Parasites of Feral Cats and Native Fauna from Western Australia: The Application of Molecular Techniques for the Study of Parasitic Infections in Australian Wildlife

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B. Sc. (Hons)

This thesis is presented for the degree of Doctor of Philosophy of Murdoch University, 2003.
I declare that this thesis is my own account of my research and contains as its main content work, which has not previously been submitted for a degree at any tertiary education institution.

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Abstract

A survey of gastro-intestinal parasites was conducted on faecal samples collected from 379 feral cats and 851 native fauna from 16 locations throughout Western Australia. The prevalence of each parasite species detected varied depending upon the sampling location. Common helminth parasites detected in feral cats included *Ancylostoma* spp. (29.8%), *Oncicola pomatostomi* (25.6%), *Spirometra erinaceieuropaei* (14%), *Taenia taeniaeformis* (4.7%), *Physaloptera praeputialis* (3.7%) and *Toxocara cati* (2.6%). The most common protozoan parasites detected in feral cats were *Isospora rivolta* (16.9%) and *I. felis* (4.5%). The native mammals were predominately infected with unidentified nematodes of the order Strongylida (59.1%), with members of the orders Rhabditida, Spirurida and Oxyurida also common. Oxyuroid nematodes were most common in the rodents (47.9%) and western grey kangaroos (27.8%). Several species of *Eimeria* were detected in the marsupials whilst unidentified species of *Entamoeba* and coccidia were common in most of the native fauna.

Primers anchored in the first and second internal transcribed spacers (ITS1 and ITS2) of the ribosomal DNA (rDNA) were used to develop a polymerase chain reaction-linked restriction fragment length polymorphism (PCR-RFLP) technique to differentiate the species of *Ancylostoma* detected in feral cats. Amplification of the ITS+ region (ITS1, ITS2 and 5.8S gene) followed by digestion with the endonuclease *Rsa*I produced characteristic patterns for *A. tubaeforme*, *A. ceylanicum* and *A. caninum*, which were detected in 26.6%, 4.7% and 0% of feral cats respectively.

*Giardia* was detected in a cat, dingo, quenda and two native rodents. Sequence analysis at the small subunit rDNA gene (SSU-rDNA) identified the cat and dingo as harbouring
*G. duodenalis* infections belonging to the genetic assemblages A and D respectively. Subsequent analysis of the SSU-rDNA and elongation factor 1 alpha (*ef1α*) identified a novel species of *Giardia* occurring in the quenda. Attempts to genetically characterise the *Giardia* in the two native rodents were unsuccessful.

Serological detection of *Toxoplasma gondii* was compared to a one tube hemi-nested PCR protocol to evaluate its sensitivity. PCR was comparable to serology in detecting *T. gondii* infections, although PCR was a much more definitive and robust technique than serology for large numbers of samples. Amplification of *T. gondii* DNA detected infections in 4.9% of feral cats and 6.5% of native mammals. The distribution of *T. gondii* does not appear to be restricted by environmental factors, which implies that vertical transmission is important for the persistence of *T. gondii* infections in Western Australia.

These results demonstrate that cats carry a wide range of parasitic organisms, many of which may influence the survival and reproduction of native mammals. As such, the large-scale conservation and reintroduction of native fauna in Western Australia must not disregard the potential influence parasites can have on these populations.
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