Salmonella transmission in wild pigs: molecular, spatial and ecological approaches

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We took an innovative approach to investigate wildlife infection transmission in an extensively distributed population of wild pigs (*Sus scrofa*) in northern Australia (2010-11). We combined molecular (integration of pig microsatellite data with *Salmonella* PFGE typing data), ecological and spatial methods. Several approaches were applied to the dataset to understand transmission and prevalence of infection at a very detailed scale. Firstly using presence/absence data we hypothesised plausible biological mechanisms for *Salmonella* prevalence. Separate logistic models were established for each hypothesis and information theoretic approaches used to choose the most likely model/s. This was used to inferred mechanisms for *Salmonella* prevalence. Secondly *Salmonella* subtyping data was used to model pair-wise genetic relatedness of all *Salmonella* isolates against a variety of covariates with the aim to quantify levels of transmission between pigs. Thirdly, measures of diversity and similarity were used to provide an additional perspective on transmission dynamics. Preliminary findings from this study show potential to be of direct value for disease control. Results so far show prevalence of infection was associated with resource rich areas (riparian zones, water bodies and pasture) and behavioural factors. However no association between prevalence and; density, environmental contamination or individual risk factors could be found. Interim analyses of pair-wise *Salmonella* relatedness data suggest that herd membership, spatial proximity and differential sex based transmission to be strong risk factors for transmission. Final results will be presented at ISVEE.