Biodiversity and Conservation Science

Bilby abundance monitoring at Warralong, Western Australia, 2021

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Warralong Greater Bilby Offset

June 2022

GOVERNMENT OF WESTERN AUSTRALIA

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Contents

Figures

Tables

Acknowledgments

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1 Background

In 2014 the Department of Biodiversity, Conservation and Attractions (DBCA) Bilby Research Team, together with Warralong community members, identified an active bilby population on the Coongan Pastoral Lease (hereafter referred to as the Coongan colony). In 2018, a collaborative project involving the Warralong Community, DBCA, Roy Hill and Greening Australia was initiated to monitor and manage this population. In 2018, preliminary surveys conducted as part of this project detected an additional bilby population on the Coongan lease, approximately 12km north-west of the Coongan colony (hereafter referred to as the River colony).

Since 2014, bilby abundance has been measured at the Coongan colony in 2016, 2018, 2019, and at the River colony in 2018 and 2019. This report documents the most recent abundance measurement recorded at the River colony in 2021.

2 Field Sampling

The field component of the 2021 Warralong bilby abundance survey involved two trips. The objective of the first trip was to locate bilby populations and delineate boundaries around areas of most recent activity. The objective of the second trip was to survey transects within the activity areas, and collect as much scat material as possible to facilitate abundance estimates using spatially explicit mark-recapture models.

The first trip was completed by DBCA scientists (two personnel) between the 23rd and 30th of July, 2021. Despite a seven-day search effort using a combination of quad bikes and light vehicles and on foot, only one bilby colony was located. This is believed to be the River colony located in previous years along the northern boundary of the Bilby Land Management Area (BLMA), with the last detection in 2019. The area containing recent bilby activity (activity from 2021) is indicated in Figure 1, and is equal to ~ 280 ha in size. The location of the previously known Coongan bilby colony located near the southern boundary of the BLMA remains unknown. Further searches for the Coongan colony will be included as part of 2022 abundance monitoring.

The second trip (August 18th-23rd) was completed by DBCA scientists (two personnel) with assistance from two Greening Australia personnel. A total of 40 scat samples were collected using the protocol outlined in Dziminski et al (2021). Samples were stored dry, at room temperature, in 30 ml tubes, approximately 1/3-filled with silica gel beads and cotton wool, until DNA extraction was undertaken. In addition, the location of burrows and tracks were also noted (Figures 2, 3, 4).

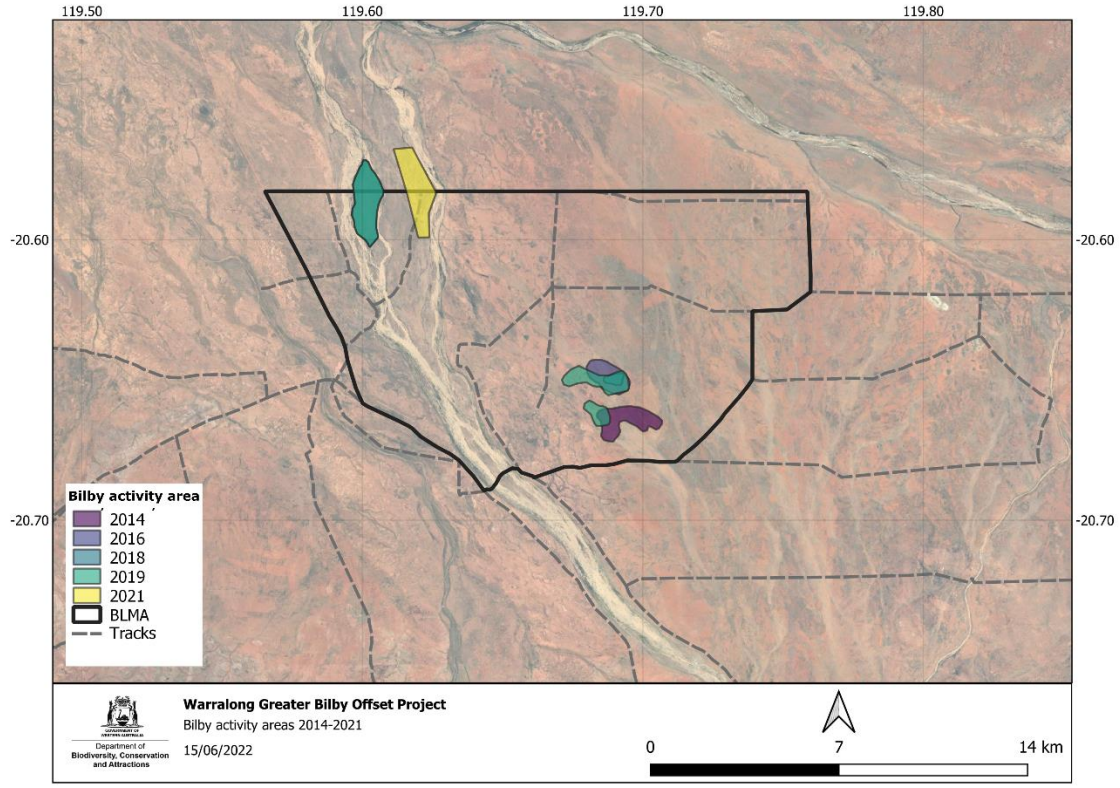


Figure 1 – Bilby activity areas recorded between 2014 and 2021 within the Bilby Land Management Area (BLMA) on Coongan Station.

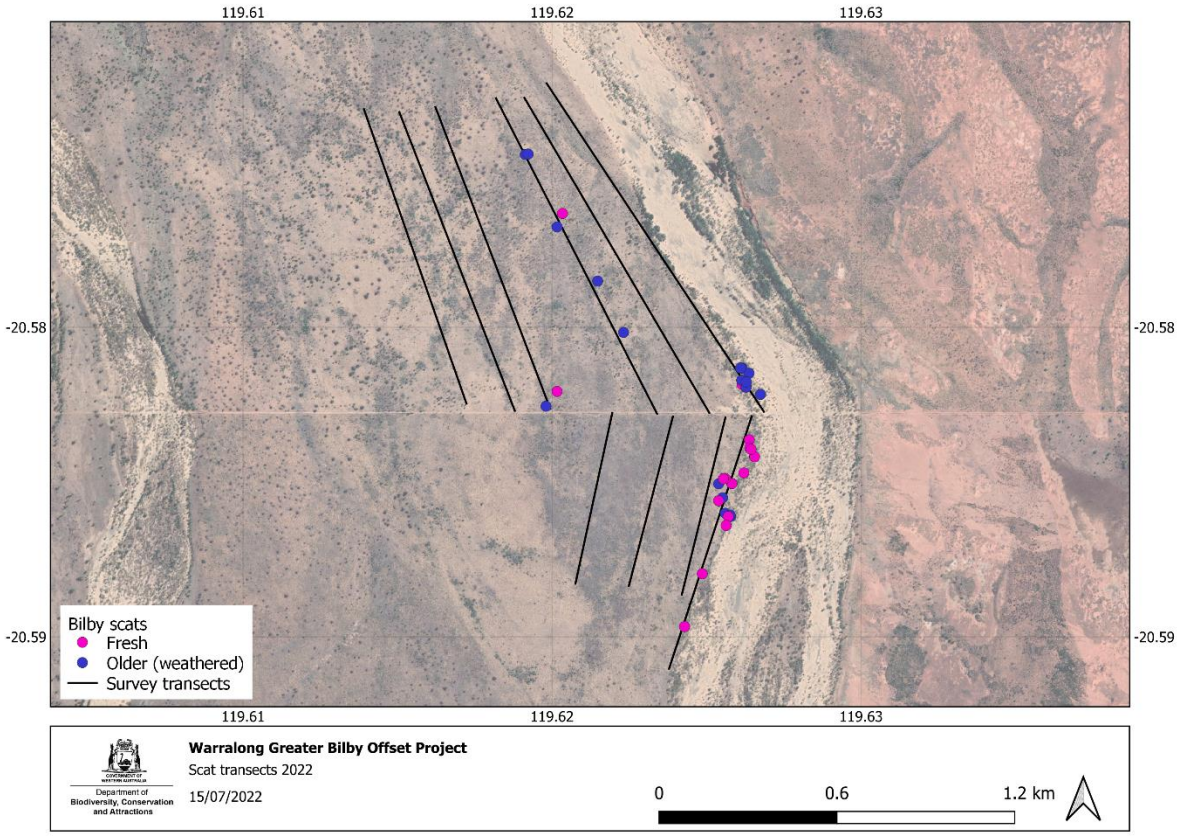


Figure 2 – Bilby sign detected as part of the 2021 bilby abundance survey on Coongan Station.

Figure 3 - An active bilby burrow detected as part of the 2021 bilby abundance survey on Coongan Station.

Figure 4 - *Bilby tracks and bilby scat detected as part of the 2021 bilby abundance survey on Coongan Station.*

3 Laboratory analyses

DNA extractions were completed using the Omega Bio-tek MagBind® Stool DNA 96 Kit (Omega Bio-tek, Norcross, GA, USA) with modifications to the manufacturer's Inhibitor Rich Protocol. DNA was screened using eight highly polymorphic microsatellite markers (Table 1). These were multiplexed into two polymerase chain reactions (PCR) using the Qiagen Multiplex PCR Plus Kit. PCR amplification was performed as described in Carpenter and Dziminski (2017). Y chromosome linked markers, to determine the sex of the individual from which the sample was obtained, were trialed on the DNA samples that were successfully genotyped (Table 1). The PCR product was then analysed on an ABI3730XL Sequencer, using GeneScanTM 500 LIZ® size standard, and genotyped using Genemapper Software 6 (Applied Biosystems, Waltham, MA, USA).

Of the 40 supplied samples, eight samples yielded DNA and amplified at enough loci to include in the identity analysis (Table 2). Genotyping using the eight loci identified at least three distinct individuals, all of which were male (Table 2). None were identified in previous abundance surveys.

Table 1 - Microsatellite and sex-linked markers used in PCR.

Locus	Fluorescent label	Reference
Multiplex 1		
B02	6-FAM	Moritz et al. (1997)
B17	VIC	Moritz et al. (1997) and Smith et al. (2009)
B56	PET	Moritz et al. (1997) and Smith et al. (2009)
B66	NED	Moritz et al. (1997)
Multiplex 2		
B55	6-FAM	Moritz et al. (1997)
B22	VIC	Moritz et al. (1997)
B41	PET	Moritz et al. (1997) and Smith et al. (2009)
B63	NED	Moritz et al. (1997)
Sex-linked markers in presence of B22 and B63 primers		
KDM5D.1	6-FAM	Brandies (2021)
HUWE1	NED	
HCFC1.2	VIC	Brandies (2021)

Table 2 - Individuals and sex identified from scat samples.

Individual	DBCA ID	Site	Sex
1	BIL0960	River Population	M
1	BIL0970	River Population	M
2	BIL0975	River Population	M
3	BIL0978	River Population	M
2	BIL0982	River Population	M
3	BIL0988	River Population	M
2	BIL0992	River Population	M
2	BIL0994	River Population	M
3	BIL0996	River Population	M

4 Abundance analysis

Due to the low number of successfully genotyped scat samples, reliably estimating bilby density using spatially explicit capture-recapture models was not possible. As such, we have used the minimum number of bilbies alive (MNA) (Krebs 1999) for the purpose of comparisons with previous abundance estimates; an abundance metric commonly used in ecology when more sophisticated measures are not available (Wauters *et al.* 2000; Abu Baker *et al.* 2017; Onodera *et al.* 2017). MNA was calculated by summing the number of animals identified at monitoring sites using genetic sequencing.

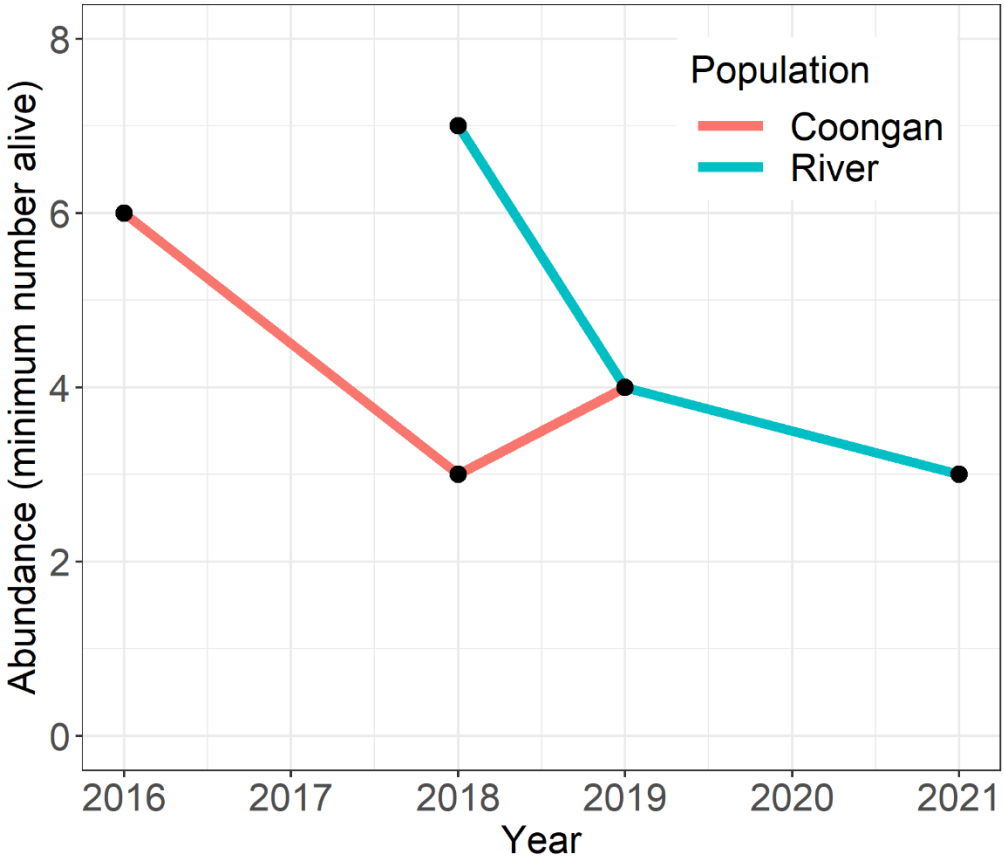


Figure 5 - Minimum number of bilbies alive derived from genotype sequencing of scats on Coongan Station between 2016 and 2021.

5 Recommendations

Feral predator management is scheduled to occur within the BLMA in June 2022. As such, we recommend further abundance surveys to occur between September – December 2022 to capture any immediate population changes. A three-month interval following baiting should be sufficient in allowing time for bilby recruits to be detectable via current abundance sampling methods, given the species' rapid reproductive cycle (Southgate *et al.* 2000). It is likely recruits will be entering the River colony in September given heavy rainfall within the study area that occurred in May is likely to have triggered bilby breeding (Berris *et al.* 2019) (Appendix 1).

In addition to the continued monitoring of the River colony, we recommend further searches are carried out to locate the Coongan colony, as well as any other additional bilby colonies or populations that may exist within the BLMA or surrounding area. Maximising the number of colonies or populations monitored is critical to facilitating the detection of changes in abundance that are resultant of management actions implemented as part of this project. It is important to note that given the 2021 abundance monitoring was limited to one colony, measuring changes in abundance as a result of management (i.e., feral predator baiting) is likely to be statistically challenging.

To facilitate locating bilby colonies, local interested community members could be trained to recognise and record bilby sign by involving them in abundance monitoring, which would also improve the likelihood of additional bilby populations being located in the future.

6 References

Brandies, P.A. (2021) Conserving Australia's iconic marsupials one genome at a time. PhD Thesis. The University of Sydney, Sydney. https://hdl.handle.net/2123/26787

Abu Baker MA, Reeve N, Conkey AA, Macdonald DW, Yamaguchi N (2017). Hedgehogs on the move: Testing the effects of land use change on home range size and movement patterns of free-ranging Ethiopian hedgehogs. *PloS one* **12**, e0180826.

Berris KK, Cooper SJ, Breed WG, Carthew SM (2019). Timing of breeding and female fecundity of the greater bilby (Macrotis lagotis) in the temperate zone of South Australia: implications for translocations of a previously widespread species. *Wildlife Research* **46**, 444–453.

Krebs CJ (1999). 'Ecological methodology'

Moritz C, Heideman A, Geffen E, McRae P (1997). Genetic population structure of the Greater Bilby *Macrotis lagotis*, a marsupial in decline. *Molecular Ecology* **6**, 925–936. doi:10.1046/j.1365-294X.1997.00268.x

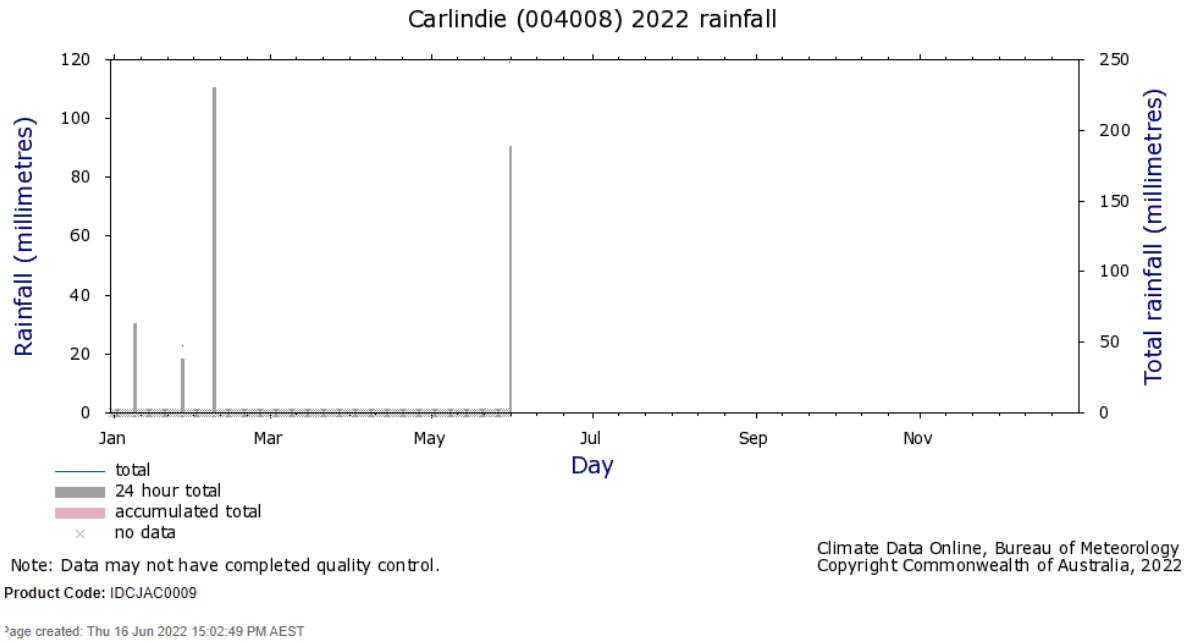
Onodera R, Akimoto Y, Shimada T, Saitoh T (2017). Different population responses of three sympatric rodent species to acorn masting—the role of tannin tolerance. *Population ecology* **59**, 29–43.

Smith S, McRae P, Hughes J (2009). Faecal DNA analysis enables genetic monitoring of the species recovery program for an arid-dwelling marsupial. *Australian Journal of Zoology* **57**, 139–148. doi:10.1071/ZO09035

Southgate R, Christie P, Bellchambers K (2000). Breeding biology of captive, reintroduced and wild greater bilbies, Macrotis lagotis (Marsupialia: Peramelidae). *Wildlife Research* **27**, 621–628.

Wauters LA, Lurz PW, Gurnell J (2000). Interspecific effects of grey squirrels (Sciurus carolinensis) on the space use and population demography of red squirrels (Sciurus vulgaris) in conifer plantations. *Ecological Research* **15**, 271–284.

7 Appendices



Appendix 1 - 2022 rainfall recorded at Carlindie Station, located approximately 37km west of Warralong community.

Appendix 2 – DBCA and Greening Australia personnel at the River bilby colony.