

Wildlife as reservoirs of disease for livestock in Australia: the case of the feral pig

Ward, M.P.¹, Cowled, B.¹, Negus, K.¹, Galea, F.², Garner, M.G.³, Laffan, S.⁴, Marsh, I.², Sarre, S.⁵ and Woolnough, A.⁶, ¹The University of Sydney, Australia, ²Primary Industries NSW, Australia, ³Department of Agriculture, Fisheries & Forestry, Australia, ⁴University of New South Wales, Australia, ⁵University of Canberra, Australia, ⁶Department of Agriculture and Food Western Australia, Australia; michael.ward@sydney.edu.au

Besides causing ecological damage and threatening native species in Australia, feral pigs potentially form a reservoir of diseases important for livestock production. These include both transboundary (e.g. foot-and-mouth disease, classical swine fever) and endemic (e.g. leptospirosis, *Salmonella*) diseases. We used *Salmonella* as a model to understand if and how FMD might spread in feral pig populations and form a reservoir which would delay or prevent disease eradication, should an incursion occur. We sampled (via aerial culling) 543 feral pigs at geo-referenced locations in a 5,000 km² study area in the remote Kimberley region of Western Australia. Both mesenteric lymph nodes and fecal samples were collected for *Salmonella* culture. In addition, fecal samples from 496 cattle in 47 geo-referenced groups cohabitating the study area with the feral pig population were collected and cultured for *Salmonella*. *Salmonella* was cultured from 240 (41%) pigs, mostly from fecal samples. A total of 39 different serotypes were isolated. *Salmonella* serotypes were further characterised using pulsed field gel electrophoresis. Nearly 100 unique pulsotypes were identified. *Salmonella* was cultured from 2% of cattle. Nine serovars were identified, but no dominant serotype was noted. There were 6 serotypes in common with feral pig isolates. Cattle isolates were more commonly recovered from areas without feral pigs. Based on PFGE analysis, cattle and pig serotypes showed only 58% similarity (compared to 84% similarity within the cattle serotypes). Spatial and molecular analysis results suggest that in this environment, feral pigs are unlikely to be an important reservoir of disease for domestic livestock.