

Livestock disease outbreaks and their impact on the evolution of trade networks

Thomas Selhorst¹, Franz Conraths², Christine Mueller-Graf¹, ¹The Federal Institute for Risk Assessment (BfR), Berlin, Germany; ²Friedrich-Loeffler Institut, Greifswald, Germany. Contact: thomas.selhorst@bfr.bund.de

Purpose

Livestock trade can represent an important route of disease transmission. Veterinary epidemiologists have analyzed the topology of trade networks to identify node and edges relevant for the distribution and the dynamics of livestock epidemics. However, this approach is valid only under the assumption of unchanged trade activity during and before an animal disease outbreak.

In order to validate this assumption, the evolution of the German pig trade network during an outbreak of classical swine fever in North Rhine Westphalia in spring 2006 was analyzed and compared with the topology during periods when relevant livestock diseases did not occur.

Methods

The analysis used the methodology of time varying graphs [1] combined with changepoint detection [2] for the identification of relevant changes in network topology. Additionally, rewiring rates [3] and loyalty indices [4] were calculated.

Results

As expected, the trade volume changed considerably close to the time of the implementation of movement restrictions. In contrast to this finding, substantial rewiring and sustainable changes in the topology of the trade network could not be identified.

Conclusion

With respect to the German pork production chain, considerable industrial specialization is obvious. Each production stage can be attributed to specialized premises or enterprises. This seems to limit the change of trade partners.

Relevance

A new set of methods is proposed in order to characterize changes in trade patterns between animal holdings caused by disease outbreaks. The supposed methodology can be applied to any contact network.

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[2] Killick, R., Eckley, I.A. (2014) changepoint: An R package for changepoint analysis. Journal of Statistical Software 58(3) 1-19.

[3] Shou C, Bhardwaj N, Lam HYK, Yan K-K, Kim PM, et al. (2011) Measuring the Evolutionary Rewiring of Biological Networks. PLoS Comput Biol 7(1)

[4] Valdano E, Poletto C, Giovannini A, Palma D, Savini L, et al. (2015) Predicting Epidemic Risk from Past Temporal Contact Data. PLoS Comput Biol 11(3).