Are we targeting the right animals? Validating network centrality as a proxy for disease risk across contrasting wildlife systems

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Contact network analysis is increasingly used in wildlife disease studies. Centrality metrics such as degree, betweenness, and closeness are widely applied as proxies for individual disease risk and could be used to inform surveillance efforts. The foundational assumption is that animals in central positions in a contact network are more likely to be exposed to pathogens and spread pathogens. However, there are a lack of empirical studies supporting this assumption in real wildlife systems. If centrality poorly predicts infection status, surveillance strategies built on network-derived risk scores might be misdirecting effort.

We present a cross-species pilot study to test this assumption using GPS telemetry data from two contrasting wildlife populations: 11 feral pigs (*Sus scrofa*, an invasive species) with linked serological results in Queensland, Australia; and 15 Baird's tapirs (*Tapirus bairdii*, an endangered species) in Costa Rica with GPS collars deployed and serological testing ongoing. These species contrast markedly in ecology, social structure, and conservation context, providing a meaningful cross-system test of whether centrality-infection relationships are generalisable.

For each species, we construct two network types: a proximity network using fine-scale spatiotemporal co-occurrence thresholds, relevant to directly transmitted pathogens such as ASF and *Brucella suis*, and a co-occurrence network using shared space use over broader temporal windows, relevant to environmentally persistent pathogens such as *Leptospira* spp. For feral pigs, we test centrality against *Brucella* spp. seropositivity using logistic regression with permutation-based null models, and against *L. pomona* antibody titre using linear regression on log-transformed values, to account for the high prevalence of this pathogen in the study population.

Preliminary results from the feral pig dataset show variable pathogen prevalence: all animals tested seropositive to *L. pomona*, 82% to Japanese encephalitis virus, and 27% to *Brucella* spp. Centrality metrics from neither the proximity nor the co-occurrence network predicted *Brucella* seropositivity. Similarly, neither network type predicted *L. pomona* titre. These results suggest that network position alone might not reliably identify animals at higher disease risk. Tapir results will be presented and will provide a critical cross-species comparison.

There is a lack of empirical evidence to support or challenge the assumptions that underpin network-based wildlife surveillance. This work addresses that gap and presents a replicable analytical framework applicable across species, pathogens, and surveillance contexts. The framework is designed to be tested in other systems and adapted where data limitations apply. These findings highlight the need to validate our strongly-held network-based assumptions before applying centrality metrics to guide surveillance efforts at the wildlife-livestock interface.

Keywords: GPS telemetry, Contact network analysis, Pathogen exposure, Wildlife-livestock interface, Wildlife disease surveillance.

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