULTS AND DISCUSSIONS (cont.)



District-to-district movements of buffalos, cattle and pigs in central Vietnam, March 2014 to July 2014. Map of Vietnam showing the point location of district centroids. Superimposed on each map are lines representing district-to-district movements for: (a) buffalos, (b) cattle, and (c) pigs

III. RESULTS AND DISCUSSIONS (cont.)

Explanatory variable	Coefficient (SE)	OR (95% CI)	P-value
Edges	-5.9250 (0.5640)	-	< 0.01
Cattle density (× 100 head per sq km) [a]	0.2810 (0.0602)	1.32 (1.18–1.49) [b]	< 0.01
Human density (× 100 head per sq km) [c]	0.0210 (0.0165)	1.02 (0.99–1.05)	0.20
GWESP [d]	1.1844 (0.4672)	3.27 (1.31–8.17)	0.01
GWESP (alpha) [e]	0.5444 (0.2143)	1.72 (1.13–2.62)	0.01
In-degree:			
1	-1.3760 (2.4656)	0.25 (0–31.71)	0.58
2	-2.6827 (3.2609)	0.07 (0–40.8)	0.41
3	-3.7639 (2.2990)	0.02 (0–2.1)	0.10
4	-4.0380 (3.9118)	0.02 (0–37.68)	0.30
5	-3.4635 (2.9260)	0.03 (0–9.69)	0.24
6	-4.0862 (2.7091)	0.02 (0–3.4)	0.13
7	-3.1856 (1.8347)	0.04 (0–1.51)	0.08
8	-4.1342 (1.6557)	0.02 (0–0.41)	0.01
9	-3.0080 (1.0197)	0.05 (0.01–0.36)	< 0.01
10	-1.8569 (0.4284)	0.16 (0.07–0.36)	< 0.01

After accounting for the confounding effect of maximum district human population density and the two network measures (geometrically weighted edgewise shared partner distribution and in-degree), **100 unit increases in maximum cattle population density** (expressed as the number of cattle per square kilometre) increased the **odds of a district-to-district connection by a factor of 1.32 (95% CI 1.18-1.49**)

III. RESULTS AND DISCUSSIONS (cont.)

3.2. Animal movement

The multivariable ERGM shows that

- After accounting for the confounding effect of maximum district human population density and the two network measures (geometrically weighted edgewise shared partner distribution and in-degree), **100 unit increases in maximum cattle population density** (expressed as the number of cattle per square kilometre) increased the **odds of a district-to-district connection by a factor of 1.32 (95% CI 1.18-1.49**)
- We propose that if FMD was detected within a given district all districts with the same community should be preferentially targeted for surveillance given their relative network 'closeness' to the index district

IV. CONCLUSIONS

- A total of 1,976 serum samples from moved animals were tested and they had relatively high positive proportion, average of 17.97% (95% CI 16.30 – 19.73%)
- Buffalo had highest proportion of positive serum samples with 68.92% (95% CI 57.10 – 79.17%), followed by cattle had 20.15% (95% CI 18.15 – 22.26%) and pig had the lowest proportion of positive serum samples with 0.25% (95% CI 0.01 – 1.39%)
- Of the 355 seropositive animals, only 65 animals were positive, average of 18.31% (95% CI 14.42 – 22.73%) or 3.29% (95% CI 2.55 – 4.17%) of the total tested (*n* = 1.976). Cattle had the highest proportion of positive probang samples, 19.47% (95% 15.17 – 24.39%), compared with buffaloes had lower proportion of 11.76% (95% CI 4.44 – 23.87%)

IV. CONCLUSIONS (cont.)

- Across the study period animals were moved more frequently from February 2014 and reached a peak during May and June 2014
- South-Central provinces often moved animal in larger numbers compared with North-Central province. The proportion of animals moved for slaughtering was highest of 51% of total movement events, followed by the purposes of raising in other places with 38% and for other purposes of 11%.
- Social network modelling indicate that if FMD was detected within a given district all districts with the same cluster should therefore be preferentially targeted for surveillance given their relative network `closeness' to the index district. Increases in the maximum cattle population density within a district increased the likelihood of two districts being connected by a livestock movement event

IV. CONCLUSIONS (cont.)

Recommendations are to carry out:

- Molecular and vaccine matching studies of the FMD virus isolated from this study to identify any molecular changes and whether current vaccine can be protective against this virus;
- Mapping the density of cattle in the central region of Vietnam and superimposing on this map the location of high in-degree districts would be a logical approach for better targeting surveillance for infectious diseases such as FMD

Acknowledgements

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