



PESTS MART

Advances in the molecular ecology of foxes

Introduction:

Foxes are highly secretive and cryptic animals. They are wary of humans, highly mobile and occur at relatively low densities across the landscape. These factors make the collection of key biological and ecological data relevant to their control, such as density and survival, challenging. Management decisions are often made without a full understanding of the fox's biology or behaviour, potentially limiting the effectiveness, and making it difficult to accurately evaluate the success of any management actions.

One response to the problem of how to directly measure the density of such an elusive species is to use a non-invasive survey technique such as an activity index (eg counts of tracks and scats). A major limitation with this method is that without identification of individual animals, and hence some understanding of their behaviour, it is difficult to attribute a change in activity to a change in population density.

“DNA analysis has become a critical addition to the traditional tools for monitoring foxes”

Advances in molecular biology and bioinformatics have permitted the development of the non-invasive analysis of DNA, otherwise known as genetic tagging¹. This technology has the ability not only to distinguish between species but also to identify individual animals. Combined with the range of non-invasive survey techniques (eg hair or scat collection), DNA analysis has become a critical addition to the traditional tools for monitoring foxes.



Image: Chris Cox

The Invasive Animals Cooperative Research Centre (IA CRC), in collaboration with the University of Canberra and the University of Western Australia, has been at the forefront of research in this area in Australia. Their most recent program was divided into five main project-elements:

- the survey and detection of foxes at low abundance for better targeted baiting and other fox control measures
- the monitoring of abundance and survival of foxes subject to lethal control methods
- the use of landscape genetics as a tool to estimate dispersal distances of foxes and define optimal management areas
- the determination of the relatedness and mainland origins of foxes in Tasmania
- the estimation of the number of breeding foxes and immigration rate onto Phillip Island in Victoria.

This factsheet contains a summary of this research program, the techniques developed and how they can inform management decisions.

To be able to apply this new technology to answer any biological fox management questions, there was a need to develop accurate methods that are reliable, flexible, and cost-effective.

DNA Analysis:

Most DNA-based techniques for species identification usually involve post-polymerase chain reaction (PCR) manipulations of samples (eg restriction digests, gel electrophoresis). These techniques add time and cost to the process, and increase the chance of contamination



Image: Invasive Animals CRC

and handling errors. The team from the IA CRC developed a highly accurate and reliable method for identifying species from DNA samples that did not require post-PCR manipulations. Instead DNA fragments are PCR amplified using a pool of species-specific primers (eg fox, cat, dog, quoll, Tasmanian devil), then identified using melt-curve analysis (MCA) to distinguish species². These researchers were also able to develop a sexing test using a similar approach³.

Remotely capturing DNA samples:

DNA samples can be collected from most parts of the fox body (eg body tissue, blood, hair, faeces). The research team found that faeces were useful for field-based collections as they were relatively long-lasting. Testing several methods of DNA extraction, it was found that the relatively quicker, cheaper method was successful in extracting sufficient DNA for species identification, even after the faeces had been on the ground for up to three months. However, the sexing test was found to be more reliable when faeces were less than three weeks old, and was maximised by the use of a more labour-intensive DNA-extraction process³.

Abundance and survival monitoring in Western Australia:

A landscape-scale experiment was conducted in the wheatbelt areas of Western Australia to use DNA analysis to estimate density and survival of foxes during a typical 1080 aerial baiting program. DNA was obtained from hair samples that were collected using hair snares. This analysis of hair samples provided significantly more individual 'captures' than conventional trapping methods typically provides, potentially allowing for more accurate and precise evaluations of the effectiveness of control. The

results identified 58 unique individuals and demonstrated a 100% knockdown of the resident fox population, indicating the effectiveness of 1080 aerial baiting programs in removing individual foxes¹.

Landscape genetics:

This project collected over 3500 fox samples from across Australia. The DNA analysis has demonstrated that foxes from Western Australia are genetically distinct from those in the eastern states, with movement virtually non-existent across the deserts of central Australia.

Foxes in Tasmania:

The survey and detection of foxes at low abundance using DNA analysis has proved reliable. It has provided independent evidence for the presence of foxes in Tasmania, and remains an important tool in the eradication program^{3,4} (see Foxes in Tasmania factsheet for more detail). So far 18 individual foxes have been successfully identified from faeces, blood and tissue samples found throughout Tasmania. There have been no recaptures of these 18 individuals.

Foxes on Phillip Island:

Foxes have been established on Phillip Island for over 100 years, and have a major impact on the populations of native wildlife, particularly breeding colonies of little penguins, *Eudyptula minor* (see Phillip Island case study for more details). Despite ongoing intensive control programs, foxes still persist. By using DNA analysis techniques, researchers have been able to measure the rates of increase of the fox population on Phillip Island. This research has shown that reproduction is the main source of population increase, with immigration from the mainland only providing a small contribution. Although fox control was shown to reduce fox densities, there was evidence that the net number of new individuals did not decline because of increased reproductive success⁵.

Further information:

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2. Berry O and Sarre S (2007). Gel-free species identification using melt-curve analysis. *Molecular Ecology Notes* 7(1): 1-4.
3. Berry O, Sarre SD, Farrington L and Aitken N (2007). Faecal DNA detection of invasive species: the case of feral foxes in Tasmania. *Wildlife Research* 34(1): 1-7.
4. Sarre S, Walsh R, Aitken N, Foster A and Mooney N (2008). *DNA detection of foxes to prevent their establishment in Tasmania*. United States Department of Agriculture Symposium in Managing Vertebrate Invasive Species, 7-9 August 2007, Fort Collins Colorado, USA, pp. 454-459.
5. Berry O and Kirkwood R (2010). Measuring recruitment in an invasive species to determine eradication potential. *Journal of Wildlife Management* 74(8): 1661-1670.