

The dissemination of *B. mallei* on between-farm animal movement

Workshops of the European Reference Laboratories for Glanders

Gustavo, Machado¹

November 16, 2021

¹North Carolina State University, College of Veterinary Medicine
<https://machado-lab.github.io/>

Table of content

1. Motivation
2. Dissemination and control questions
3. Results
4. Discussion and conclusion

Acknowledgement



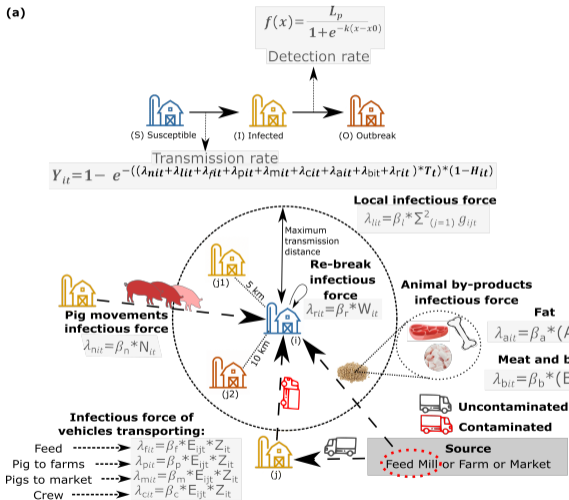
Dr. Nicolas Cardenas

Funding: Fundesa-RS

Motivation

1. Approximately 80 % of between-farm transmission are driven by the movement of animals.
2. Remain unknown the contribution of other routes in the propagation of diseases among food-animal populations.

(a)



(b) Model parameters

- β_n = Transmission rate of between farm pig movements
- β_l = Local transmission rate
- β_f = Transmission rate of between farm movements of vehicles transporting feed
- β_p = Transmission rate of between farm movements of vehicles transporting pig to farm
- β_m = Transmission rate of between farm movements of vehicles transporting pig to market
- β_c = transmission rate of between farm movements of vehicles transporting crew to farms
- β_a = Fat in the delivered feed rate
- β_b = Meat and bone in the delivered feed rate
- β_r = Re-break rate
- N = Number of asymptomatic and infected farms that sent pigs to "I"
- g = Gravity model with barrier effect
- E = Edge weight
- Z = Time vehicle stay on the farm
- A = Amount of fat in the meal
- B = Amount of meat and bone in the meal
- F = Pig population in the farm
- W = Re-break probability based on the time after last outbreak
- T = Monthly seasonality index
- H = Biosecurity index
- L = Detection probability
- x_0 = Average time detection
- x = Time post virus introduction
- k = Logistic growth rate

Modes of between-farm transmission

1. **Network.**
2. Distance (local transmission).
3. Transportation vehicles.
4. Vectors.
5. Environmental.

Detection

- Surveillance (clinical)-> most effective early detection.

Control

Detection

- Surveillance (clinical)-> most effective early detection.
- Trace-back.

Control

Detection

- Surveillance (clinical)-> most effective early detection.
- Trace-back.
- Whole herd testing.

Control

Detection

- Surveillance (clinical)-> most effective early detection.
- Trace-back.
- Whole herd testing.

Control

- National or sub-national standstill.

Detection

- Surveillance (clinical)-> most effective early detection.
- Trace-back.
- Whole herd testing.

Control

- National or sub-national standstill.
- Implementation of control areas (zones).

Detection

- Surveillance (clinical)-> most effective early detection.
- Trace-back.
- Whole herd testing.

Control

- National or sub-national standstill.
- Implementation of control areas (zones).
- Movement permits and contact tracing.

Detection

- Surveillance (clinical)-> most effective early detection.
- Trace-back.
- Whole herd testing.

Control

- National or sub-national standstill.
- Implementation of control areas (zones).
- Movement permits and contact tracing.
- Depopulation (complete or test and removal).

Detection

- Surveillance (clinical)-> most effective early detection.
- Trace-back.
- Whole herd testing.

Control

- National or sub-national standstill.
- Implementation of control areas (zones).
- Movement permits and contact tracing.
- Depopulation (complete or test and removal).
- Vaccination.

Dissemination and control questions

- Spread can occur by direct or indirect contact with an infected animal.
 - Ingestion of feed or water that has been contaminated by nasal discharges from infected animals.
 - Crowded conditions.
 - Acute or chronic disease.
1. Can it spread via animal movement?
 2. What would be the best way to stop propagation?

1. Dynamics of Glanders disease on between-farm movements.
2. Characterized the spatial and temporal patterns of the horse networks and identified regional trade communities.
3. Establish possible *B. mallei* causal paths between farms.

Real-time movement data

National policy

- Every animal or sub product movement must complete an electronic request (mandatory).
- Penalty notice.
- Premise identification, lat and long, reason of the movement, number of animals.

Real-time movement data

Sport



Fair/sales



Every site must provide:
1. Farm ID.
2. Lat & long.
3. Population.



11/12/2020



01/10/2021

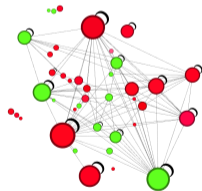
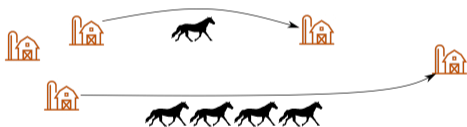


Movement data

1. 103,000 registered horse farms.
2. 537,159 horses.
3. All between farm movements from January 2014 to December 2016.
4. *B. mallei* infection (n = 30) and 10 in 2017 and 2018.

Network analysis

1. Farm locations represent the “nodes”.
2. Movements between farm “edges”.



Association between animal movements and *B. mallei* outbreaks

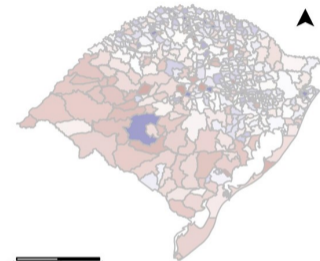
1. To test the hypothesis of direct association between animal movement and *B. mallei* via the k-test.
2. Possible outbreaks that may occur within n steps from an infected node.
3. All between farm movements from January 2014 to December 2016.
4. The contact network for the movements involving infected movements was traced.

Results

Network

a

Accumulated



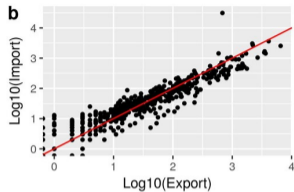
Animal trade

Exporter

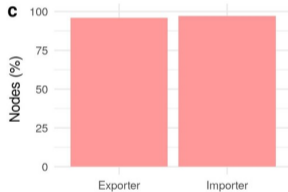
Balance

Importer

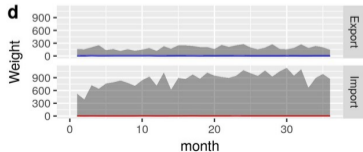
b



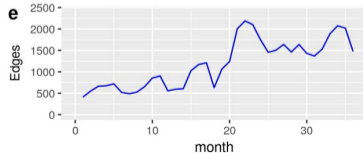
c



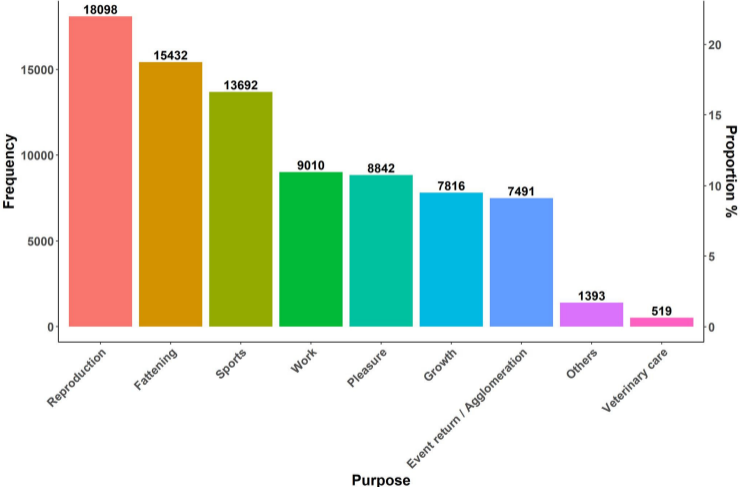
d



e



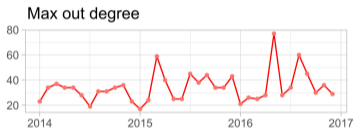
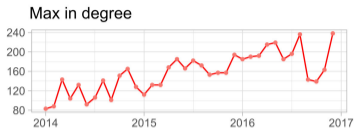
Network



General network metrics

Parameter	Municipality	Farm
Nodes	491	38,263
Edges	59,161	82,293
Mean of horses per movement	2.83	10.51
Graph density	0.050	4.24×10^{-5}
Max value of in degree	183	3868
Max value of out degree	184	400
Max size of GWCC	488 (99.39%)	30470 (79.63%)
Max size of GSCC	476 (96.94%)	6606 (17.26%)
Diameter	8	26
Mean of the shortest path	2.86	6.29

Temporal network metrics

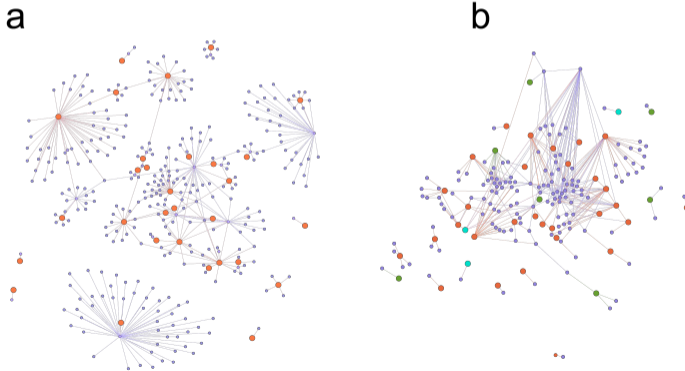


In- and out-going from infected farms

Contact chain	Measure	2014 n=8	2015 n=16	2016 n=23	All years
In-going	IQR	(1-423)	(5-861)	(1-1351)	(2-5115)
	Maximum value	758	1394	1858	5908
	Median value	4	22	3	2185
Out-going	IQR	(2 -726)	(4-1172)	(2-1075)	(4-5679)
	Maximum value	1101	2034	2204	12537
	Median value	3	96	12	1858

Infected network

- a) Each red circle (infected) represents a farm where at least one horse tested positive.
- b) Green and pink circles represent the positive farms in 2017 and 2018.



Outbreak associations with the network metrics at the farm level

Variable (cutoff)	Univariable analysis		Multivariable analysis			
	p-value	OR (CI 95%)	b	SE	OR (CI 95%)	p-value
Betweenness						
≤2,706.82	–	–	–	–	–	–
>2,706.82	0.02	2.50 (2.22–2.83)	–	–	–	–
Closeness centrality in						
≤0.0001459	–	–	–	–	–	–
>0.0001459	0.94	1.00 (0.99–1.01)	–	–	–	–
Closeness centrality out						
≤0.0002577	–	–	–	0.47	–	–
>0.0002577	0.001	4.46 (3.72–5.35)	1.63	–	5.11 (4.31–60.7)	<0.001
In degree						
≤73	–	–	–	0.42	–	–
>73	0.05	2.05 (1.82–2.32)	0.87	–	2.40 (2.01–2.86)	0.03
Out degree						
≤81	<0.001	–	–	–	–	–
>81	–	3.57 (3.26–3.90)	–	–	–	–
Degree total						
≤153	0.04	–	–	–	–	–
>153	–	3.02 (2.73–3.34)	–	–	–	–
PageRank						
≤0.005425	0.20	–	–	–	–	–
>0.005425	–	1.77 (0.99–2.06)	–	–	–	–

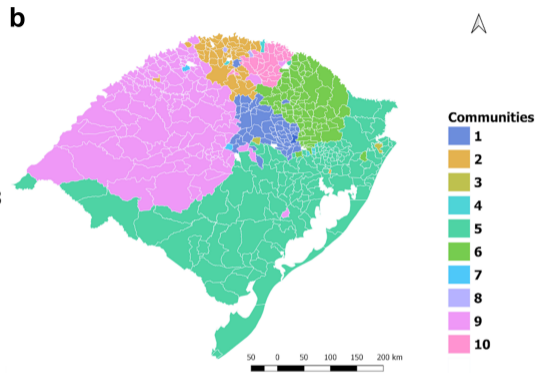
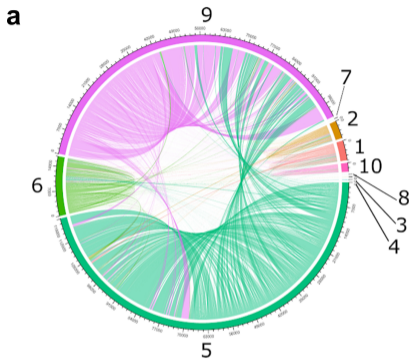
Discussion and conclusion

- The reinforcement of active surveillance in farms with a high in degree within the infected network in Rio Grande do Sul, Brazil (control).

- The reinforcement of active surveillance in farms with a high in degree within the infected network in Rio Grande do Sul, Brazil (control).
- 10 communities, suggesting that infected horses tend to readily move between the farms of a given community and later reach farms of other communities.

- The reinforcement of active surveillance in farms with a high in degree within the infected network in Rio Grande do Sul, Brazil (control).
- 10 communities, suggesting that infected horses tend to readily move between the farms of a given community and later reach farms of other communities.
- The outbreaks of *B. mallei* showed a clear causal association through the network paths, two steps!!.

- The reinforcement of active surveillance in farms with a high in degree within the infected network in Rio Grande do Sul, Brazil (control).
- 10 communities, suggesting that infected horses tend to readily move between the farms of a given community and later reach farms of other communities.
- The outbreaks of *B. mallei* showed a clear causal association through the network paths, two steps!!.
- OR 2.40 and 5.11, in-degree and centrality, local and a more complex dynamics.



1. So many assumptions.
2. Currently only including animal movement.
3. Questions about the trace-back and movement restriction implemented by the state.
4. All animals transported are required by law to be tested for *B. mallei* (?).

- Network information has the potential to inform *B. mallei* control.
- **Mathematical simulation** could provide a better inside to the over all dynamics.
 - Local transmission.
 - Environmental transmission.
 - Proper farm closure intervention.
- Questions about the trace-back and movement restriction implemented by the state.

Questions?

