Forensic Science provides evidence for use in courts of law. Wildlife forensics is not commonly available to wildlife authorities, but can provide evidence to prosecute people who are illegally trafficking in wildlife.

Feral pigs are a very significant invasive species. They are referred to as triple-threat animals because they cause damage to the environment, agricultural losses, as well as a threat to biosecurity and potentially human health (because of the diseases they can carry). Feral pigs eat livestock, damage fences and infrastructure, and they have the potential to spread many diseases, including “foot and mouth disease”, if it makes its way into Australia.

The molecular ecology of feral pigs was investigated to understand their social and population genetic structure.

**Methods and results**

We developed a highly variable set of highly discriminatory short tandem repeat (DNA-profiling) markers (Figure 1) and used them to identify individual Australian wild pigs. These genetic markers are identical to those used in ‘CSI forensics’. The theoretical probability of identity (PID) for these markers was that 1 in 662 billion feral pigs would share exactly the same DNA profile. This meant we were able to identify a particular pig with a high degree of certainty (Figure 2).

Samples from adult animals were collected over their distribution range across south-western Australia (Figure 3). Using DNA-profiling markers, we identified seven feral pig populations that had moderate genetic diversity (mean = 58%) and displayed a high level of difference between the populations (mean $R_{ST} = 0.180$).

We have been able to discriminate translocated pigs from those dispersing naturally (Figure 3), even over the large distances considered (in the order of hundreds of kilometres). If natural dispersal was occurring over these very large distances, then there would, presumably, be an equally likely chance of detecting an immigrant in any population over the entire study area, which we did not.

**FIGURE 1** Gel of the DNA profiles used to identify individual feral pigs

**FIGURE 2** Genetic fingerprinting enables us to profile the animals from different populations, and then identify any individuals that have a genotype that is different from this
The genetic structure of feral pig populations revealed anomalies in some individuals. We found recently colonised regions that had previously been un-infested by feral pigs. We also found evidence where animals from geographically isolated areas had been introduced into established feral pig populations; these populations were in areas that were in close proximity to public road access and towns.

Conclusions and recommendations

DNA profiling offers enormous potential in wildlife forensic casework, indicating where there has been illegal dumping of animals. Detecting the movement of vertebrate pests for malicious intent like illegal hunting is a serious management problem for the control of feral pigs in sensitive conservation and agricultural areas.

Illegal dumping adds to the natural expansion of invasive species, further complicating efforts of local population eradication. The technology developed was able to identify that illegal movement was not isolated to the present generation or a specific cohort of pigs in the south-west of Australia, suggesting that translocation of pigs has been ongoing. The identification of illegally transported stock will be important to identify in any exotic disease outbreak, as such activities may severely compromise the ability to control the incident.

Prosecution of persons involved in illegally transporting declared pests would be difficult without the evidence provided by genetic testing. DNA markers revealed that there were high levels of variability and inter-population differentiation in allele frequencies among populations in this study, which would enable prosecution and correct assignment of individuals (or tissue) from their population of origin with high (> 99.99 %) certainty.

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References


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FIGURE 3 Graphs used to identify pigs that were illegally dumped, presumably by recreational hunters. In Denbarker, all the pigs sampled were likely to have Denbarker parents, but in the Perth Hills, there was evidence of pigs that did not have Perth Hills parentage.