
R08.3 On the interaction between bovine and bubaline trade network in epidemic spreading

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Abstract

The Italian cattle movement network has been extensively studied in the literature (Bajardi et al., 2011) while the Italian buffalo network has not been investigated. Throughout the peninsula there are several farms that breed buffaloes and more than 60% of these also breed cattle. Such situation highlights potential transmission of pathogens between the two species. In order to study the interaction between the two networks we considered a pathogen, *Q-Fever*, that can infect both species and also humans. It is a dangerous disease for humans, but, since it is usually asymptomatic in animals, it is often neglected. This pathogen is widespread among cattle and buffaloes in Campania region (Ferrara et al., 2022).

We want to study if the buffalo network can support the diffusion of the pathogen and spread it to the cattle network through those farms that breed both species. To do this, we consider a SIS model. Since the diagnosis is complicated and usually carried out at herd level, the epidemiological units of our model are the farms. An infectious farm is a farm where at least one animal is infectious.

A susceptible farm that receives animals from an infectious farm will also become infectious according to a defined probability of infection.

We randomly infect a small subset of the buffalo farms (0.05% of all the farms), and then simulate the diffusion of the pathogen using real movement data between 2017 and 2020, aggregated by week. Given the above considerations, we considered a low probability of "healing" among the farms, 0.1%.

In Table 1 (<https://www.veterinariaitaliana.izs.it/index.php/GEVET23/article/view/3247/1405>) we can observe the results of 100 different simulations for different infection probabilities.

From this analysis, it can be concluded that the interaction between the buffalo and the cattle network is not negligible. Indeed, the buffalo network may support the spread of a pathogen and is able to

spread it within the cattle network through those farms that breed both species. Further work could include a more in-depth study of both the buffalo network and the interaction between the two species in the multidimensional network. In addition, improving the model by considering surveillance in the cattle network might be interesting to observe the impact that the buffalo network would have by itself.

References

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