

Monitoring the abundance of greater bilbies

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Background

The greater bilby (*Macrotis lagotis*) is a culturally and taxonomically significant marsupial, playing an important role as an ecosystem engineer through extensive digging and burrowing activity. Bilbies are under threat from changed and inappropriate fire regimes, feral predators and degradation of habitat from introduced herbivores and vegetation clearing, and are listed as vulnerable in Western Australia, nationally and on the IUCN Red List. Their range has contracted to approximately 20 percent of that prior to European settlement. Bilbies are difficult to trap and observe in the wild, making traditional capture-mark-recapture and spotlighting monitoring methods inappropriate and inefficient. Vegetation prevents efficient spotlighting across the majority of the bilby's range, and it does not account for the proportion of animals underground. Counting tracks or burrows has been shown to be an unreliable indicator of abundance.



We developed a reliable technique to monitor bilby abundance using non-invasively collected genetic material from faecal pellets (scats) combined with spatially explicit capture-recapture (SECR) analyses. This technique has been trialled and successfully implemented at bilby populations across WA.

Abundance monitoring technique

Population delineation and transect allocation

Once a population is identified, the boundary of activity is delineated by plotting the extent of fresh bilby sign, using GPS enabled devices. Bilby populations shift between years, requiring this step to be completed prior to subsequent monitoring events. Wild populations are often isolated and distinct; however, where bilby activity extends across a much larger area, for example reintroduced populations such as at Matuwa (formerly Lorna Glen Station), areas can be subsampled. Transects are allocated within the boundary of the activity area to ensure that the population is evenly sampled, and to avoid sampling unoccupied areas. Transects can be traversed on foot, all-terrain vehicle or vehicle at walking pace, depending on vegetation and terrain. The start and end points of each transect are plotted at the commencement and completion of each transect and the path can also be recorded.

Scat collection

Scats are systematically collected along transects. Bilby scats are easily distinguished from other species and are easy to find, as diggings provide a clear visual cue: 95 percent of scats are found at diggings (Fig. 1). It is also important to search the spoil of diggings as 29 percent of scats are buried within it. Diggings also assist in aging the scats. Digging spoil that is hard and weathered indicates the scats may be old, whereas loose, darker spoil indicates a more recent dig and fresher scat. Scats at very eroded and weathered diggings are probably older than two weeks, are less likely to yield DNA and are not collected. Clearly decomposed or broken up scats are also not collected. The GPS co-ordinates of each sample location and details are recorded electronically in apps such as Mobile Data Studio or Fulcrum.

Scats are collected in 30 mL labelled vials, approximately one third filled with silica gel beads and a cotton wool ball on top (Fig. 2). This ensures samples are kept dry and the cotton wool prevents scats from breaking up. The lid of the vial or a small stick, only used for the one sample, is used to move scats into the vial. Pellets in a group in contact with or very close to each other are from one individual and stored in one vial. These procedures ensure cross-contamination from different individuals does not occur. Scats should be maintained at ambient temperature and not be exposed to extreme heat or sunlight once collected. Moisture degrades DNA, so sampling should therefore be undertaken during the dry season, and at least two weeks since any rain event.



Fig. 1. Bilby digging with scats.

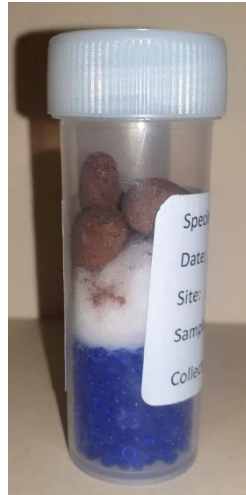


Fig. 2. Vial with sample.

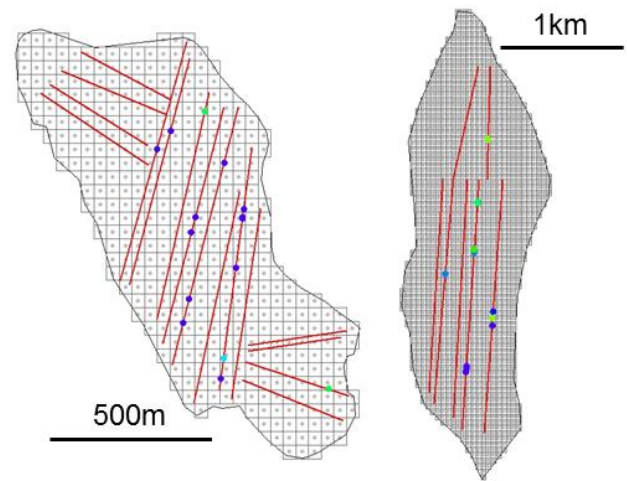


Fig. 3. Examples of bilby population monitoring sites. Red lines represent transects and coloured points represent individual bilby genotypes identified from collected scats.

DNA extraction, genotyping and SECR analysis

DNA is extracted in the laboratory and genotyping is undertaken using highly-polymorphic bilby-specific microsatellite markers. This indicates the number of individuals identified and 'recaptured' on the transects sampled (Fig. 3).

SECR analyses then allow us to gain a population abundance or density estimate for the overall area within the population boundary or across a greater area for subsampled populations. DBCA scientists can provide assistance with planning, genotyping and analyses for bilby monitoring, and the authors can be contacted at the email addresses above.

Findings

We verified the application of this technique against a recently reintroduced known founding population, which demonstrated its reliability. The technique has now been implemented by DBCA, consultants and industry to monitor bilby abundance across Western Australia, including in the Pilbara, Kimberley, Rangelands and inland deserts. Use of this monitoring technique has provided better information for managing bilby populations.

The technique has been used extensively in partnership with Traditional Owners across the Kimberley and inland deserts where small and large populations exist, with the largest known wild population documented at 44 individuals. Wild bilby populations in the Pilbara are relatively small (up to 19 individuals) and isolated, which means they can be highly susceptible to threats, with two populations becoming extirpated during monitoring. A reintroduced population at Matuwa increased sevenfold over nine years from 144 to at least 971 individuals. This demonstrates that when threats are managed appropriately across a large area, bilbies can rapidly increase in number without the need for predator exclusion fencing.

Management implications

- A reliable monitoring technique using non-invasive genetic sampling, reducing the need for unnecessary disturbance to bilbies and reduced time and resource requirements is now available.
- This standardised monitoring technique allows for robust comparisons of population size between populations, and within populations over time and is useful in measuring the effectiveness of management actions.
- It can be used to conduct population genetic analyses to estimate the relationship and connectivity of populations and family groups.

Further information

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