Results of the second PMA3 Biodiversity Monitoring Survey of the PNG LNG Upstream Project Area, 10–31 May 2017

Edited by Stephen J. Richards

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Cover image: The Rainbow Treefrog (*Litoria iris*) is a conspicuous member of the frog fauna on Hidges Ridge where adults glue their eggs to leaves overhanging forest pools and roadside ditches.
Back cover image: Shovel-billed Kookaburra (*Clytoceyx rex*).

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Stephen J. Richards (Editor)

A Report to ExxonMobil PNG Limited from the 2017 PMA3 Biodiversity Monitoring Program

This report is dedicated to the memory of our friend and colleague Dr Ken Aplin, who passed away in January 2019.

Ken was a key member of the PMA3 biodiversity monitoring team, a mentor to aspiring Papua New Guinean mammalogists, and a valued colleague and friend. His interests and expertise spanned many fields, and the results of Ken's research in New Guinea over nearly four decades will be an enduring legacy. He will be sorely missed.

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Acronyms and Abbreviations

asl	Above sea level
BAA	Biodiversity Assessment Area
CEPA	Conservation and Environment Protection Authority
CITES	Convention on International Trade in Endangered Species of Wild Fauna and Flora
DD	Data Deficient (IUCN threat category)
EIS	Environmental Impact Statement
EN	Endangered (IUCN threat category)
GLMM	Generalised Linear Mixed Model – a statistical test
GPS	Global Positioning System
IFC	International Finance Corporation
IUCN	International Union for the Conservation of Nature
km	Kilometers
LC	Least Concern (IUCN threat category)
LNG	Liquefied Natural Gas
m	meters
mm	millimeters
NT	Near Threatened (IUCN threat category)
pers. obs.	Abbrev. 'personal observation'
PNG	Papua New Guinea
Project	PNG LNG Project
RAI	Relative abundance index
ROW	The pipeline right of way including associated access roads
sp.	Abbrev. 'species' (singular)
spp.	Abbrev. 'species' (plural)
WMA	Wildlife Management Area

Glossary of Technical Terms

Central cordillera	Refers to the central mountainous spine of New Guinea that runs from the eastern edge of the Vogelkop Peninsula in Indonesian New Guinea to the eastern tip of mainland PNG.
Community structure	The taxonomic composition of a community; species assemblage.
Conservation listed species	Includes: (1) species listed under the IUCN Red List as threatened (Critically Endangered, Endangered or Vulnerable), Near Threatened or Data Deficient; (2) species listed as Protected under the PNG Fauna (Protection and Control) Act 1966; (3) species listed under CITES Appendix I or II.
Diversity	In its broadest sense the concept of biological diversity can refer to multiple organizational levels including (but not limited to) genes, variants and subspecies, species, and ecosystems. In this report the term 'diversity' is restricted to the meaning 'numbers of species' (the most common definition) except where other forms of diversity are also being discussed, when the specific term 'Species Richness' is used.
Endemic	Belonging exclusively or confined to a particular place.
New species	A species new to science, discovered for the first time during the PMA3 surveys
Protected	Species listed as Protected under the Papua New Guinea Fauna (Protection and Control) Act 1966.
Restricted range	Species which have a total historical breeding range of less than 50,000 km2.
Taxa	Plural of taxon; a systematic division (e.g. more than one species, genera, etc.).
Taxonomic	Taxonomy is the science of identifying, naming and classifying living organisms.
Undescribed species	A species that has not yet been formally named. It may be a new species or it may be known previously from other locations.

Report Summary

Montane forest canopy at Hides Ridge

Background and aims

The Upstream Project Area of the Papua New Guinea Liquefied Natural Gas (PNG LNG) Project supports considerable biodiversity values. These were summarised in ExxonMobil PNG Limited's (EMPNG) Biodiversity Strategy as (i) extensive intact forest, (ii) high floristic diversity, (iii) high faunal diversity, (iv) endemic species, (v) unique assemblages of species, (vi) species of conservation concern, and (vii) biodiversity of importance to local communities for resource use and cultural and spiritual purposes.

To evaluate the success of its commitment to safeguarding these biodiversity values, and to determine whether the Project is successfully meeting the four major objectives of the Biodiversity Strategy – *Maintain the intactness of the Upstream area as a whole*; *Conserve the priority ecosystems*; *Protect focal habitats*; and *Account for residual impacts* (EMPNG PNG LNG Biodiversity Strategy; available online) – EMPNG has developed a series of four Programmed Monitoring Activities (PMAs). One of these, Programmed Monitoring Activity 3 (PMA3), provides high-quality information on trends in species diversity and abundance in the Upstream area of the PNG LNG Project in order to detect changes that may be associated with the development of Project infrastructure.

PMA3 conducts rapid biodiversity surveys to collect quantitative, repeatable data on species presence, relative abundance and trends in species diversity in two Biodiversity Assessment Areas (BAAs) in areas affected by the PNG LNG Project: the first at Hides Ridge (BAA 1), and the second on the Agogo Range near Moro (BAA 2). The first PMA3 biodiversity survey program was conducted during June–July 2015 and the results were presented to EMPNG in 2016 and subsequently published in a public document (Richards 2017). That report provided baseline data on biodiversity in the two BAAs against which future monitoring surveys could be compared, found limited evidence for impacts of the linear infrastructure corridors on a suite of flora and fauna groups, and presented a series of recommendations for improving the PMA3 monitoring program to ensure that it best supports EMPNG's goal to safeguard biodiversity values in the Upstream Project Area.

The PMA3 monitoring program is scheduled to be conducted biennially. This document reports the results of the May 2017 PMA3 biodiversity monitoring survey and compares them with data on species diversity and trends obtained during 2015 to identify and interpret any trends in species presence, abundance and diversity in the vicinity of Project infrastructure.

Survey dates

10th– 31st May 2017 (Camera traps 10th May–30th August 2017)

Brief description of the survey area

Detailed descriptions of environments in the Upstream Project Area are presented in the Project EIS, and the region's biodiversity values are summarised further in the EMPNG Biodiversity Strategy. A comprehensive description of the local environments in BAA 1 and BAA 2, including forest structure and classification, is presented in Richards (2017), so only a brief summary is presented here.

Extensive forest cover remains within both BAAs, and gradients in vegetation composition and structure with elevational change are evident. Both BAAs lie within the high-rainfall belt that extends across the southern slopes of PNG's central cordillera and annual rainfall totals in excess of 4,000 mm with limited seasonality ('continuously heavy'; McAlpine et al. 1983) are typical.

The locations of both BAAs are shown in Figure 1.

BAA 1: 21–31 May 2017.

BAA 1 was established on Hides Ridge in Hela Province. It covers elevations between 2,100 and 2,750 m above sea level (asl), and was divided into two elevational bands, with three survey transects located at 2,100–2,400 m asl in the area between Wellpad C and Wellpad D, and three transects at 2,660–2,780 m asl located between Wellpads E and G (Figures 2–4).

BAA 2: 10–19 May 2017.

BAA 2 is located on the Agogo Range near Moro in Southern Highlands Province (Figure 1). Two survey transects were established at elevations of 1,000–1,080 m asl in the area west of Arakubi Quarry and east of the pipeline right of way (ROW), and three survey transects at elevations of 1,340–1,410 m asl in the vicinity of KP107 (Figures 5–7).

Camera traps were deployed from 10th May to 30th August 2017.

Survey approach

Surveys for butterflies, frogs, non-volant mammals (rodents) and bats were conducted on the 11 permanent transects established during the 2015 PMA3 survey (Figures 2–7): six transects established in BAA 1 along the Hides Ridge access road and pipeline ROW (Figures 2–4), and five permanent transects in BAA 2 established along the pipeline ROW at KP107 (Figures 5–6) and adjacent to the Arakubi Quarry (Figures 5, 7). Each of these 11 transects extended for 220–250 m into the forest and were approximately perpendicular to the ROW or forest edge. Coordinates for all transects are presented in Appendix 1. In addition, camera trapping surveys were undertaken in the same elevational bands in each of BAA 1 and BAA 2 but the activities were carried out at some distance from the transects to avoid regular disturbance of camera trapped areas. Locations of camera trap arrays are illustrated in Figures 3–4 (BAA 1) and 6–7 (BAA 2).

A detailed rationale for the use of permanent transects to detect potential impacts of Project activities on species presence and trends is presented in Richards (2017). Perpendicular alignment of transects with respect to linear infrastructure samples a gradient of potential disturbance that is greatest at the forest edge and progressively less so with increasing distance into the forest. The impacts of 'edge effects' on most groups of organisms, including greater light and wind penetration, and dust and noise pollution, are likely to attenuate rapidly and the 220–250 m transects should extend beyond any major impacts.

Although patterns in species abundance and distributions along the transects were evident from the first (2015) survey results, quantitative data collected over time at the same sites using the same methods will be a more powerful indicator of any changes that are occurring, including in the more sheltered areas of forest remote from the forest edge.

Survey modifications for 2017 PMA3 monitoring program

Several modifications were made to the PMA3 survey program in response to results of the 2015 survey:

1. Invertebrates comprise the most diverse group of animals in tropical forests but were not represented in the 2015 PMA3 monitoring program. To address this gap the 2017 PMA3 survey evaluated the potential to incorporate butterflies, a well-known group of insects frequently included in monitoring studies, into the long-term biodiversity monitoring program. Results of this study are included in this report.

2. Long-term studies of vegetation regeneration along the ROW, and of weed distribution and dispersal, are being conducted for or by EMPNG in the Upstream Project Area, with several long-term plant plots located in the vicinity of the PMA3 transects. A decision was therefore made that the vegetation studies initiated during 2015 would not provide sufficient value over the long term and this component of PMA3 was discontinued.

3. A pilot study to test the effectiveness of camera-traps for monitoring bird and mammal populations was conducted during the 2015 PMA3 surveys and proved to be highly successful. In contrast, mist-netting for birds proved to be unviable due to various logistical constraints and the rugged limestone terrain. The decision was therefore made to replace the mist-netting survey with an expanded program of camera trapping in 2017. The expanded focus on camera-trapping of birds and mammals also precluded the detailed examination of ROW impacts on birds using Acoustic Recorders for this report.

Major results

A summary of the major results is presented below.

Taxon accounts

Butterflies

A total of 31 individuals representing 18 butterfly species was documented, including nine species from BAA 1 and nine species from BAA 2. No species considered to be of conservation significance were encountered and two thirds of the species were represented by a single capture. Although there was a clear trend for maximum numbers of individuals and species to be captured at the edge of the ROW in both BAAs, an insufficient number of butterflies were detected to undertake meaningful analyses of butterfly abundance and assemblage structure during this survey.

Given the extremely low numbers of butterflies encountered during the 2017 PMA3 monitoring survey it is recommended that this component of the PMA3 monitoring program be discontinued.

Frogs

A total of 34 species of frogs was documented using a combination of Visual and Audio Encounter Surveys (VAES) and Acoustics Recorders along permanent transects that run perpendicular to linear infrastructure in BAA 1 at Hides Ridge and BAA 2 on the Agogo Range near Moro. Three species that were detected during 2015 were not encountered on transects during 2017, and two additional species that were not detected during 2015 were found on transects during 2017.

Five of the undescribed species documented during 2015 have now been formally described in the scientific literature, but nearly half of the frog species encountered in 2017 remain undescribed (n= 16; 47%). All of these were previously known to occur in the Upstream Project Area. The two IUCN Data Deficient species documented in 2015, *Choerophryne burtoni* and *Oreophryne notata*, were both documented during the 2017 survey and there appear to be no threats to these species in either BAA.

Species diversity and composition differed substantially between the two BAAs, with eight frog species found on Hides Ridge in BAA 1, 27 species on the Agogo Range near Moro in BAA 2, and only one species (3%) shared between them. Analyses of data from the VAES searches and Acoustic Recorders, and comparisons with data from 2015, found a significant effect of elevation on species diversity and community composition but no evidence for temporal shifts in species diversity or composition with increasing distance from the ROW and associated roads in either BAA.

Analysis of the abundance of potential edge effect 'Indicator Species' at increasing distances from linear infrastructure did not identify any species that was obviously associated with the forest edge, or conversely with the forest interior, but various species were shown to be relatively common at specific altitudinal bands. The multi-faceted approach to analysing patterns of distribution and relative abundance are providing important context data within which any future potential change may be compared.

To date, establishment of the linear infrastructure clearings in BAA 1 on the Hides spine-line and in BAA 2 on the Agogo Range near Moro has had no detectable impacts on local frog populations.

Camera traps

More than 80 species were documented in 5,506 independent photographic events from 71 functioning cameras in both BAAs. Thirteen of these species had not previously been recorded in the BAAs, and a number of them were not previously known from the broader Kikori basin. Nine conservation listed species were camera trapped, including five IUCN Threatened species – the Eastern Long-beaked Echidna (*Zaglossus bartoni*), Pademelon (*Thylogale* sp.), Goodfellow's Tree Kangaroo (*Dendrolagus goodfellowi*), Western Montane Tree Kangaroo (*D. notatus*) and Papuan Eagle (*Harpyopsis novaeguineae*) – three Near Threatened species and one Data Deficient species. The Near Threatened Small Dorcopsis (*Dorcopsulus* cf. *vanheurni*) was the most frequently camera trapped of all species with more than 950 photographic events recorded across all sites.

Multi-model comparisons (using Akaike information criterion (AICc)) and model averaging revealed a correlation between animal activity rates and distance from infrastructure (roads or clearings) in six species. Most species demonstrated higher activity rates further from infrastructure clearings at the BAA 2 sites, and a reverse pattern at Hides High (BAA 1) with higher activity nearer to clearings. Two widespread species – Raffray's Bandicoot (*Peroryctes raffrayana*) and Small Dorcopsis – shifted the direction of their response to distance from clearings across the BAAs.

Terrain effects offer an alternative and parsimonious explanation for this observation—steeper terrain is present closer to clearings at BAA 2 and further from clearings at BAA 1, so that most observed patterns can be explained by animals avoiding the steepest ground.

The highest number of forest incursions by humans and dogs, and the lowest photographic event rates for hunting-sensitive species, were recorded at the BAA 1 sites. Hunting-sensitive species were rarest at Hides Low, where pooled activity rates of widespread (study area-wide) taxa were significantly lower than at all other sites.

Small non-volant mammals (Rodents)

A total of 12 species of rodents was trapped during the 2017 survey, four of which were not detected during 2015. No IUCN listed (above Least Concern) mammal species were recorded by trapping, but five species are yet to be formally described in the scientific literature. Trapping results in 2017 were lower than the previous survey, with a total of 53 individuals captured in 2017 compared with 133 in 2015. However these capture rates are relatively high compared to many other studies.

Statistical analysis of the mammal trapping data indicate that diversity and total captures were not significantly different at increasing distances from the linear infrastructure, across elevation bands, or between survey years. The results of this study find no evidence for negative impacts of linear infrastructure on native rodents in either BAA.

One of the additional species detected during 2017 was a Black Rat, *Rattus rattus*, which is a commensal pest species. One Black Rat was captured in BAA 1 at 2,200 m at the edge of transect H2, which suggests that this species may be moving along the linear infrastructure on Hides Ridge. The introduced rat *Rattus exulans*, which was documented at KP107 during the 2015 survey, was not encountered there in 2017.

The introduction of the genome-scale SNP-based genetic identification system, which incorporated all samples sequenced previously, as well as samples collected from all novel captures in 2017, confirmed the species identities of all morphological-based identifications, and was particularly useful for identifying species boundaries between the most closely related taxa.

Bats

A total of 20 bat species was detected by acoustic recordings, and nine echolocating species of bat from the Hipposideridae, Miniopteridae, Rhinolophidae and Vespertilionidae, and two small blossom bats from the Pteropodidae, were captured in nets or harp traps. Based on both captures and acoustic recordings from the 2015 and 2017 surveys, a total of 26 bat species has now been documented during the PMA3 monitoring program. Two of these are species possibly new to science, and a third undescribed species is deemed to be present on the basis of a unique echolocation call.

Statistical tests showed that the bat assemblages were significantly different above and below 2,000 m, with higher diversity at lower elevations in BAA 2. This was due mainly to a greater number of species in BAA 2 that forage in edge habitats (small Emballonuridae) and a greater number of forest interior species (Hipposideridae and Rhinolophidae).

In contrast to the results from the 2015 survey, bat diversity was significantly greater at the open edge of sampling transects compared to the forest interior. This was a trend noticed at 1,000 m in 2015, but the 2017 survey brought greater statistical power to analyses, and the patterns were also obvious from an examination of Indicator Species indices. This difference reflects an influx of species that forage in edge and open flight spaces (mainly the small Emballonuridae, also Miniopteridae), particularly in BAA 2. These species have benefitted from the creation of additional forest-edge habitats.

The combined results from both the 2015 and 2017 surveys suggest that forest adjacent to the ROW and associated roads has so far retained its value for bats.

Table 1. Number of species documented during the 2017 PMA3 Surveys, number estimated to be new to science and/or undescribed, and the number of species holding an IUCN threat classification above Least Concern.

	Butterflies	Frogs	Camera traps (birds and mammals)	Non-volant Mammals	Bats	TOTALS
Total Species	31	34	80+	12	20	**177**
Undescribed Species	0	16	?	5	1+	**22+**
IUCN Species	0	2	9	0	0	**11**

Threats

Two major ongoing threats to biodiversity values in BAA 1 and BAA 2 were identified during the 2015 survey (apart from risks of mortality to dispersing animals from traffic). These were 1) decreasing habitat quality adjacent to the ROW due to edge effects (e.g. Andrews et al. 2015) and 2) improved access to the forest by humans (for hunting and gardening) and by invasive species, both native and exotic.

Edge effects

The 2017 survey again found no conclusive evidence for negative impacts of 'edge effects' in the animal groups studied. Several species of bats at lower elevations in BAA 2, and one frog at Hides Ridge in BAA 1 appear to have benefitted from the creation of linear infrastructure associated with the pipeline ROW and associated roads, and the camera trap study revealed several terrestrial birds and mammals with higher activity rates nearer to infrastructure clearings at some sites. Initial camera trapping evidence for negative edge effects in some cases is confounded by possible terrain effects which will be investigated further in subsequent sampling years.

Hunting, and predation pressure by dogs

The improved accessibility into formerly remote areas of forest following construction of the linear ROW infrastructure and associated roads has led to an increase in both direct hunting pressure by local people and predation by dogs. The highest number of forest incursions by humans and dogs was recorded on Hides Ridge (BAA 1), where camera traps recorded the capture of an Eastern Long-beaked Echidna. The presumedly higher levels of hunting pressure at Hides Ridge were correlated with consistently lower photographic rates on camera traps for hunting-sensitive species in BAA 1. Hunting pressure is difficult to quantify, and impacts on local wildlife populations are best measured by monitoring population trends over time, so the 2017 camera trapping dataset provides a useful baseline against which to measure future changes.

Removal of trees along linear infrastructure

Removal of trees by local people for construction materials and other purposes was documented on or adjacent to three survey transects during the 2017 survey: one at the forest edge (0 m) at Transect H2 in BAA 1, one at the forest edge (0 m) at Transect M2 in BAA 2 and one c 200 m inside the forest adjacent to Transect M4 at Arakubi in BAA 2.

In all three cases single trees were felled causing damage to surrounding vegetation, and at Transects H2 and M2 this shifted the location of the forest edge by several metres. Impacts, if any, of these disturbance events will be monitored over time.

Exotic rodents

During 2015 exotic rodent species were detected only at KP107 in BAA 2 where they were confined to the forest edge, and at Hides Gas Conditioning Plant. During 2017 *Rattus exulans*, which had been detected at KP107 in 2015, was not detected there. However, a single specimen of the Black Rat, *Rattus rattus*, was encountered at transect H2 on Hides Ridge during the 2017 survey. The risk of short-term expansion of exotic rodents beyond the immediate forest edge is likely quite low, but their presence in BAA 1 carries with it a risk of the transfer of novel pathogens to native wildlife. This can happen through interspecific contact including predation (e.g. quoll eating exotic rat) and attempted interbreeding (e.g. native and exotic *Rattus* spp.) or through environmental contamination (water, soil etc). The spread of new pathogens to native wildlife populations is acknowledged globally as a threat to biodiversity.

Major conclusions

1. Results of the 2017 PMA3 survey indicate that both BAAs retain high biodiversity values for all surveyed taxa, with both areas continuing to support many rare, conservation listed, restricted range and hunting-sensitive species. Numerous conservation significant species that were not encountered during 2015 were documented during the 2017 survey, including a number of additional species not previously recorded from the Kikori basin.

2. Low capture rates precluded detailed analyses of abundance and assemblage composition for butterflies on transects in BAA 1 and BAA 2 and this group appears to be unsuitable for long term monitoring at these sites.

3. There have been no detectable temporal shifts in frog or rodent species diversity or composition since establishment of the PMA3 monitoring program in 2015 along linear clearings in BAA 1 on the Hides spine-line and in BAA 2 on the Agogo Range near Moro.

4. Statistical tests (and greater statistical power from the 2017 survey) highlighted the significantly greater bat diversity in open areas at the start of transects compared to the remaining recording sites in the forest interior during the 2017 survey, which reflects an influx of species that forage in edge and

open flight spaces, particularly in BAA 2. These species have benefitted from creation of additional forest-edge habitats.

5. Improved accessibility along the ROW and Project roads has facilitated hunting by local people and predation by dogs, particularly on Hides Ridge where hunting pressure was reflected in low camera trap detection rates for hunting-sensitive species.

6. Results of the expanded camera trapping study reinforce the utility of this method for documenting rare and elusive hunting sensitive fauna. The expanded 2017 study generated statistically useful datasets that have provided significant insights into edge and terrain effects in a variety of species, and into hunting and predation pressure on conservation significant species adjacent to Project infrastructure.

7. Overall, the results of the 2017 PMA3 survey indicate that the biodiversity values of the Upstream Project Area remain intact - there was no unequivocal evidence that edge effects negatively influence the presence or behaviour of any species.

8. However increases in hunting pressure and feral dog predation and the potential spread of exotic rodent species, both potentially associated with installation of the pipeline ROW and associated roads, remain the two major factors that may threaten biodiversity values in the BAAs.

General recommendations

1. **Butterfly monitoring**
   Butterflies are not a suitable target for biodiversity monitoring programs at Hides Ridge and the Agogo Range due to low detection rates, and this taxon should not be monitored in future.

2. **Reassessment of VAES transect sampling for frogs**
   Because most frog species were encountered by both Visual and Audio Encounter Surveys (VAES) and Audio Recorders, we recommend that the use of VAES be reassessed after the 2019 survey due to the logistical difficulties associated with conducting field work at night. It may be possible in future to rely on Acoustic Recorders as the sole survey method.

3. **Continued use of improved genetic assessment methods**
   Genetics-based identification has provided a foundation for reliable comparisons between sites, survey years and investigators for multiple taxa during the PMA3 surveys by providing a robust mechanism for species identifications in groups that contain morphologically cryptic fauna. During 2017 we adopted a new genomics-based set of genetic markers to provide greater clarity around the species boundaries of closely-related taxa encountered on the surveys. The 'RADseq' DNA sequencing method has provided a more powerful method for understanding the relationships of taxa encountered and we recommend that it be continued as the PMA3 program moves forward.

4. **Collecting fine-scale habitat data to support the camera trapping program**
   The expanded camera trapping program was successfully implemented in 2017 and should be adopted for 2019 and in subsequent survey years. To better understand the observed patterns of distribution of species detected by camera traps, additional information on fine-scale vegetation variables at trapping sites should be collected for consideration in future modelling. A relevant sampling protocol has already been developed, and we recommend adding one more member to the camera trapping team to assist with this data collection during the 2019 survey.

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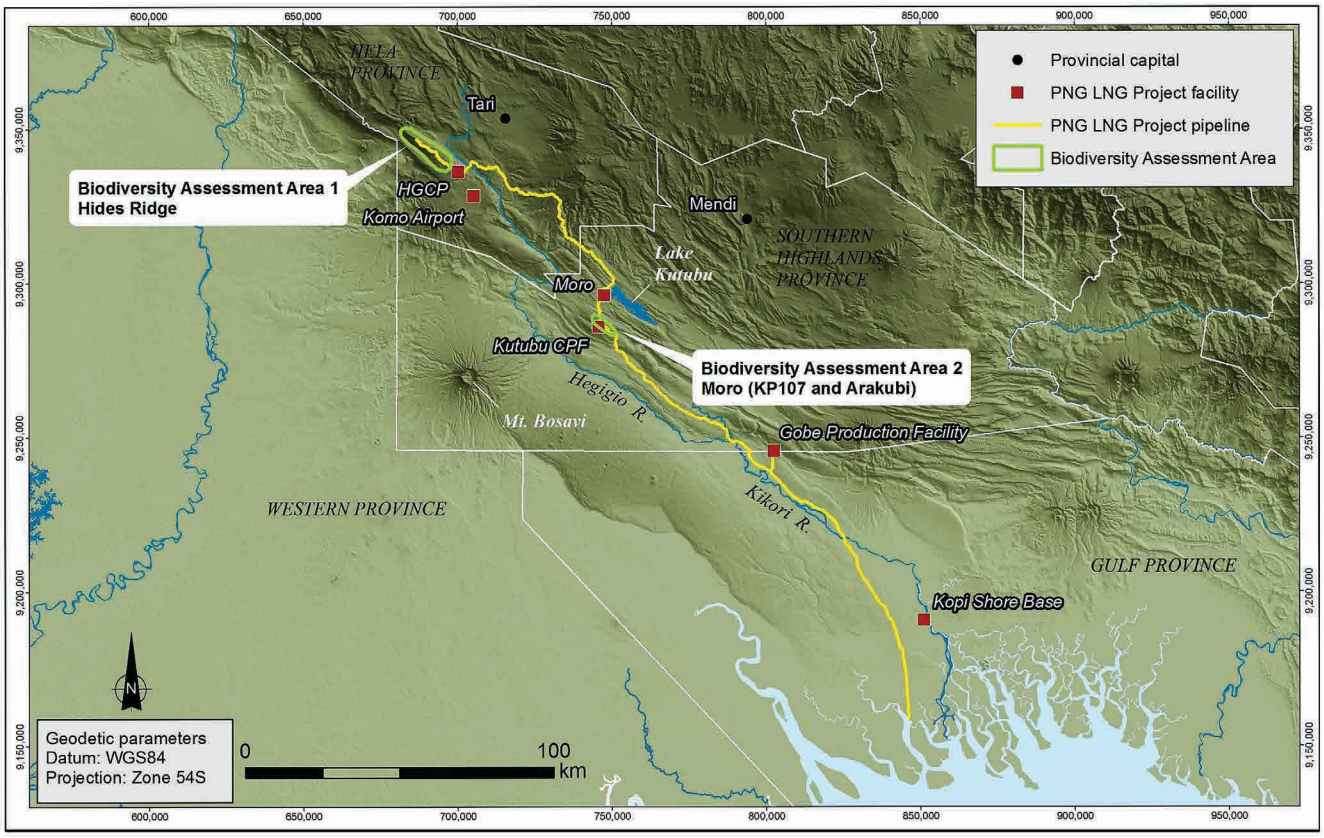

Figure 1. Regional map showing location of the two BAAs surveyed during the PMA3 surveys.

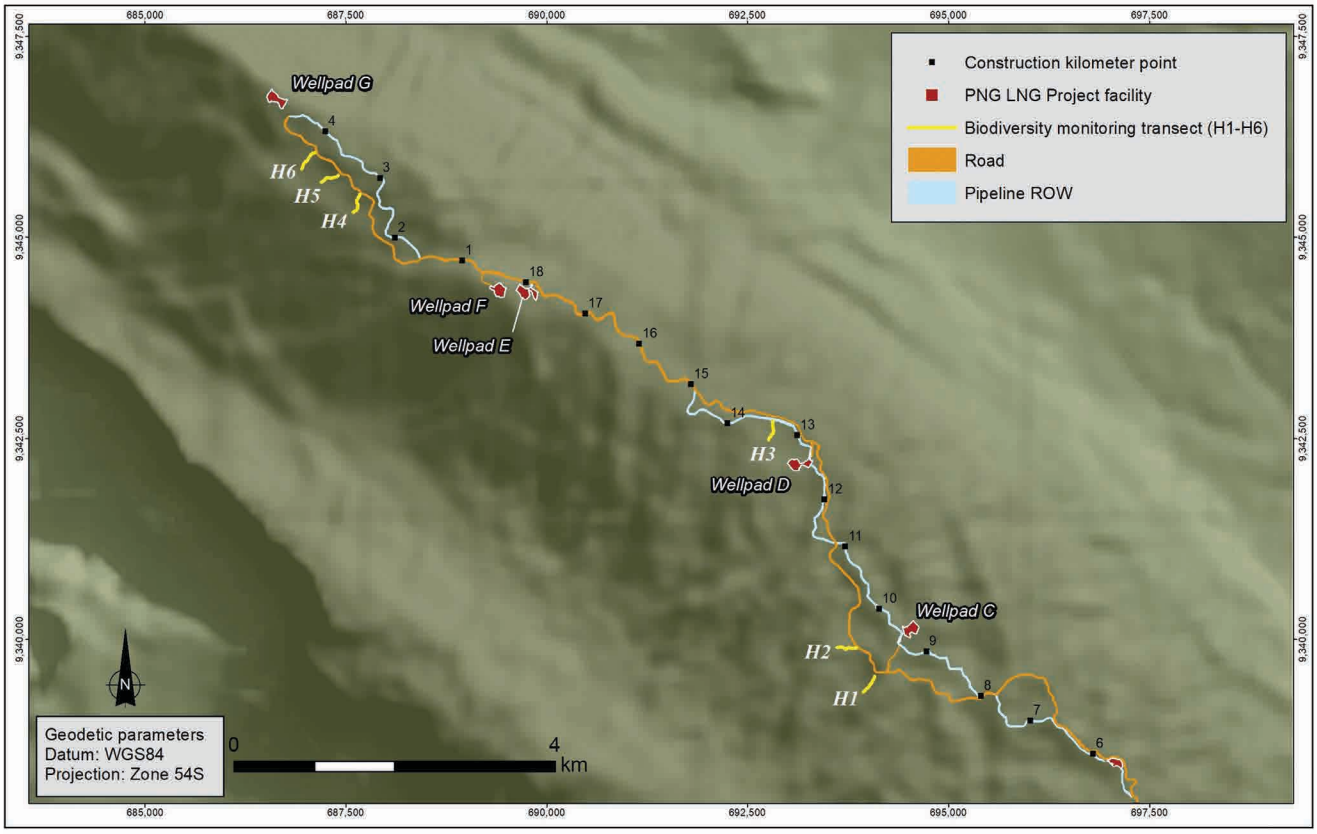

Figure 2. Map showing locations of the six major transects in BAA 1.

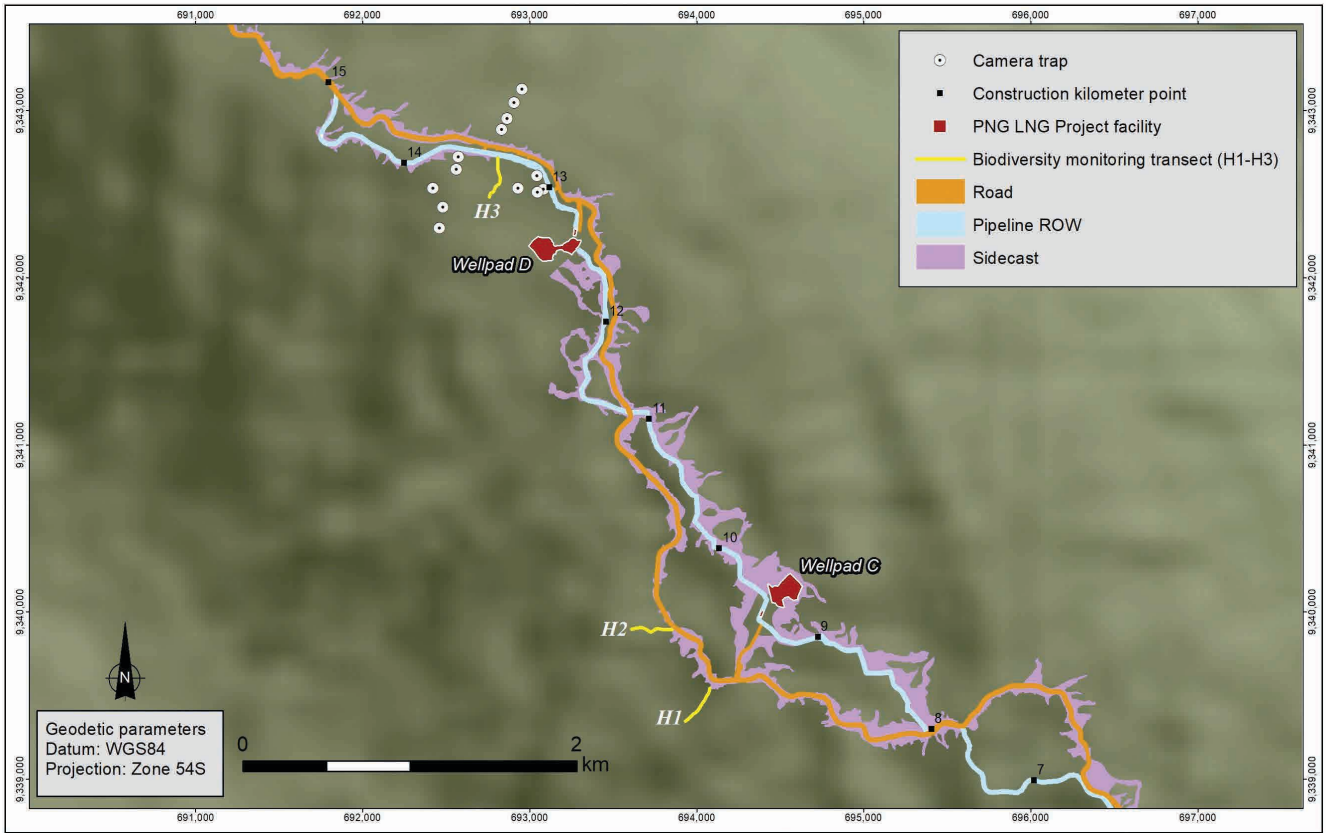

Figure 3. Map of lower elevations in BAA 1 showing details of Transects 1–3, and camera trap arrays.

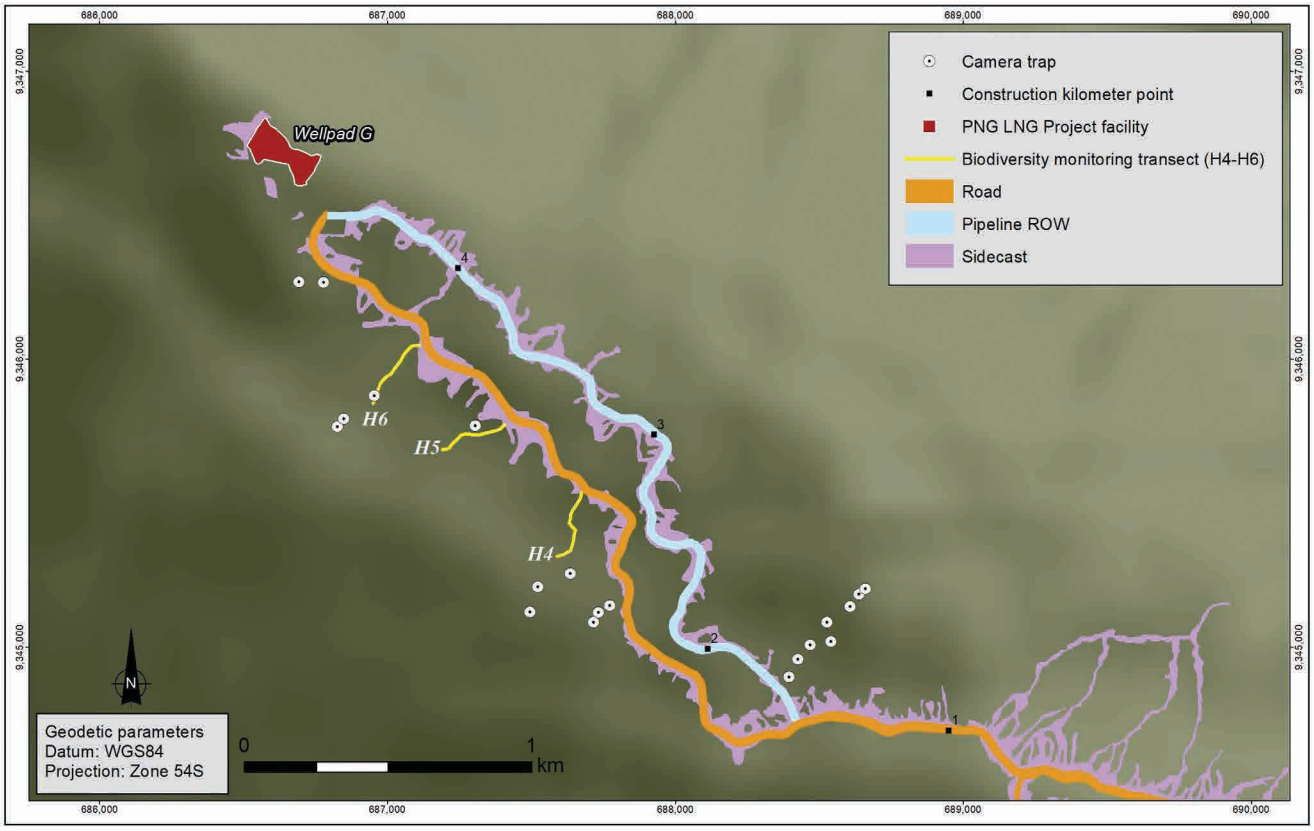

Figure 4. Map of upper elevations in BAA 1 showing details of Transects 4–6 and camera trap arrays.

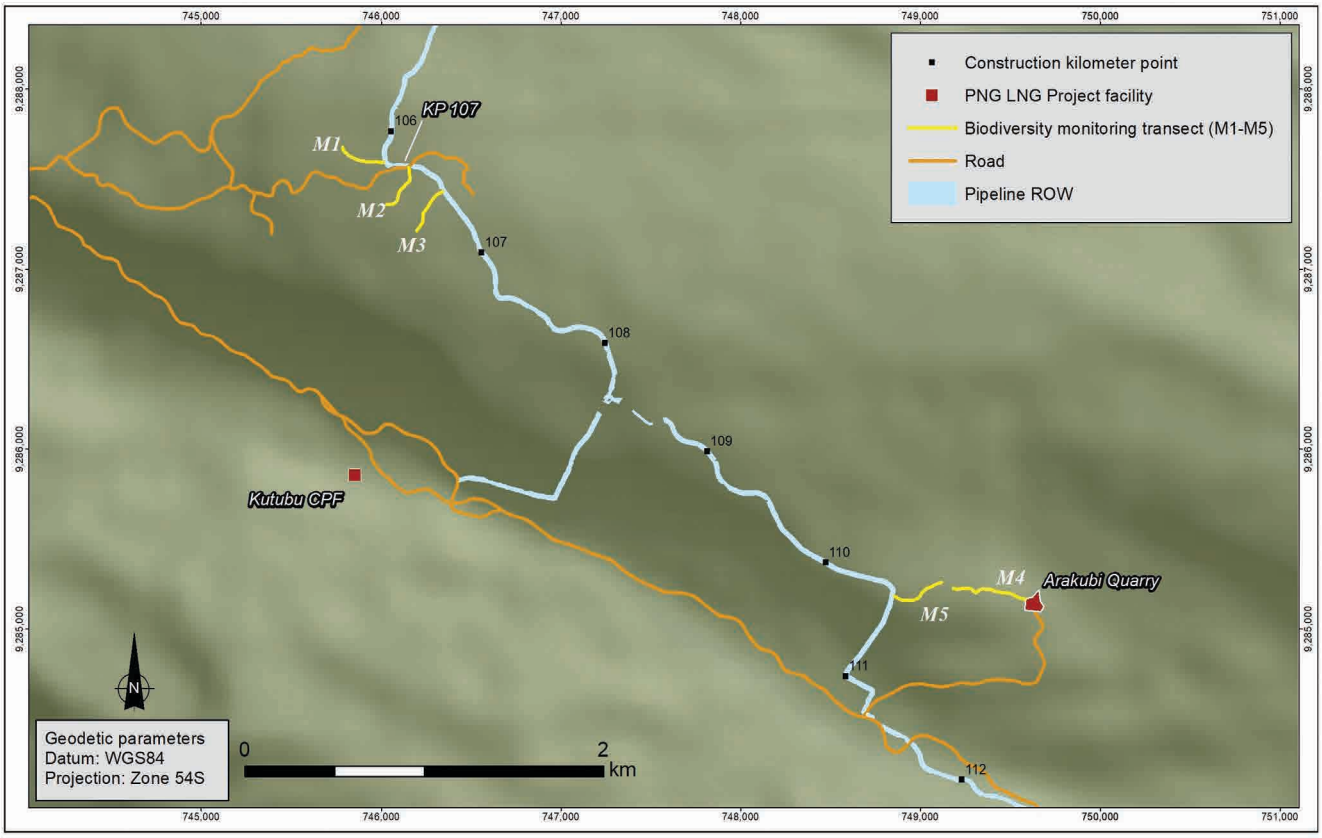

Figure 5. Map showing locations of the five major transects in BAA 2.

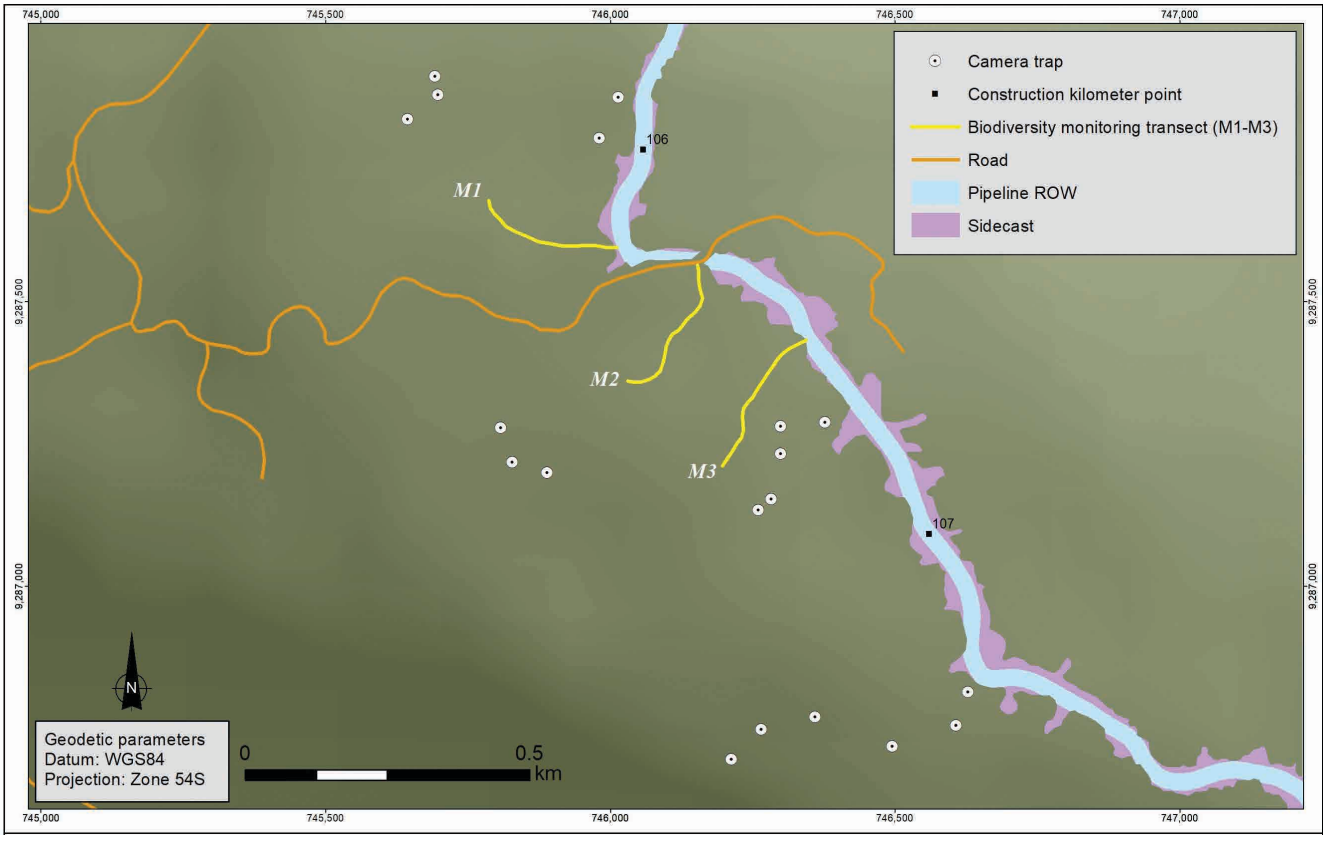

Figure 6. Map showing locations of the three major transects and camera trap arrays at KP107 in BAA 2.

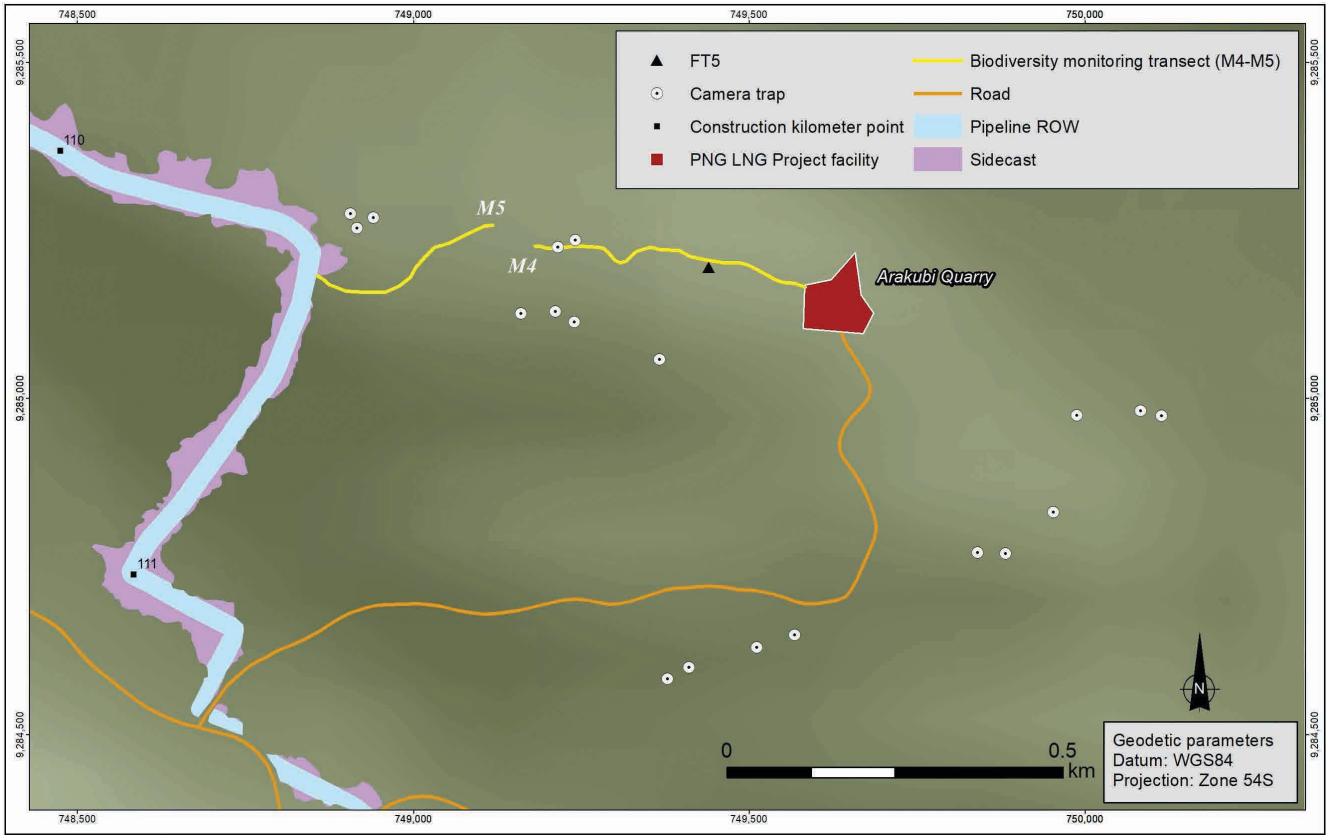

Figure 7. Map showing locations of the two major transects and camera trap arrays at Arakubi Quarry in BAA 2.

Appendix 1. Coordinates and elevations (at start) for each of the 11 standard survey transects established in BAA 1 and BAA 2.

BAA	Transect	Position	Coordinates	Elevation (m)
1	H1	Start	S5.97229° E142.75333°	2140
1	H1	End	S5.97416° E142.75198°	
1	H2	Start	S5.96915° E142.75127°	2150
1	H2	End	S5.96913° E142.74908°	
1	H3	Start	S5.94369° E142.74177°	2285
1	H3	End	S5.94579° E142.74132°	
1	H4	Start	S5.91835° E142.69531°	2685
1	H4	End	S5.92036° E142.69456°	
1	H5	Start	S5.91621° E142.69289°	2745
1	H5	End	S5.91699° E142.69095°	
1	H6	Start	S5.91372° E142.69021°	2730
1	H6	End	S5.91553° E142.68877°	
2	M1	Start	S6.44023° E143.22424°	1390
2	M1	End	S6.43950° E143.22221°	
2	M2	Start	S6.44051° E143.22552°	1380
2	M2	End	S6.44236° E143.22442°	
2	M3	Start	S6.44169° E143.22724°	1365
2	M3	End	S6.44368° E143.22594°	
2	M4	Start	S6.46206° E143.25662°	995
2	M4	End	S6.46152° E143.25299°	
2	M5	Start	S6.46124° E143.25242°	1050
2	M5	End	S6.46192° E143.25004°	

Chapter 1 – Butterflies

Pagi S. Toko

Graphium weiskei from Hides Ridge

Summary

Background and aims

Butterflies are among the best-studied of invertebrates and they have been useful targets for biodiversity monitoring because they are taxonomically well known, easily surveyed, and they occur in many different habitats. Three methods for monitoring butterflies were trialed during the 2017 PMA3 surveys, at Hides Ridge in Biodiversity Assessment Area 1 (BAA 1) and near Moro on the Agogo Range (BAA 2):

1. Pollard walks were conducted on 200 m survey transects that extended into the forest from the edge of EMPNG's pipeline right of way (ROW).

2. Fruit bait traps were placed at 20 m intervals along each 200 m transect and left for 24 hours.

3. Paper lures, which are particularly attractive to hesperiid butterflies, were placed on low foliage at 20 m intervals along each transect and checked after 2 hours.

This report presents the results of the butterfly monitoring survey to determine whether 1) there is any evidence that the ROW is having an impact on butterfly populations at Hides Ridge and the Agogo Range near Moro and 2) whether one or more of the techniques trialed during this survey are suitable for long term population monitoring at these sites.

Major results

A total of just 30 individuals representing 18 butterfly species was collected, with nine species detected in BAA 1 and nine in BAA 2. There was no overlap in species composition between the two BAAs.

Pollard walks along transects produced the largest number of butterfly records, accounting for 25 individuals of 15 species. Fruit bait traps produced just five records from four butterfly species, and paper lures did not produce any records.

Although there was a trend for more butterflies to be detected at the forest edge, insufficient data were obtained to conduct detailed analyses of butterfly assemblages in order to assess the potential impacts of linear infrastructure.

Conclusions

Low capture rates precluded detailed analyses of abundance and assemblage composition on transects in BAA 1 and BAA 2.

It is concluded that butterflies are not a suitable target for biodiversity monitoring programs at Hides Ridge and the Agogo Range and this taxon will not be monitored in future.

Introduction

The island of New Guinea supports about 5% of global biodiversity, most of it endemic, and has a unique geological and cultural history (Sekhran and Miller 1995). New Guinea boasts more than 1000 butterfly species, with about 900 of these occurring in Papua New Guinea (Novotny and Toko 2002; Tennent 2006). Butterflies are frequently used in biodiversity monitoring projects because they are taxonomically well known, easily surveyed, and they occur in many different habitats (Pearson 1994; Kerr et al. 2000).

The Moro and Hides areas of Southern Highlands and Hela provinces are located on Papua New Guinea's central cordillera and are known to harbor a rich montane biodiversity. Exxon Mobil PNG Limited (EMPNG) has constructed a pipeline right of way (ROW) and associated roads in these areas (the Upstream Project Area) to extract Liquefied Natural Gas and pipe it from the highlands to the coast. The pipeline runs through extensive areas of forest that were recognized

as having significant biodiversity values, and in order to provide high quality information on trends in species diversity in the vicinity of the ROW, EMPNG established a biodiversity monitoring program (PMA3) near Moro and on Hides Ridge. The first field survey for the PMA3 biodiversity monitoring program was conducted in 2015 and those results are summarized in Richards (2017). The 2015 survey did not assess trends in species diversity for any group of invertebrates and, because invertebrates constitute the majority of animal species in tropical forest environments, an attempt was made during the 2017 survey to establish a butterfly monitoring program using transects established in 2015.

Methods

Study sites

The butterfly monitoring project utilized the same transects that were established for other taxonomic groups during the 2015 PMA3 survey. These included six transects in Biodiversity Assessment Area 1 (BAA 1) on Hides Ridge and five transects in BAA 2 on the Agogo Range near Moro. The locations of the two BAAs and the altitudes and locations of each transect, and a description of the habitats in both BAAs, are provided in the Report Summary.

Survey methods

Butterfly surveys were conducted by the author and Mr Chris Dahl, occasionally with assistance from Anita Mosby or Rebekah Ilave from the EMPNG biodiversity team. We trialed three different methods to monitor butterflies on existing transects – 1) 'Pollard walks', 2) fruit baits and 3) paper lures, to assess their potential for quantitatively assessing butterfly abundance and assemblage composition in the Upstream Project Area. We used the first 200 meters of transects that were established perpendicular to the ROW during 2015 to assess the impact of linear infrastructure on a range of animal taxa (see Richards 2017). Surveys were conducted within a 10 m wide band (5 m on either side of the transect centre-line). The aim was to document changes in butterfly abundance, diversity and species composition along a disturbance gradient between the forest edge at the ROW and less/undisturbed forest 200 m from the forest edge.

Butterfly transects (Pollard walk)

The 'Pollard walk' is a method commonly used by ecologists for sampling butterflies (Moore 1975; Pollard 1977; Pollard et al. 1993). This method provides quantitative assessment of butterfly abundances, species richness and diversity in long term monitoring studies or for rapid comparative studies. It follows a simple protocol where a transect of certain length and width is prescribed and the recorder walks along it at a uniform pace and records each butterfly species found. Pollard walks may be 'time constrained', and they are frequently replicated at different times of the day to detect butterflies with different diel activity patterns. Although the technique has been criticized because it may not adequately consider the potentially significant role of butterfly ecology and behaviour, and of habitat and weather conditions on capture rates (Wikström et al. 2009; Pellet et al. 2012), the Pollard walk is still regarded as one of the best methods for sampling butterfly abundances and populations.

Each 200 m transect was marked at 20 m intervals. Pollard walks along each transect lasted for about 30 minutes with approximately 2–3 minutes spent walking within each 20 m segment, recording the location (segment) where each butterfly was detected. Transects were sampled twice, by walking slowly from 0 m to 200 m and then after 30 minutes returning to the start of the transect at the same pace. It therefore took approximately 90 minutes (30 minutes in one direction, 30 minutes wait and 30 minutes to return) to complete a 'set' of Pollard walks on a transect. The start and finish time for each set of Pollard walks was recorded. We sampled each transect twice, when possible on different days, once in the morning and once in the afternoon. For each transect we recorded canopy cover, and immediately prior to each walk we noted weather conditions including cloud cover because these factors can contribute to the activity levels of butterflies (Wikström et al. 2009). We captured resting and flying butterflies using a butterfly net attached to a 2 m aluminum pole and documented some specimens using binoculars.

Butterfly specimens were identified using Parsons (1999). Some butterflies that were not captured and could not be identified to species level were identified only to genus. Some voucher specimens were returned to the Binatang Research Center laboratory in Madang where they were carefully processed as museum specimens. Photographs of each specimen were also taken. Details of the Pollard walk survey design and schedule are presented in Appendix 1.1.

Fruit baits

Fruit baits are frequently used to study insect feeding guilds, and several studies (e.g. Barlow et al. 2007) have used fruit baits to study fruit feeding butterflies in different forest types. Fruit bait traps are simple and convenient, and are an efficient method for sampling butterflies that are attracted to rotting fruit and animal carcasses (Young 1975; Krenn et al. 2001), especially those in the subfamilies Amanthusiinae and Satyrinae in the Nymphalidae family. This method is particularly successful in tropical forests that have extended or year-round fruit-yielding seasons. Although fruit traps are simple and effective, the bias towards higher capture rates of species that are more attracted to certain chemical cues than others (Hughes et al. 1998) must be considered during interpretation of survey results.

We used the van Someren Rydon fruit trap design (DeVries 1987). This trap is a cylinder (65 cm deep x 25 cm diameter) enclosed by black nylon netting. The top of the cylinder is covered by strong cloth to provide shelter from the rain while the bottom rim of the cylinder is attached to a wooden plate by six small hooks, leaving a 2 cm gap that allows the butterflies to enter the cylinder. Fruit bait is placed on the wooden platform and when butterflies enter the trap through the gap at the base of the cylinder to access the bait, they normally climb or fly upwards after feeding, becoming trapped. One of the traps used during the PMA 3 monitoring survey is illustrated in Figure 1.1.

Fruit bait was made from chopped pieces of pineapple, banana and pawpaw mixed with 4–5 table spoons of sugar crystals and 3–4 cups of water to speed up fermentation. The bait was stored in air tight plastic bags and left to ferment for 24–48 hours.

Fruit bait traps were placed at three sampling stations at 0 m, 100 m and 200 m along the transects that were surveyed during Pollard walks. At each station we set up one bait trap, which contained a plate full of rotten fruit on the wooden base and was positioned approximately 3–4 m above the ground to avoid predation by terrestrial animals. Traps were placed strategically in open spaces under the canopy where butterflies are more likely to be active and after 24 hours they were checked, butterflies that had been trapped in the last 24 hours were recorded, and bait traps were removed, cleaned, and moved to another sampling station. Each sampling station was sampled only once, and all specimens captured were identified in the same way described for Pollard walks. Details of the bait trap survey design and schedule are presented in Appendix 1.2.

Paper Lures

Many butterflies are known to feed on mud, animal excrement and secretions, a behavior called puddling (Molleman 2010) that provides supplementary nutrients. Some skipper butterflies (Hesperiidae) are attracted to bird droppings, probably to obtain supplementary sodium that may enhance their mating physiology and behaviour (Boggs et al. 2004; Molleman et al. 2005).

To attract hesperiid butterflies we constructed paper lures that imitate bird droppings and soaked them in urine. Lures comprised 10–15 small pieces of white paper (approximately 1–3 cm in diameter) placed within a radius of 5 meters on the leaves of shrubs and small understory trees at sampling stations at 0, 100 and 200 m of the survey transects. The lures look and smell like bird droppings, and stick to the leaves for up to 3 days depending on rainfall. We checked lures for butterflies within 1–2 hours of their placement, for approximately 2–5 minutes at each station during Pollard walks, once during the outward walk from 0–100 m along the transect and again during the return walk. The sampling design for paper lure surveys is presented in Appendix 1.3.

Results

Species composition, diversity and abundance

An insufficient number of butterflies were detected to undertake meaningful analyses of butterfly abundance and assemblage structure during this survey. A total of just 31 individuals representing 18 butterfly species was documented (Table 1.1), including nine species from BAA 1 and nine species from BAA 2. Two thirds of the species were represented by 'singletons' where only one individual was caught, so it was also not possible to construct species accumulation curves. Figure 1.1 illustrates the number of individuals and species captured at 20 m intervals along 200 m transects extending into the forest perpendicular to the ROW. There is a clear trend for maximum numbers of individuals and species to be captured at the edge of the ROW in both BAAs, with another peak at the 200 m point for both individuals and species in BAA 2.

Assessment of methodology

The Pollard walk method was the most successful for documenting butterflies in both BAAs, detecting 25 individuals of 15 species (Table 1.2). In contrast fruit bait traps captured only five individuals from four species, and no butterflies were detected at paper lures.

Table 1.1 Total number of individuals and species of butterflies captured at BAA 1 and BAA 2 with all trapping methods combined.

	BAA 1	BAA 2	Total
Individuals	20	11	31
Species	9	9	18

Table 1.2. Summary of butterflies documented using different trapping methods on all transects in BAA 1 and BAA 2.

Family	Subfamily	Species Name	IUCN	BAA 2						BAA 1		
				Arakubi			KP107			Hides		
				Fruit Bait	Paper Lure	Pollard Walk	Fruit Bait	Paper Lure	Pollard Walk	Fruit Bait	Paper Lure	Pollard Walk
Lycaenidae	Satyrinae	*Mycalesis duponchelii*	NE			1	1					
Nymphalidae	Lycaeninae	*Philiris montigena*	NE									6
Nymphalidae	Pierinae	*Delias clathrata*	NE									1
Nymphalidae	Pierinae	*Delias endela*	NE									4
Nymphalidae	Pierinae	*Delias microsticha*	NE									2
Nymphalidae	Pierinae	*Delias geraldina*	NE						1			
Nymphalidae	Satyrinae	*Melanitis amabilis*	NE			1						
Nymphalidae	Satyrinae	*Mycalesis discobolus*	NE						2			
Nymphalidae	Satyrinae	*Mycalesis* sp.										1
Nymphalidae	Satyrinae	*Platypthima ornata*	NE									1
Nymphalidae	Satyrinae	*Platypthima homochroa*	NE									1
Papilionidae	Nymphalinae	*Cethosia cydippe*	NE	1								
Papilionidae	Papilioninae	*Graphium eurypylus*	NE									2
Papilionidae	Papilioninae	*Graphium weskei*	NE									2
Pieridae	Morphinae	*Morphopsis biakensis*	NE	1								
Pieridae	Morphinae	*Taenaris onolaus*	NE				1					
Pieridae	Morphinae	*Taenaris* sp.		1								
Pieridae	Satyrinae	*Mycalesis terminus*	NE			1						
				3		**3**	**2**		**3**			**20**

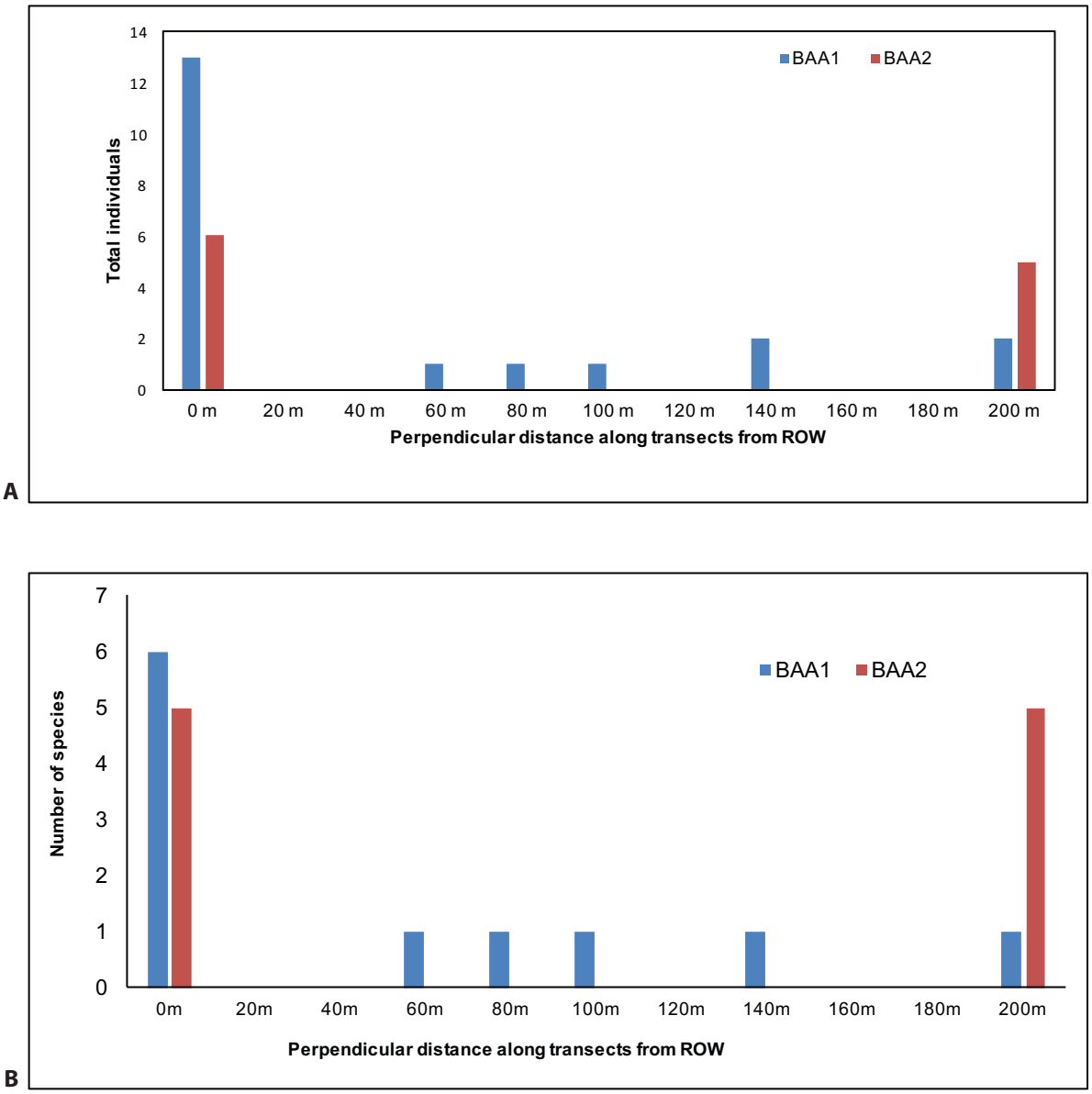

Figure 1.1. The number of individuals (A) and species (B) of butterflies encountered on all transects in each BAA during the 2017 survey.

Discussion

The results of this survey show some evidence of unequal distribution of butterfly species along forest disturbance gradients, with most captures occurring at the forest edge. This result is not surprising because many forest butterflies fly in open sunny areas, especially in forest gaps or along rivers (Brown and Hutchings 1997). However the extremely low capture rate in the forest interior was surprising, particularly because some transects intersected sunny gaps deep in the forest.

Many studies have shown that forest fragmentation, depending on the size and connectivity of fragments, can have both positive and negative effect on species distributions, diversity and composition (e.g. Pardini et al. 2005; Echeverría et al. 2007) and butterflies are one of the groups that has shown mixed responses to forest fragmentation and cleared corridors. For example while some forest disturbance regimes can be harmful to butterflies, some habitat-specialist and habitat restricted butterflies such as *Euptoieta claudia* from the Nymphalidea family can increase their diversity in response to disturbance (Haddad and Baum 1999). The pipeline ROW in the Upstream Project Area provides an excellent opportunity to study the impacts of forest fragmentation and edge effects on butterflies, but unfortunately capture rates on all transects were too low to reach any confident conclusions regarding possible impacts of linear infrastructure on local butterfly assemblages.

Given that cloudy conditions and rain are frequent in the Upstream Project Area it is likely that extended periods of time in the field, with substantially more replication of sampling, would be required to obtain data sufficiently robust for meaningful analysis.

Finally, we did not detect any butterfly species that are considered to be of conservation concern. All of the butterflies encountered are species with broad distributions along the central cordillera of New Guinea.

Conclusions

1. Thirty individual butterflies representing 18 species were detected during this survey. Diversity was the same at Hides Ridge (BAA 1) and on the Agogo Range (BAA 2) with nine species documented at each site.

2. No species considered to be of conservation significance were encountered.

3. Pollard walks along transects were the most efficient sampling method. Fruit bait traps detected just five butterflies, and paper lures failed to detect any butterflies.

Recommendations

1. Given the extremely low numbers of butterflies encountered during the 2017 PMA3 monitoring survey it is recommended that monitoring of this taxon be discontinued.

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Plate 1

Figure 1.2. Butterfly bait trap at Hides Ridge

Figure 1.3. *Cethosia cydippe* caught in bait trap in BAA 2

Figure 1.4. *Delias clathrata* from Pollard walk in BAA 2

Figure 1.5. *Delias endela* captured during Pollard walk at Hides Ridge

Figure 1.6. *Taenaris onolaus* caught in bait trap at Arakubi in BAA 2

Appendix 1.1.
Summary of the design, schedule and environmental variables recorded for the Pollard walk surveys (initials PT = Pagi Toko, CD = Chris Dahl, RI = Rebecca Ilave, AM = Anita Mosby).

Date	Location	Study Sites	Transect	Start Time	Finish Time	GPS at 0 meters	GPS at 200 meters	Transect direction	Cloud Cover at start	Canopy Cover	Weather Condition	Recorder
11/5/17	BAA 2	Arakubi Quary	M4	9:30	10:00	S6.46206° E143.25662°	S6.46152° E143.25299°	0 m–200 m	100%	75%	Cloudy, light rain	PT, CD
11/5/17	BAA 2	Arakubi Quary	M4	10:30	11:00	S6.46152° E143.25299°	S6.46206° E143.25662°	200 m –0 m	100%	75%	Cloudy, light rain	PT, CD
11/5/17	BAA 2	KP107	M3	13:30	14:00	S6.44169° E143.22724°	S6.44368° E143.22594°	0 m–200 m	100%	100%	Cloudy, light rain	PT, CD
12/5/17	BAA 2	Arakubi Quary	M4	9:15	9:50	S6.46206° E143.25662°	S6.46152° E143.25299°	0 m–200 m	100%	75%	Cloudy, light rain	PT, CD
12/5/17	BAA 2	Arakubi Quary	M5	10:34	11:00	S6.46192° E143.25004°	S6.46124° E143.25242°	200 m–0 m	100%	100%	Cloudy, light rain	PT, CD
12/5/17	BAA 2	Arakubi Quary	M5	11:30	12:00	S6.46124° E143.25242°	S6.46192° E143.25004°	0 m–200 m	100%	100%	Cloudy, light rain	PT, CD
12/5/17	BAA 2	Arakubi Quary	M4	12:30	13:00	S6.46152° E143.25299°	S6.46206° E143.25662°	200 m – 0 m	75%	75%	Patches of cloud, light rain	PT, CD
13/5/17	BAA 2	Arakubi Quary	M4	9:18	9:36	S6.46206° E143.25662°	S6.46152° E143.25299°	0 m–200 m	100%	75%	Misty, wet & chilly. Gloomy day	PT, CD
13/5/17	BAA 2	Arakubi Quary	M4	12:22	12:40	S6.46152° E143.25299°	S6.46206° E143.25662°	200 m – 0 m	100%	75%	Misty, wet & chilly. Gloomy day	PT, CD
13/5/17	BAA 2	Arakubi Quary	M5	10:30	11:58	S6.46192° E143.25004°	S6.46124° E143.25242°	200 m – 0 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, CD
13/5/17	BAA 2	Arakubi Quary	M5	11:30	12:00	S6.46124° E143.25242°	S6.46192° E143.25004°	0 m–200 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, CD
13/5/17	BAA 2	KP107	M2	13:47	14:15	S6.44051° E143.22552°	S6.44236° E143.22442°	0 m–200 m	50%	100%	Patches of cloud, light rain	PT, CD
13/5/17	BAA 2	KP107	M2	14:40	15:00	S6.44236° E143.22442°	S6.44051° E143.22552°	200 m –0 m	50%	100%	Patches of cloud, light rain	PT, CD
13/5/17	BAA 2	KP107	M1	15:15	16:10	S6.43950° E143.22221°	S6.44023° E143.22424°	200 m –0 m	50%	100%	Patches of cloud, light rain	PT, CD
14/5/17	BAA 2	KP107	M3	12:10	12:40	S6.44169° E143.22724°	S6.44368° E143.22594°	0 m–200 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, CD
14/5/17	BAA 2	KP107	M3	13:00	13:20	S6.44368° E143.22594°	S6.44169° E143.22724°	200 m –0 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, CD
14/5/17	BAA 2	KP107	M2	13:40	14:14	S6.44051° E143.22552°	S6.44236° E143.22442°	0 m–200 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, CD
14/5/17	BAA 2	KP107	M2	13:30	14:45	S6.44236° E143.22442°	S6.44051° E143.22552°	200 m –0 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, CD

Date	Location	Study Sites	Transect	Start Time	Finish Time	GPS at 0 meters	GPS at 200 meters	Transect direction	Cloud Cover at start	Canopy Cover	Weather Condition	Recorder
15/5/17	BAA 2	KP107	M2	12:42	13:01	S6.44051° E143.22552°	S6.44236° E143.22442°	0 m–200 m	100%	75%	Gloomy, light rain	PT, CD
15/5/17	BAA 2	KP107	M2	13:30	13:55	S6.44236° E143.22442°	S6.44051° E143.22552°	200 m –0 m	100%	75%	Gloomy, light rain	PT, CD
15/5/17	BAA 2	KP107	M1	14:00	14:25	S6.44023° E143.22424°	S6.43950° E143.22221°	0 m–200 m	100%	75%	Gloomy, light rain	PT, CD
15/5/17	BAA 2	KP107	M1	14:40	15:00	S6.43950° E143.22221°	S6.44023° E143.22424°	200 m–0 m	100%	75%	Gloomy, light rain	PT, CD
16/5/17	BAA 2	KP107	M2	12:14	12:30	S6.44051° E143.22552°	S6.44236° E143.22442°	0 m–200 m	100%	100%	Gloomy, light rain	PT, CD
16/5/17	BAA 2	KP107	M2	12:50	12:50	S6.44236° E143.22442°	S6.44051° E143.22552°	200 m–0 m	100%	100%	Gloomy, light rain	PT, CD
16/5/17	BAA 2	KP107	M1	13:30	13:40	S6.44023° E143.22424°	S6.43950° E143.22221°	0 m–200 m	100%	100%	Gloomy, light rain	PT, CD
16/5/17	BAA 2	KP107	M1	13:50	14:15	S6.43950° E143.22221°	S6.44023° E143.22424°	200 m–0 m	100%	100%	Gloomy, light rain	PT, CD
17/5/17	BAA 2	KP107	M1	8:48	9:15	S6.44023° E143.22424°	S6.43950° E143.22221°	0 m–200 m	25%	100%	Clear sunny morning	PT, CD
17/5/17	BAA 2	KP107	M1	10:15	10:45	S6.43950° E143.22221°	S6.44023° E143.22424°	200 m–0 m	25%	100%	Clear sunny morning	PT, CD
18/5/17	BAA 2	KP107	M1	9:15	9:37	S6.44023° E143.22424°	S6.43950° E143.22221°	0 m–200 m	25%	100%	Clear sunny morning	PT, CD
18/5/17	BAA 2	KP107	M1	10:00	10:30	S6.43950° E143.22221°	S6.44023° E143.22424°	200 m–0 m	25%	100%	Clear sunny morning	PT, CD
22/5/17	BAA 1	Hides	H1	9:30	10:05	S5.97229° E142.75333°	S5.97416° E142.75198°	0 m–200 m	75%	100%	Cloudy, sunny patches, wet under-storey	PT, CD
22/5/17	BAA 1	Hides	H1	10:30	11:00	S5.97416° E142.75198°	S5.97229° E142.75333°	200 m–0 m	75%	100%	Cloudy, sunny patches, wet under-storey	PT, CD
22/5/17	BAA 1	Hides	H3	13:00	13:30	S5.94369° E142.74177°	S5.94579° E142.74132°	0 m–200 m	100%	100%	Cloudy, sunny patches, wet under-storey	PT, CD
22/5/17	BAA 1	Hides	H3	14:00	14:28	S5.94579° E142.74132°	S5.94369° E142.74177°	200 m–0 m	100%	100%	Cloudy, sunny patches, wet under-storey	PT, CD
23/5/17	BAA 1	Hides	H5	14:50	15:17	S5.91621° E142.69289°	S5.91699° E142.69095°	0 m–200 m	100%	100%	Gloomy, light rain droplets	PT, CD
23/5/17	BAA 1	Hides	H5	13:30	14:00	S5.91699° E142.69095°	S5.91621° E142.69289°	200 m–0 m	100%	100%	Gloomy, light rain droplets	PT, CD
23/5/17	BAA 1	Hides	H3	9:12	10:00	S5.94369° E142.74177°	S5.94579° E142.74132°	0 m–200 m	100%	100%	Cloudy, sunny patches, wet under-storey	PT, CD

Date	Location	Study Sites	Transect	Start Time	Finish Time	GPS at 0 meters	GPS at 200 meters	Transect direction	Cloud Cover at start	Canopy Cover	Weather Condition	Recorder
23/5/17	BAA 1	Hides	H3	10:30	11:00	S5.94579° E142.74132°	S5.94369° E142.74177°	200 m–0 m	50%	100%	Clear fine day, patches of cloud	PT, CD
24/5/17	BAA 1	Hides	H5	10:00	10:30	S5.91621° E142.69289°	S5.91699° E142.69095°	0 m–200 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, AM
24/5/17	BAA 1	Hides	H5	11:00	11:30	S5.91699° E142.69095°	S5.91621° E142.69289°	200 m–0 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, AM
24/5/17	BAA 1	Hides	H4	13:00	13:30	S5.91835° E142.69531°	S5.92036° E142.69456°	0 m–200 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, CD
24/5/17	BAA 1	Hides	H4	14:00	14:30	S5.92036° E142.69456°	S5.91835° E142.69531°	200 m –0 m	100%	100%	Misty, wet & chilly. Gloomy day	PT, CD
24/5/17	BAA 1	Hides	H1	15:55	16:24	S5.97229° E142.75333°	S5.97416° E142.75198°	0 m–200 m	100%	100%	Cloudy, sunny patches, wet understorey	PT, CD
24/5/17	BAA 1	Hides	H1	16:40	17:10	S5.97416° E142.75198°	S5.97229° E142.75333°	200 m –0 m	100%	100%	Cloudy, sunny patches, wet understorey	PT, CD
25/5/17	BAA 1	Hides	H2	9:17	9:47	S5.96915° E142.75127°	S5.96913° E142.74908°	0 m–200 m	100%	100%	Cloudy, sunny patches, wet understorey	PT, CD
25/5/17	BAA 1	Hides	H2	10:30	11:10	S5.96913° E142.74908°	S5.96915° E142.75127°	200 m –0 m	100%	100%	Cloudy, sunny patches, wet understorey	PT, CD
25/5/17	BAA 1	Hides	H4	13:36	14:05	S5.91835° E142.69531°	S5.92036° E142.69456°	0 m–200 m	100%	100%	Cloudy, sunny patches, wet understorey	PT, CD
25/5/17	BAA 1	Hides	H4	14:30	14:58	S5.92036° E142.69456°	S5.91835° E142.69531°	200 m –0 m	100%	100%	Cloudy, sunny patches, wet understorey	PT, CD
26/5/17	BAA 1	Hides	H2	8:47	9:25	S5.96915° E142.75127°	S5.96913° E142.74908°	0 m–200 m	0%	100%	sunny morning, clear day, chilly	PT, RI
26/5/17	BAA 1	Hides	H2	9:55	10:25	S5.96913° E142.74908°	S5.96915° E142.75127°	200 m –0 m	0%	100%	sunny morning, clear day, chilly	PT, RI

Date	Location	Study Sites	Transect	Start Time	Finish Time	GPS at 0 meters	GPS at 200 meters	Transect direction	Cloud Cover at start	Canopy Cover	Weather Condition	Recorder
26/5/17	BAA 1	Hides	H6	13:30	14:00	S5.91372° E142.69021°	S5.91553° E142.68877°	0 m–200 m	100%	100%	Cloudy, sunny patches, chilly & wet	PT, CD
26/5/17	BAA 1	Hides	H6	14:30	15:00	S5.91553° E142.68877°	S5.91372° E142.69021°	200 m –0 m	100%	100%	Cloudy, sunny patches, chilly & wet	PT, CD
27/5/17	BAA 1	Hides	H3	9:47	10:23	S5.94369° E142.74177°	S5.94579° E142.74132°	0 m–200 m	100%	100%	Cloudy, sunny patches, chilly & wet	PT, CD
27/5/17	BAA 1	Hides	H3	10:50	11:20	S5.94579° E142.74132°	S5.94369° E142.74177°	200 m –0 m	100%	100%	Cloudy, sunny patches, chilly & wet	PT, CD
28/5/17	BAA 1	Hides	H6	14:00	14:30	S5.91372° E142.69021°	S5.91553° E142.68877°	0 m–200 m	100%	100%	Misty, chilly & wet. Gloomy day	PT, CD
28/5/17	BAA 1	Hides	H6	15:00	15:30	S5.91553° E142.68877°	S5.91372° E142.69021°	200 m –0 m	100%	100%	Misty, chilly & wet. Gloomy day	PT, CD
29/5/17	BAA 1	Hides	H4	9:45	10:15	S5.91835° E142.69531°	S5.92036° E142.69456°	0 m–200 m	0%	100%	Sunny morning, clear day, chilly	PT, RI
30/5/17	BAA 1	Hides	H6	9:20	10:10	S5.91372° E142.69021°	S5.91553° E142.68877°	0 m–200 m	0%	100%	Sunny morning, clear day, chilly	PT, RI

Appendix 1.2. Sampling design for the fruit bait trap survey.

Site	Transect	Date	Activity	Trap Method	Time of activity		
					0m	100m	200m
BAA2	M1	17.05.17	setup	Fruit Bait	10:15	10:35	10:45
		18.05.17	pull down		10:00	10:25	10:35
	M2	15.05.17	setup	Fruit Bait	13:30	13:43	13:56
		17.05.17	pull down		8:45	9:04	9:17
	M3	14.05.17	setup	Fruit Bait	12:10	12:32	12:40
Agogo Range		15.05.17	pull down		12:42	12:52	13:03
	M4	12.05.17	setup	Fruit Bait	12:30	12:54	13:00
		13.05.17	pull down		12:22	12:33	12:42
	M5	11.05.17	setup	Fruit Bait	10:30	10:50	11:05
		12.05.17	pull down		10:34	10:50	11:00
BAA1	H1	22.05.17	setup	Fruit Bait	9:30	9:47	10:05
		23.05.17	pull down		10:30	10:45	11:02
	H2	25.05.17	setup	Fruit Bait	9:17	9:27	9:40
		26.05.17	pull down		8:47	8:10	9:25
	H3	26.05.17	setup	Fruit Bait	13:30	13:55	14:02
Hides Ridge		27.05.17	pull down		10:50	11:10	11:20
	H4	28.05.17	setup	Fruit Bait	14:00	14:17	14:35
		29.05.17	pull down		9:45	10:00	10:15
	H5	23.05.17	setup	Fruit Bait	14:50	15:02	15:17
		24.0.5.17	pull down		11:00	11:15	11:35
	H6	29.05.17	setup	Fruit Bait	13:30	13:40	14:05
		30.05.17	pull down		9:20	9:42	10:10

Appendix 1.3. Sampling design for the paper lure survey method.

Site	Transect	Date	Activity	Trap Method	Time of activity		
					0m	100m	200m
BAA2	M1	17.05.17	setup	Paper Lure	8:48	9:05	9:15
		17.05.17	checked		10:15	10:35	10:45
	M2	16.05.17	setup	Paper Lure	12:14	12:25	12:35
		16.05.17	checked		12:50	13:01	13:10
	M3	14.05.17	setup	Paper Lure	12:10	12:32	12:40
Agogo Range		14.05.17	checked		13:02	13:18	13:35
	M4	12.05.17	setup	Paper Lure	9:15	9:33	9:50
		12.05.17	checked		12:30	12:45	13:01
	M5	12.05.17	setup	Paper Lure	10:30	10:50	11:05
		12.05.17	checked		11:32	11:46	12:02
BAA1	H1	24.05.17	setup	Paper Lure	15:55	16:12	16:24
		24.05.17	checked		16:40	17:09	17:15
	H2	25.05.17	setup	Paper Lure	9:17	9:27	9:47
		25.05.17	checked		10:30	10:48	11:10
	H3	23.05.17	setup	Paper Lure	9:12	9:35	10:00
Hides Ridge		23.05.17	checked		10:50	11:10	11:20
	H4	25.05.17	setup	Paper Lure	13:36	13:52	14:09
		25.05.17	checked		14:30	14:43	15:02
	H5	23.05.17	setup	Paper Lure	14:50	15:02	15:17
		23.05.17	checked		15:45	16:08	16:17
	H6	26.05.17	setup	Paper Lure	13:30	13:40	14:05
		26.05.17	checked		14:30	14:50	15:02

Chapter 2 – Frogs

Stephen J. Richards, Kyle N. Armstrong and Chris Dahl

A male *Oreophryne flavomaculata* guards its eggs glued to a leaf in forest at KP107

Summary

Background and aims

To determine whether linear infrastructure created by ExxonMobil PNG Limited's pipeline right-of-way (ROW) and Project roads is having an impact on frogs in the Upstream Project Area, we have established a program to monitor frog populations and communities in two Biodiversity Assessment Areas (BAAs) at Hides Ridge (BAA 1) and on the Agogo Range near Moro (BAA 2). The monitoring program, scheduled to occur every two years, was initiated in 2015 using 1) Visual and Audio Encounter Surveys (VAES) and 2) automated sound recording of frog calls (Acoustic Recorders). The second monitoring survey was conducted during May 2017 along the same permanent transects established adjacent to linear infrastructure during 2015.

This report presents the results of the 2017 monitoring survey and compares them with the 2015 results to assess whether there is currently evidence that Project infrastructure is having an impact on frog populations in either BAA.

Major results

A total of 34 species of frogs was documented using a combination of both survey methods along permanent transects that run perpendicular to infrastructure clearings in BAA 1 at Hides Ridge and BAA 2 on the Agogo Range near Moro. Three species that were detected during 2015 were not encountered during 2017. In contrast two additional species that were not detected during 2015 were found on transects during 2017.

Of the 108 species by transect detection events from both survey methods, 60 (55.5%) were detected by both survey methods, 26 (24.1%) were detected only by Acoustic Recorders and 22 (20.4%) were detected only by VAES. However overall 30 of the 34 species (88%) were detected at least once by both survey methods and just four species (12%) were detected only by VAES. No species were detected on automated sound recordings that were not also encountered during VAES transect surveys.

Species diversity was significantly lower at higher elevations, and both diversity and composition differed between the two BAAs, with eight frog species found in BAA 1, 27 species in BAA 2 and only one species (3%) shared between them. However, analyses of data from both the VAES and the Acoustic Recorders found no evidence in either BAA for shifts in species diversity or composition with increasing distance from infrastructure clearings.

The new genome-scale DNA identification framework developed for this survey has enhanced our ability to provide consistent identifications across surveys and a way of confirming the allocation of call types, specimens and names. It is a useful tool for the PMA3 program because many of the frog taxa encountered on the survey remain undescribed, and the taxonomic status of others remains poorly resolved. The same framework has immense potential for application nation-wide.

Conclusions and recommendations

Results of the 2017 PMA3 survey indicate that there have been no detectable temporal shifts in frog diversity and composition since establishment of the PMA3 monitoring program in 2015 along linear clearings in BAA 1 on the Hides spine-line and in BAA 2 on the Agogo Range near Moro.

The biodiversity values of frogs in these areas remain intact.

The two survey methods used gave complementary results, but Acoustic Recorders generated more robust data for statistical analyses. We recommend that VAES transects be continued in 2019 because they facilitate collection of data to improve species identification capacity and enhance the accuracy of call-based monitoring. However the ongoing value of the VAES method should be reassessed after the 2019 survey.

Introduction

Amphibians are excellent indicators of environmental conditions because their thin permeable skin makes them vulnerable to subtle changes in both aquatic and terrestrial environments. Frogs were identified as a core taxon in EMPNG's Biodiversity Strategy, and the presence of a distinct assemblage of torrential-stream dwelling treefrogs (Family Pelodryadidae) was partly responsible for upland rainforest streams being recognised as focal habitats. However many frog species in New Guinea do not use aquatic habitats for reproduction, instead depositing large, yolk-filled eggs on plants or under litter on the forest floor where they hatch directly into froglets (Anstis et al. 2011). All New Guinean species in the diverse family Microhylidae are known or expected to reproduce this way (Menzies 2006) and as a result this group dominates the frog faunas of karst habitats in Papua New Guinea.

The karst environments of Hides Ridge in BAA 1 and on the Agogo Range near Moro in BAA 2 are characterised by limited flowing water so the PMA3 frog monitoring program was designed to document the diversity (here also called 'species richness') and composition (which species are present) of microhylid frog communities. The frog monitoring program was initiated in May 2015 to document frog diversity and community composition in both BAAs using quantitative, repeatable sampling techniques that provided baseline data against which future changes in frog diversity and community composition could be measured, and assessed whether frog diversity and community composition changed with increasing distance from Project infrastructure. Results of the 2015 field survey are summarised in Richards and Armstrong (2017). Here we present the results of the second frog monitoring survey, conducted during May 2017.

Methods

Frog surveys in 2017 were conducted along the same permanent transects that were established during 2015, on Hides Ridge (BAA 1) between 22–29 May, and on the Agogo Range in the Moro area (BAA 2) between 14 May–20 May (Figure 1 in Report Summary). Each of these BAAs was divided into two survey 'sites' that differed in elevation:

- Hides Ridge (BAA 1):
  - Transects H1–3: between Wellpad C and Wellpad D, at elevations of 2,100–2,400 m asl.
  - Transects H4–6: between Wellpad E and Wellpad G, at 2,660–2,780 m asl.

- Moro area (BAA 2):
  - Transects M1–3: on the Agogo Range in the vicinity of KP107, at 1,340–1,410 m asl.
  - Transects M4–5: west of Arakubi Quarry and east of the pipeline ROW, at 1,000–1,070 m asl.

Surveys for frogs on transects

The two quantitative methods used to document frogs along transects in both BAAs are described in detail by Richards and Armstrong (2017) and a brief summary of each is provided below.

Visual and Audio Encounter Surveys (VAES)

VAESs provide counts of the numbers of frogs of each species seen and heard on 100 m transects marked at 20 m intervals. Most of the VAES transects start at the edge of, and run perpendicular to, linear infrastructure clearings, and thus allow for comparison of species diversity and assemblage composition at increasing distances from the forest edge. In the case of FT5 (see Figure 7 in Report Summary), the VAES transect starts at a sharp transition from regrowth forest (previously cleared for the quarry) to original forest. Coordinates for the beginning and end of each VAES transect are presented in Appendix 2.1.

Surveys were conducted by two searchers with headlamps and a digital recorder who walked slowly along each 100 m transect, noting each frog seen in each 20 m interval within a 5 m band (2.5 metres on either side of the transect path)

or heard within a 10 m band (5 metres on either side of the transect path). Each transect was sampled twice, normally on non-consecutive nights. The first survey each night started between approximately 19:30–21:00, and the second survey of the night started by 22:00. A standard set of environmental data (rainfall, temperature etc.) was recorded at the start of each VAES. A sample data sheet is provided in ExxonMobil (2016).

Each frog encountered was identified, whether it was seen or heard (or both) was noted, and its location on the transect (which 20 m segment, i.e. distance from the forest edge) was noted. A small number of voucher specimens were taken to provide tissue samples for DNA barcoding that will support future efforts to make robust and consistent identifications across successive surveys. VAES transects generally overlap with two Acoustic Recorders, positioned at 5 m and 70 m from the forest edge. This is not the case for Transect 6 in BAA 1 and Transect 5 in BAA 2 for which VAES data were not obtained.

Audio monitoring with acoustic recorders

During the 2015 survey unattended acoustic recordings generated by Wildlife Acoustics Song Meter SM3 recorders (hereafter 'Acoustic Recorders') provided high quality data on calling frogs from standardised recording effort at known distances into the forest from the disturbance zone.

The 2015 survey design for Acoustic Recorders was replicated in 2017. Acoustic Recorders were placed at three recording sites at increasing distances from the forest edge (5 m, 70 m and 170 m) on transects H1–6 established in BAA 1 and M1–5 in BAA 2 (Figures 2–7 in Report Summary). Recording units were placed 65 and 100 m apart to reduce the likelihood that an individual frog would be detected by more than one unit. The microphone of the recorder set at the 5 m position on each transect was oriented to maximise reception of signals from the edge habitat adjacent to the open area over the road. Units recorded continuously in WAV format at a sampling rate of 48 kHz for two consecutive nights at each recording site on each transect, giving a total of 36 recording nights over an 8-night survey period for BAA 1, and 30 recording nights over a 6-night survey period for BAA 2 (Table 2.1).

A summary of the design is presented in Table 2.1 and coordinates for each recording location are presented in Appendix 2.2. Unless otherwise specified, for the purposes of this chapter the abbreviation 'ROW' is used to refer to linear infrastructure including both the pipeline right-of way and associated roads.

Table 2.1. Summary of the experimental design and frog acoustic recording site placements.

BAA	Elevation	Transect	Distance from forest edge			Total nights
			5 m	70 m	170 m	
BAA 1	'2,700 m'	H4—2,700 m (2,681–2,696 m)	2	2	2	36
Hides Ridge		H5—2,750 m (2,726–2,756 m)	2	2	2	
		H6—2,730 m (2,725–2,736 m)	2	2	2	
	'2,200 m'	H1—2,150 m (2,148–2,163 m)	2	2	2	
		H2—2,200 m (2,171–2,229 m)	2	2	2	
		H3—2,300 m (2,296–2,327 m)	2	2	2	
BAA 2	'1,400 m'	M1—1,400 m (1,397–1,405 m)	2	2	2	30
Agogo Range		M2—1,380 m (1,315–1,397 m)	2	2	2	
		M3—1,380 m (1,369–1,389 m)	2	2	2	
	'1,000 m'	M4—1,030 m (995–1,041 m)	2	2	2	
	Arakubi Quarry	M5—1,050 m (1,051–1,073 m)	2	2	2	

Audio and visual monitoring of frogs at Wellpad D on Hides Ridge

A small pond adjacent to Wellpad D was identified in the PNG LNG Project Environmental Impact Statement (EIS) as a significant habitat for frogs on Hides Ridge in BAA 1. It provides one of the few habitats for aquatic frogs in BAA 1 and, as well as supporting a population of the Rainbow Treefrog (*Litoria iris*), it is the only known locality for an undescribed, spike-nosed treefrog discovered during the EIS surveys. We conducted one VAES night survey for 30 minutes around the edge of the pond on 27 May 2017 and documented the species present, based on both calls and visual detection. We estimated the abundance of each species based on visual detection only, in categories of 0, 1–10 and >10 and noted the presence and abundance of gelatinous egg masses of the Rainbow Treefrog hanging from low vegetation (0, 1–10, >10 clumps).

A Frontier Labs Bioacoustic Recorder (BAR) was also deployed at the pond for two consecutive nights, 27 and 28 May 2017, with the microphone angled across the centre of the pond. The resulting data for analysis were selected using the same methods described for Acoustic Recorders placed on transects.

Data synthesis and statistical analyses

VAES data

The number of individual frogs seen and heard in each transect interval (0–20, 20–40 m, etc. from the forest edge) was tabulated. For analysis, this was reduced to a table of presence/absence of each species in each transect interval, with species scored as present regardless of whether they were seen or heard. Data from both survey nights on the same transect interval was combined.

Acoustic data

Sixty-six nightly recordings collected from the 11 transects were analysed. To improve the efficiency of call detection on SM3 recordings, frog presence was scored using a method modified slightly from the approach used in 2015. For each 24-hour recording period at each site we again analysed the five 1-hour sound files starting at (or closest to) 19:00 to 23:00 inclusive (recording time 19:00 to 00:00). However in contrast to the 2015 process where three 5-minute sections: 15–20 mins, 35–40 mins and 55–60 mins of each 1-hour file were both observed and listened to, in 2017 the entire 60 minutes of each of the five 1-hour files was scanned visually in 30 s blocks noting the presence/absence of calls for each species.

Indicator Species

In the previous 2015 survey (Richards and Armstrong 2017), we present a matrix of Relative Abundance values to help interpretations of which species were contributing the greatest amount of signal to overall patterns. These values were also used to identify species that might be most sensitive to changes in their environment, either by responding positively by increasing their abundance at forest edges, or decreasing their presence and withdrawing to the forest interior. For the 2017 survey, we instead calculated a metric that is more sensitive to the association of individual species with particular sites and environmental conditions— Dufrêne and Legendre's (1997) Indicator Species index. This also gives an indication of the relative commonness or rarity of individual species. Species found in many habitat types tend to have low scores, and higher scores are apparent when a species is associated with one treatment or condition.

For this study, inter- and intra-specific trends in the Indicator Species index were examined by elevation and by distance from the linear infrastructure values. This exercise helped to identify species that might be more or less vulnerable to impacts associated with the roads and ROW.

Statistical Analysis

Statistical analyses were conducted separately on data obtained from the VAES transects and the acoustic recordings. We did not combine the data for analysis because there was not 100% compatibility between the two sampling designs (there was no VAES search conducted at transect H6 in BAA 1 and acoustic sample sites at transect M5 did

not correspond with VAES transect FT 5 in BAA 2); and secondly, because we wished to explore further the relative contributions of the two datasets to assess whether it may be possible to phase out VAES surveys in future without compromising the study objectives.

Frog diversity was compared across elevations and distances from linear infrastructure between years by fitting a Generalised Linear Mixed Model by Maximum Likelihood to the data. Variation in community composition (i.e. the mix of species found on each transect) was explored for each of the VAES and acoustic recording datasets by calculating the Bray-Curtis Dissimilarity Index and then performing Non-metric Multidimensional Scaling (NMDS). The NMDS is an ordination that grouped sites in two-dimensional space on the basis of the similarity/dissimilarity of the mix their component species.

All analyses were conducted and output plots were produced using a modified version of the custom-written [R] language statistical computing language script that was developed for the 2015 surveys.

DNA barcoding

The PMA3 study uses genetic markers in the frog, bat and small mammal components for different reasons (Armstrong and Aplin 2017). In the frog component, which monitors responses in the frog community to potential changes in the forest habitats adjacent to the ROW, frog species are recognised primarily from their distinct species-specific calls. Not all frog species in the PMA3 study areas have taxonomically stable names, and a significant proportion of taxa encountered in the 2015 study were undescribed taxa. Thus, genetic markers were used to give confirmation of identities, provide greater clarity on species boundaries in very closely related taxa by assessing phylogenetic relationships, provide a genetic perspective of apparent novelty, and provide a genetics-based voucher for call types. Mitochondrial genetic markers (12S) were used to refine the field identifications by associating representative individuals of many of the call types with the context of published mitochondrial sequences used for phylogenetic studies of microhylid frogs (Richards and Armstrong 2017). However, there are limitations in the power of mitochondrial genes for giving information on species boundaries (review in Collins and Cruikshank 2012). When seeking to fill knowledge gaps on the relationships of taxa in the PMA3 study and extend the comparative genetic framework, it was deemed more efficient to create a new framework using genome markers. This genetic framework will provide a genetic basis for consistent identifications for frogs in future, particularly of individuals that cannot be identified by their calls (e.g. females, froglets) or by using morphological criteria (e.g. eggs, tadpoles, adults of morphologically cryptic species).

We developed a new comparative genetic framework using a genome-scale sequencing approach. 'Reduced representation' genome sequencing approaches rely on Single Nucleotide Polymorphisms (SNPs; many thousands of single variable sites from random locations across the entire chromosome area) to give a considerably refined view of the boundaries between species. Using genome-scale markers for genetics-based identification of frogs in industry projects is unprecedented in Papua New Guinea and such broad screens of taxa using this method are uncommon globally. We used an approach called 'DArTseq' (Kilian et al. 2003; Grewe et al. 2015), which is the commercial equivalent of an identical widely-used technique called 'RADseq' (restriction site-associated DNA sequencing; Peterson et al. 2012). A custom-written [R] language analysis script was used to tidy and filter the genotype matrix supplied after bioinformatic processing conducted by the commercial service (Diversity Arrays Pty Ltd, Canberra). Individuals and loci that had insufficient coverage were removed, and an Neighbour-Joining distance phenogram was produced using the packages 'ape' (Paradis and Schliep 2018) and 'phytools' (Revell 2012), based on a concatenated string of the full trimmed fragments (as against concatenate SNPs). Figtree version 1.4.3 software was used to display the tree and prepare it for illustration. A second Maximum Likelihood tree was also generated using concatenated fragments, which was almost identical.

Results and Discussion

A species list showing the frog species recorded on each transect within the two BAAs is presented in Table 2.2, which also illustrates the call detection method (VAES survey and Audio Recorder) for each species on each transect. Species blocked in grey were encountered in 2015 but not in 2017. A summary of species detections at increasing distances from the disturbance edge are also presented for VAES transects in Appendix 2.3 and for Acoustic Recorders in Appendix 2.4.

Table 2.2. Summary of species encountered on each transect in both BAAs, indicating the call detection method for each encounter (V = VAES; A = Acoustic Recorder).

	BAA 2					**BAA 1**					
	1,000 m asl		1,400 m asl			2,200 m asl			2,700 m asl		
Species	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5	H6
PELODRYADIDAE											
Litoria iris											
Litoria sp. 1 'yellow legs'	V	A	AV	V	V						
LIMNODYNASTIDAE											
Lechriodus aganoposis											
MICROHYLIDAE											
Asterophrys slateri	AV	AV	A	A							
Austrochaperina laurae			V	AV	V						
Austrochaperina sp. 2 'long call'	AV	AV									
Callulops omnistriatus	A	AV	AV	AV	AV						
Callulops wilhelmanus									A	AV	
Choerophryne alainduboisi	V	AV	AV	AV	AV						
Choerophryne brevicrus							V	V	V	V	
Choerophryne burtoni			A	AV							
Choerophryne crucifer											
Choerophryne multisyllaba			AV	AV	AV						
Choerophryne murrita			V		A						
Choerophryne sp. 1 'arboreal'						AV	AV	AV			
Choerophryne sp. 2 'tiny'						V		AV			
Cophixalus wempi			V	V	AV						
Cophixalus sp. 1 'musical call'			A	AV	AV						
Cophixalus sp. 2 'tiny'			A	AV	AV						
Cophixalus sp. 5 'peeping call'			A	AV							
Cophixalus sp. 6 'loud grunter'						AV	AV	A			
Copiula sp. '2-note call'	V	AV									
Hylophorbus richardsi						V					
Hylophorbus sp. 1 'slow call'			A	AV	AV						
Hylophorbus sp. 2 'fast call'	AV	AV	A	A	AV						
Liophryne schlaginhaufeni		AV									
Oreophryne anamiatoi						V	AV				
Oreophryne flavomaculata	A	A	AV	AV	AV						
Oreophryne notata	A	A	AV	AV	A	AV	AV	AV	AV	AV	A
Oreophryne oviprotector	AV	AV									
Oreophryne pseudunicolor	AV	AV	A	AV	A						
Oreophryne sp. 2 'ratchet call'		V	AV	A	A						
Oreophryne sp. 6 'rasping call'	A	AV									
Sphenophryne cornuta	AV	AV	V		V						

	BAA 2					BAA 1					
	1,000 m asl		1,400 m asl			2,200 m asl			2,700 m asl		
Xenorhina sp. 1 'slow call'	AV	AV									
Xenorhina sp. 2 'fast call'				V							
Gen. nov. sp. nov.		V									
Species Richness Acoustic	11	15	15	15	13	3	4	4	2	2	1
Species Richness VAES	10	14	11	15	12	6	5	4	2	3	—
Total Species Richness	14	17	19	18	16	6	5	5	3	3	1

Overview of the frog fauna

A total of 34 species of frogs was documented on the permanent transects, including eight species in BAA 1 and 27 species in BAA 2 (Table 2.2; examples in Figures 2.8–2.19). Thirty-three of the 34 species (97%) belong to the family Microhylidae, a group characterised by direct embryonic development that is dominant in karst habitats where freestanding water is rare. This is a slightly higher percentage than in 2015 (92%) because two of the three non-microhylid species recorded during 2015 were not detected on transects in 2017, while two additional microhylid species that were not recorded in 2015 were detected in 2017. One additional non-microhylid frog species was encountered on Hides Ridge in 2017, but the single specimen of an unidentified torrent-dwelling treefrog (*Litoria*) was not on a transect and given the lack of suitable breeding habitat was probably not resident and it is not considered further here. Although the Rainbow Treefrog, *Litoria iris*, was not found on transects in 2017 this species was abundant in roadside ditches and at a small pond at Wellpad D during the survey.

Elevational trends in frog diversity and community composition

The frog fauna in BAA 2 is substantially more diverse than that encountered on Hides Ridge, with more than three times as many species (27 vs 8) detected there; and the pronounced reduction in frog diversity with increasing elevation that was reported following the 2015 survey was observed again in 2017. Figure 2.1 illustrates the rapidly dropping species richness with increasing elevation that was documented in both years. In both years elevation was the major factor influencing differences in the number of species on transects in both BAAs (Table 2.3, 2.4; Figure 2.1) and GLMM analysis of 2017 data demonstrated that these differences are significant, with lower elevation sites having significantly higher diversity than high elevation sites (Table 2.4). This pattern is widely repeated in the mountains of New Guinea (e.g. Richards 2007; Richards and Dahl 2011; Tallowin et al. 2017).

Table 2.3. Summary of means ± standard deviation in 2017 for frog diversity at each distance from the road or ROW, elevation and a comparison between survey year, for the two different frog survey methods.

Distance (m)	Acoustic recordings	Distance (m)	VAES transects
5	5.54 ± 3.53	0-20	3.05 ± 1.57
70	5.41 ± 3.39	20-40	3.35 ± 2.25
170	5.32 ± 3.67	40-60	3.30 ± 2.32
—		60-80	3.40 ± 2.28
—		80-100	4.25 ± 2.34
Elevation (m)	Acoustic recordings	Elevation (m)	VAES transects
1,000	8.25 ± 3.02	1,000	4.40 ± 2.52
1,400	8.94 ± 1.51	1,400	5.27 ± 1.66
2,200	3.89 ± 0.83	2,200	2.17 ± 1.18
2,700	1.56 ± 0.51	2,700	1.80 ± 0.41
Year	Acoustic recordings	Year	VAES transects
2015	5.03 ± 2.79	2015	3.14 ± 1.89
2017	5.82 ± 4.06	2017	3.80 ± 2.38

Within BAA 1 the lower diversity at the high elevation sites (~2,600–2,750 m asl, with 3 species) compared to the low elevation sites (2,100–2,400 m asl, with 7 species) is of slightly less magnitude than was documented in 2015 but this was because three species known to occur at the low sites were not encountered on transects there in 2017. Two of these (*Callulops wilhelmanus* and *Lechriodus aganoposis*) appear to occur at low densities in the 2,100 to 2,400 m elevational band on Hides Ridge so their absence was not surprising; the other, *Litoria iris*, is a species that normally occurs around small ponds that are absent from the transects, so their presence during 2015 was surprising and their absence during 2017 was not unexpected. Two of the three species recorded at the high elevations in BAA 1 were also found at the low elevations in that BAA; the other, *Callulops wilhelmanus*, was heard calling at low elevations in BAA 1 but was not encountered on a transect using either detection method.

In contrast to BAA 1 where the high elevation band has a frog community that is a subset of the low elevation band, there was a high turnover of species between the two elevation bands in BAA 2. Just 10 of the 27 species (37%) found in BAA 2 were detected at both KP107 (1,400 m asl) and Arakubi (1,000 m asl) despite these sites being in close proximity and having similar numbers of species (20 and 17 respectively).

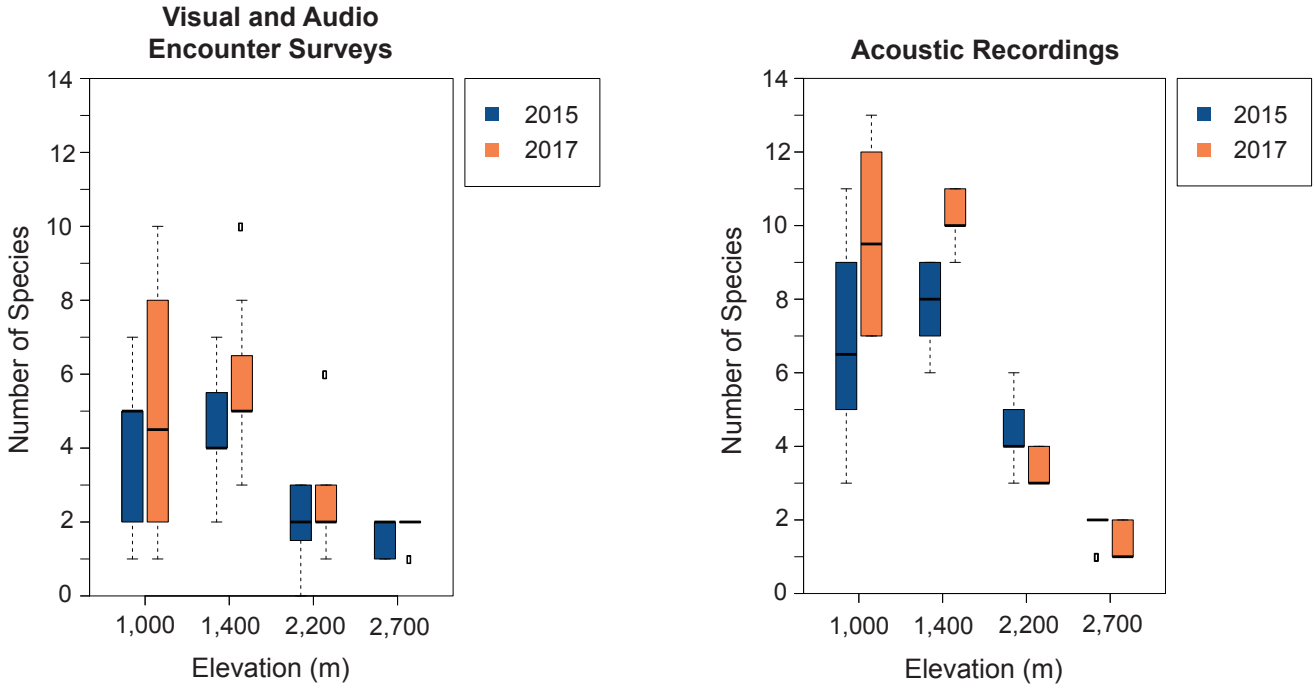

Figure 2.1. Summary of frog diversity (as number of species, or richness) at different elevations based on data from VAES transects (left) and acoustic recordings (right) in 2015 and 2017. For each of the two plots, data are pooled across all distances from linear infrastructure. Boxplot components are: central bar—median; boxes—inter-quartile range, with second quartile group below median, third quartile group above median; bars—minimum and maximum values of quartile groups; circles—outliers.

Although less diverse, the frog communities in BAA 1 are not simply a sub-set of the frogs found in BAA 2, with only one species, *Oreophryne notata*, that was documented in BAA 1 during 2017 also occurring in BAA 2 (Table 2.2). Another species, *Lechriodus aganoposis*, that was found rarely in both BAAs during 2015 was not encountered in either BAA during 2017. Hides Ridge remains an important habitat for a distinctive suite of high-elevation frogs, several of which are undescribed and known from few or no other localities.

Table 2.4. Summary of the tests of the Generalised Linear Mixed Model (values from the Analysis of Deviance table; Type III Wald chi-square tests) and post hoc pairwise comparisons to test for the influence on frog diversity of elevation and distance from the road or ROW, and year (2015 & 2017) for each of the acoustic recording and the VAES data sets (only significant pairs shown; values are elevations in metres; Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1). Model coded in [R] as: m <- lmer(total_richness ~ dist + elev + year + dist*elev + elev*year + dist*year + dist*elev*year + (1 | transect), data = y, REML = FALSE).

Acoustic recordings	**Chi-square**	**df**	**P**	**Pairwise**
Distance	0.73	2	0.69 NS	All NS
Elevation	37.83	3	<0.001***	1,000 > 2,200** 1,000 > 2,700*** 1,400 > 2,200*** 1,400 > 2,700*** 2,200 > 2,700*
Year	19.73	1	<0.001***	2015 < 2017***
Distance*Elevation	15.65	6	0.016*	—
Distance*Year	13.52	2	0.001**	—
Elevation*Year	45.58	3	<0.001***	—
Distance*Elevation*Year	14.21	6	0.027*	—
VAES transects	**Chi-square**	**df**	**P**	**Pairwise**
Distance	4.95 (10.47)	4	0.29 (0.033)	(0-20 < 80-100*)
Elevation	7.62 (26.25)	3	0.054 (<0.001***)	(1,000 > 2,200^) (1,000 > 2,700^) (1,400 > 2,200**) (1,400 > 2,700**)
Year	0 (6.56)	1	1 (0.010*)	(2015 < 2017*)
Distance*Elevation	9.59	12	0.65	—
Distance*Year	9.21	4	0.056	—
Elevation*Year	0.11	3	0.98	—
Distance*Elevation*Year	13.54	12	0.33	—

These differences in composition of frog communities at different elevations are also demonstrated by Multi-dimensional Scaling (NMDS) ordinations of species presence based on each of the VAES transect and acoustic recording datasets in 2015 and 2017 (Figure 2.2). NMDS ordinations emphasise the strong differentiation not only between frog communities in each of the elevational zones in BAA 2, but also between the BAA 1 and BAA 2 frog communities. It is interesting to note that the ordination based on acoustic recordings showed a consistent difference between species composition of the high and low Hides Ridge sites in both years (Figure 2.2) that was not detected by the VAES data. Given the high species overlap between these two sites this minor discrepancy is difficult to interpret. VAES searches detected more species than Acoustic Recorders in BAA 2 and so detected more component species in the low elevation band than the Acoustic Recorders, presumably generating a greater disparity between the two elevational bands than was evident in the Acoustic Recorder data.

Overall, the frog community documented on transects at the highest elevation site (~2,700 m asl) in BAA 1 remains substantially a subset of the species occurring at the lower site, and the only species from the upper sites (*Callulops wilhelmanus*) that was not detected in the lower elevation band at Hides was encountered there near our transects.

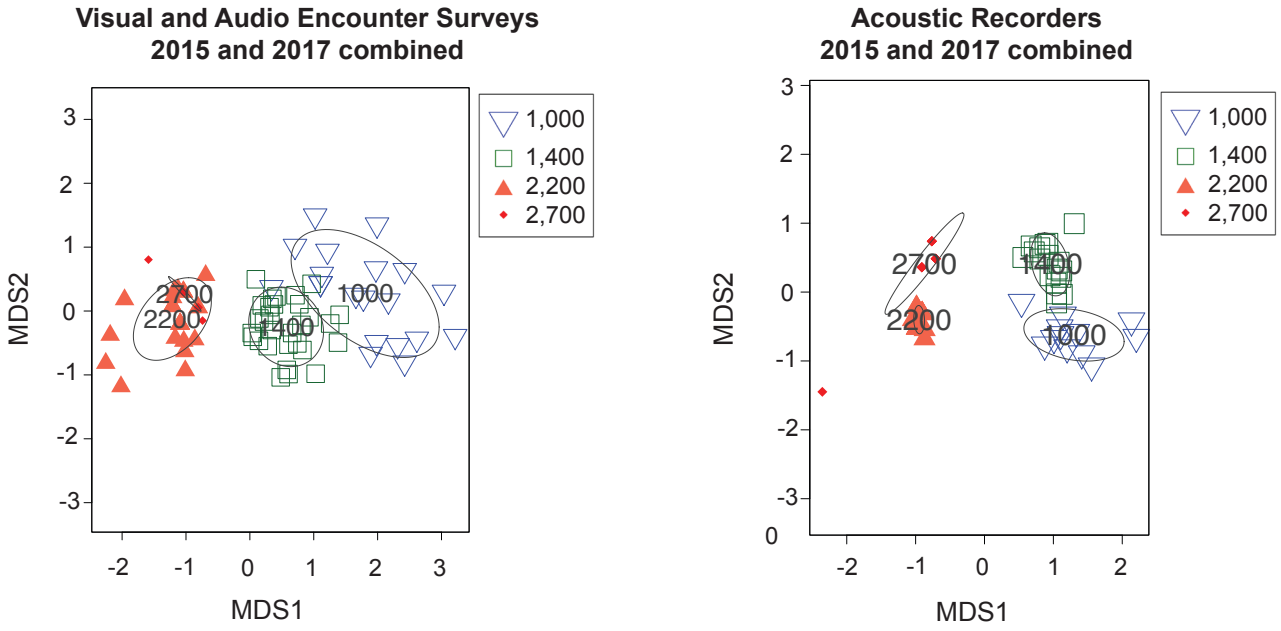

Figure 2.2. Multi-dimensional Scaling (NMDS) ordinations summarising patterns of species composition at different elevations within the BAAs in 2015 and 2017(confidence ellipses are one standard deviation).

Significant species and taxonomic uncertainties

Taxonomic studies since the 2015 survey have resulted in the formal descriptions of five frog species that were undescribed at that time, and resolution of the taxonomy of several other species of uncertain taxonomic status. A summary of the taxonomic changes that have been incorporated into species tabulations in this report is presented in Appendix 2.5.

Other taxonomic considerations include:

1. Attempts to extract further DNA from a tiny frog of the morphologically conservative genus *Oreophryne* (*Oreophryne* sp. 1 'tiny') following the 2015 survey were not successful and, given the similarity of this 'species' to the larger sympatric *Oreophryne notata*, which was not available for the 2015 DNA analysis, we cannot discount that they represent juveniles of this species and they are removed from the list of species recorded from Hides Ridge pending further studies.

2. The taxonomic status of frogs referred to *Oreophryne notata* from KP107 and Arakubi requires confirmation. The call of this frog in BAA 2 is similar to that of *O. notata* recorded (and vouchered) on Hides Ridge in BAA 1, but no specimens have been captured due to its arboreal habit. It is possible that the population referred to *notata* at the lower elevation BAA 2 sites represents a hitherto unidentified and undescribed species of *Oreophryne*. For the purposes of this report we consider the populations in BAA 1 and BAA 2 to represent the same species but if future DNA and morphological comparisons show otherwise then this will further strengthen the already substantial differences documented between the frog communities in BAA 1 and BAA 2.

3. The identity of several small arboreal frogs of the genus *Oreophryne* with 'rattling' calls in BAA 2 remains uncertain because these tree-dwelling frogs are rarely seen calling. DNA barcoding reveals the presence of at least two species at KP107 (Figure 2.3), and at least one additional species (*Oreophryne oviprotector*) occurs at Arakubi. However there appears to be more variation among rattling calls at KP107 than would typically occur within two species. For the purposes of this report we consider that only two species of 'rattling' *Oreophryne* occur at KP107: *O. flavomaculata* and an unidentified species referred to as *Oreophryne* sp. 2 'ratchet call'. Resolving the possibility that two species' calls are included in what we classify as *O. flavomaculata* remains a high priority for future surveys.

For the purposes of data analysis and interpretation in this report we also combined two species, *Cophixalus* sp 2 'tiny A' and *Cophixalus* sp 3 'tiny B', that were identified during the 2015 survey, into a single 'species'. These are referred to here as *Cophixalus* sp. 2 'tiny' because the two species are impossible to distinguish morphologically in the field, and there is uncertainty about which of two known call types are produced by each species. The presence of these two genetically deeply divergent species was confirmed by DNA barcoding and both genetic types occur at KP107 (Richards and Armstrong 2017). Given the species' morphological and apparently ecological similarity, they are therefore combined in this report. Associating call types to each of these species will permit future species discrimination during both VAES and Acoustic Recorder surveys so this is a high priority for the 2019 survey.

Species of conservation significance (IUCN-Listed)

Two species of frogs that have an IUCN red list status greater than Least Concern were documented during 2015. Both of these species were again present in 2017 and there appears to be no threat to these populations. Each is illustrated in Richards and Armstrong (2017).

***Choerophryne burtoni* (IUCN Data Deficient)**

Originally described from near Moran, this small (males <13 mm), long-snouted frog is now known from a number of additional sites in the mountains of south-central PNG (Kraus 2010, Richards and Dahl 2011). It was detected only along transects at KP107 in BAA 2 where its conspicuous calls were heard during both 2015 and 2017.

***Oreophryne notata* (IUCN Data Deficient)**

This is a small (<18 mm) frog with a distinct, pale upturned 'U' mark on the lip. It is an arboreal species found in mossy high-elevation forest in south-central Papua New Guinea. Its loud and distinctive 'peeping' call and relatively high abundance on the Hides Ridge make it a candidate for long-term acoustic monitoring there. The taxonomic status of frogs referred to this species from BAA 2 requires confirmation.

Frogs at Wellpad D on Hides Ridge

Large numbers of Rainbow Treefrogs were present around the small pond at Wellpad D during the 2017 survey, when numerous gelatinous egg masses were also observed hanging from fringing vegetation. Numbers of both adult frogs and egg masses exceeded the highest abundance class (>10) during the 30 minute survey, and calls of this species were present on 100% of the BAR recordings analysed.

Although no other pond-breeding frogs were observed at this site, several calls that are reminiscent of the clicking vocalisations produced by small spike-nosed frogs of the *Litoria pronimia* group were detected on the BAR. These may represent the undescribed, spike-nosed treefrog that was discovered at (and is still known only from) this site during the EIS surveys. However no individuals of this new species were seen at the pond in 2015 or 2017, and its call remains unknown. Furthermore, *Litoria iris* produce complex call repertoires comprising complex series of clicks and buzzes, and it is possible that the atypical calls documented at the pond represent a poorly-documented call type produced by *Litoria iris*. Additional direct observations of frog calling behavior at the pond during future surveys will be required to

clarify the status of these calls. In the meantime formal description of the spike-nosed frog from Wellpad D is underway based largely on genetic data.

DNA barcoding

Following the 2017 PMA3 monitoring survey we expanded the genetic identification program to incorporate additional tissue vouchers from both BAAs, and we also expanded the breadth of 'context' material included from across Papua New Guinea in order to better understand the relationships of species from the Upstream Project Area with other described and undescribed species. Results are presented in Figure 2.3.

The genome-scale DNA sequencing significantly improved our ability to accurately identify several species, and contributed greatly to our understanding of both the diversity and composition of frog assemblages in both BAAs. For example, at BAA 1 the first available DNA sample of the species previously referred to as *Oreophryne*? Sp. 5 'loud grunter' supported new studies revealing that this species is correctly placed in the genus *Cophixalus*, and that it is a species new to science that is known only from the Upstream Project Area. It has been renamed *Cophixalus* sp. 6 'loud grunter' in this report (Table 2.2, Appendix 2.5). Similarly, DNA barcoding confirmed that the species previously referred to as *Cophixalus* sp. 4 'rasping call' belongs in the genus *Oreophryne* and it is here referred to *Oreophryne* sp. 6 'rasping call', an as yet scientifically undescribed species known to have a broad distribution extending outside of the Upstream Project Area.

The genome-scale DNA identification framework developed here can be considered a prototype for a much larger nation-wide system of genetics-based identification, and within the context of the PMA3 study it continues to establish a framework for consistent identifications across surveys and a way of confirming the allocation of call types, specimens and names. It continues to be a useful tool for the PMA3 program given that many of the frog taxa encountered on the survey are either known to science but undescribed, or completely new to science.

Figure 2.3. Neighbour Joining distance phenogram showing the relationship of DNA-barcoded captures on the 2015 and 2017 PMA3 surveys to other taxa with available sequences (Köhler and Günther 2008; Rittmeyer et al. 2012). Red = PMA3 taxa.

Influence of Project infrastructure on species diversity, community composition and relative abundances

Local environmental changes close to the forest edge (collectively termed 'edge effects'), including lower humidity and greater extremes of temperature, might be expected to reduce frog diversity there or result in changes to community structure with more 'climate tolerant' frogs replacing forest-interior species closer to clearings. We analysed the VAES and acoustic recording data in various ways to explore the potential relationship between distance from the primary forest edge and frog species diversity (= richness) and community composition.

Graphical summaries of species diversity recorded in 2015 and 2017 at increasing distances from the forest edge on each of the VAES transects, and by acoustic recordings, are shown in Figures 2.4 and 2.5. It is apparent from Figure 2.4 that there is at most a slight suggestion of an increasing trend in species diversity with increasing distance from infrastructure at KP107 in both the VAES and Acoustic Recorder data sets, and the statistical analysis using GLMM (Table 2.4) found no significant influence of distance from infrastructure on species diversity, whether measured by the VAES transect method or acoustic recordings. Indeed a reverse trend, with an apparent drop in diversity with increasing distance from infrastructure, was detected by Acoustic Recorders (only) in the 2,200 m asl elevational band in BAA 1 during 2015 and this trend is also seen, though barely so, in the acoustic survey data from 2017.

The consistency of this overall lack of response across elevations during both survey periods is clearly illustrated in Figure 2.5, which shows a similar pattern in the number of species detected at each distance category in the four elevational bands separately for each survey method.

GLMM analysis supports the hypothesis that, overall, the influence of distance from infrastructure on species diversity was not statistically significant for either survey method during 2017, with only one pairwise comparison of all distance segments across all transects at both BAA's returning a significant difference (and that for VAES surveys only; Table 2.4). Although the detection of several significant interaction terms (Table 2.4) points to some complex relationships between some factors, these are difficult to interpret, especially given the relatively low statistical power of the models and they are not considered further here.

The 2017 results are similar to those obtained in 2015 indicating that there has not been a temporal shift in species diversity since 2015 and strongly suggesting that the linear infrastructure in BAA 1 and BAA 2 is currently having no detectable impact on local frog communities.

The GLMM analysis did identify that species diversity on each transect increased significantly between 2015 and 2017 (Table 2.4), despite slightly fewer species being detected overall. This may reflect the refined method for detecting calls during processing of 2017 acoustic recordings, and this possibility will be assessed during future survey programs.

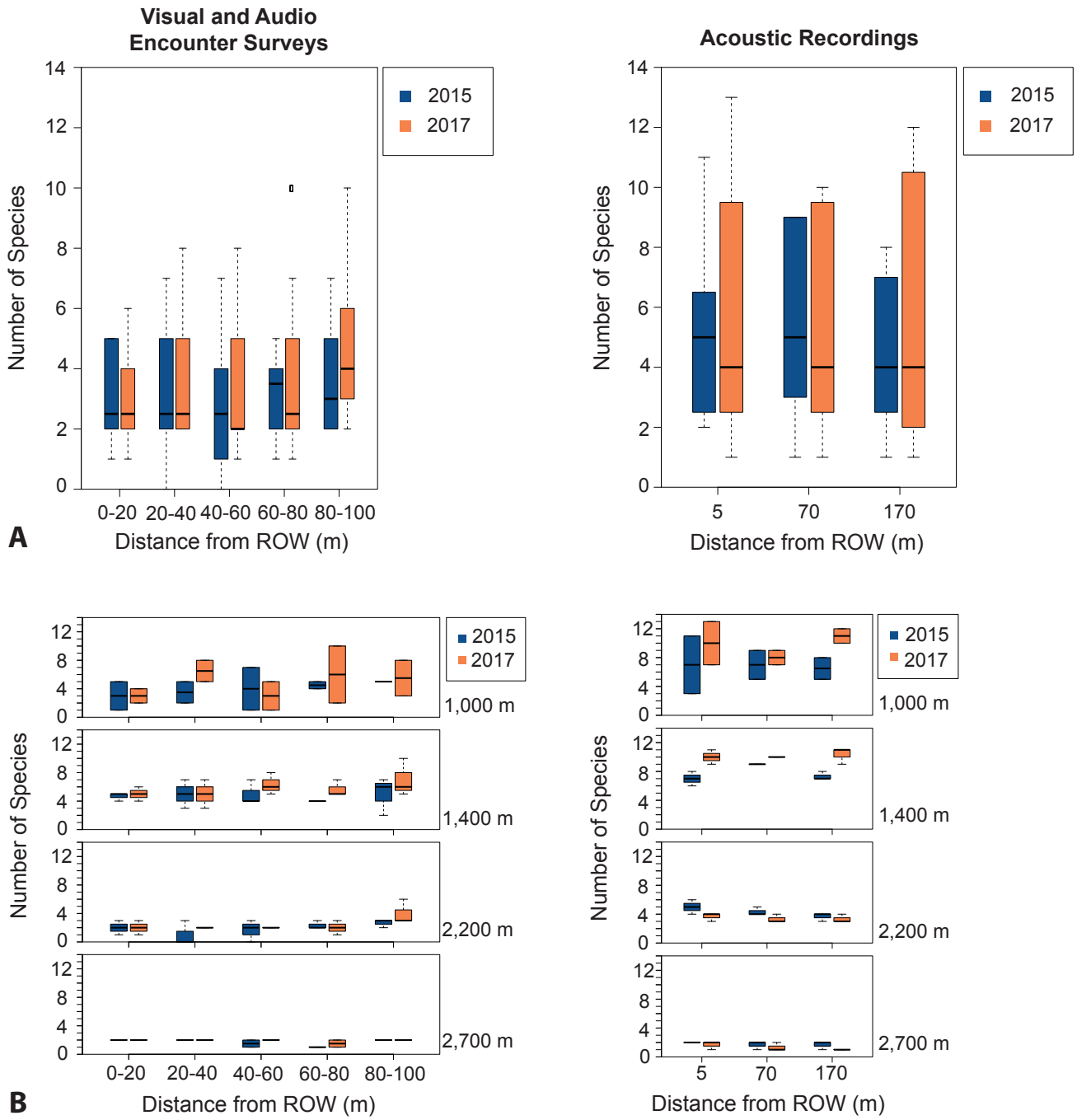

Figure 2.4. Summary of frog diversity (as number of species) at different distances from the forest edge based on data from VAES transects (left column) and the acoustic survey (right column) in 2015 and 2017. For each of the two series, the uppermost graphs (A) are pooled across all distances, while those below are for each of the elevational zones (B). See figure 2.1 for explanation of boxplots.

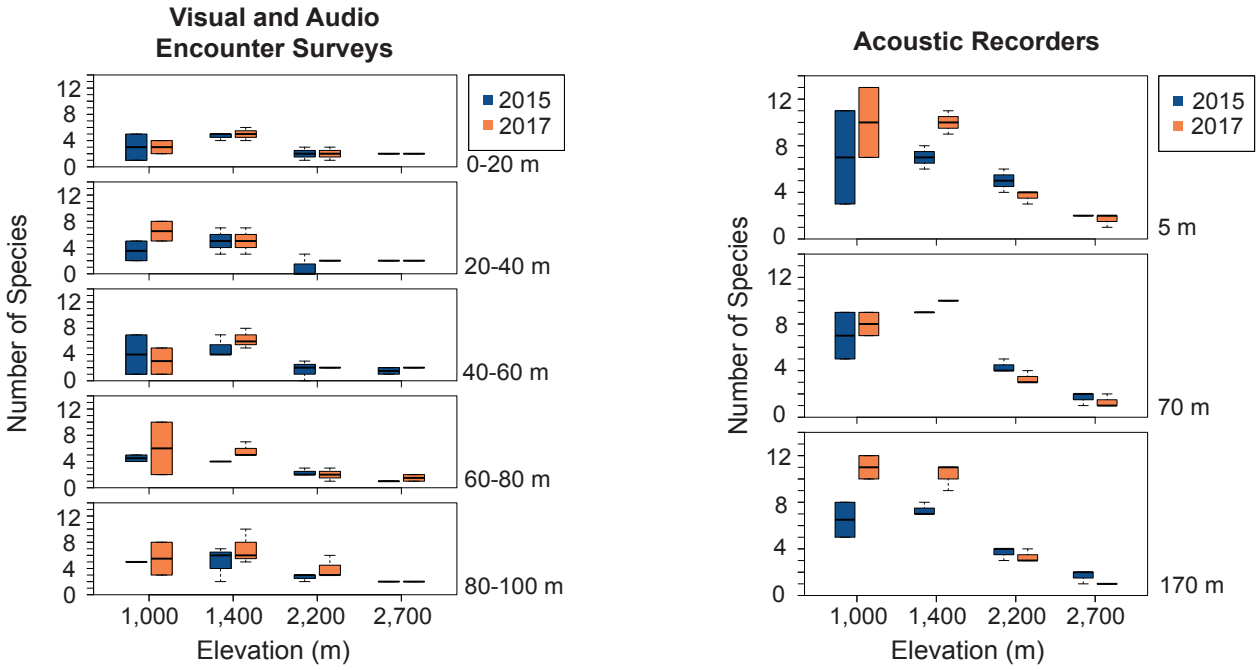

Figure 2.5. Summary of frog diversity (as number of species) by elevation for each distance from Project infrastructure based on data from VAES transects (left column) and the acoustic survey (right column) in 2015 and 2017.

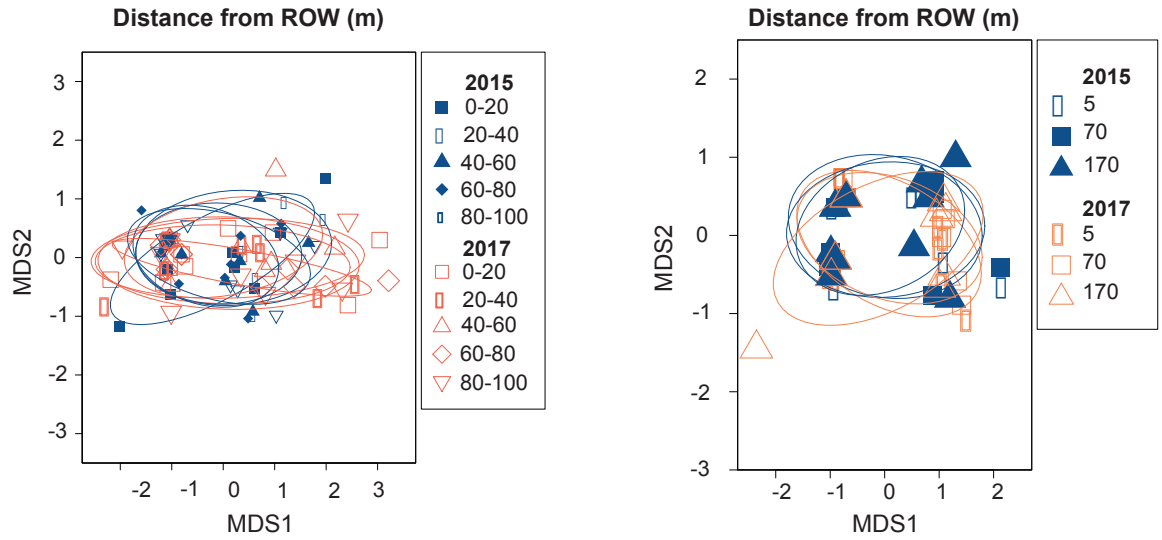

Figure 2.6 Multi-dimensional Scaling (NMDS) ordinations summarising patterns of species composition at different distances from the road or ROW based on each of the VAES transect (left) and acoustic recording (right) datasets in 2015 and 2017 (confidence ellipses are one standard deviation).

The lack of evidence for detectable impacts of Project infrastructure on frog communities in BAA 1 and BAA 2 is further supported by NMDS analyses based on the VAES and acoustic recording datasets, neither of which shows any differentiation of frog communities based on distance from linear infrastructure in either 2015 or 2017 (Figure 2.6).

These analyses have been based on presence/absence data and are relatively insensitive to impacts associated with Project infrastructure that have altered the relative commonness or rarity of different species but without causing actual species losses from the communities. The Indicator Species index is expected to be more sensitive to such changes, because it allows for a species to be still present but at reduced numbers due to deleterious impacts from being nearer to Project infrastructure, or to be present in higher than normal numbers if it is advantaged by the near-edge conditions. Figure 2.7 shows trends in the Indicator Species Indices derived from each of the VAES transect and acoustic recording datasets in 2017 and 2018.

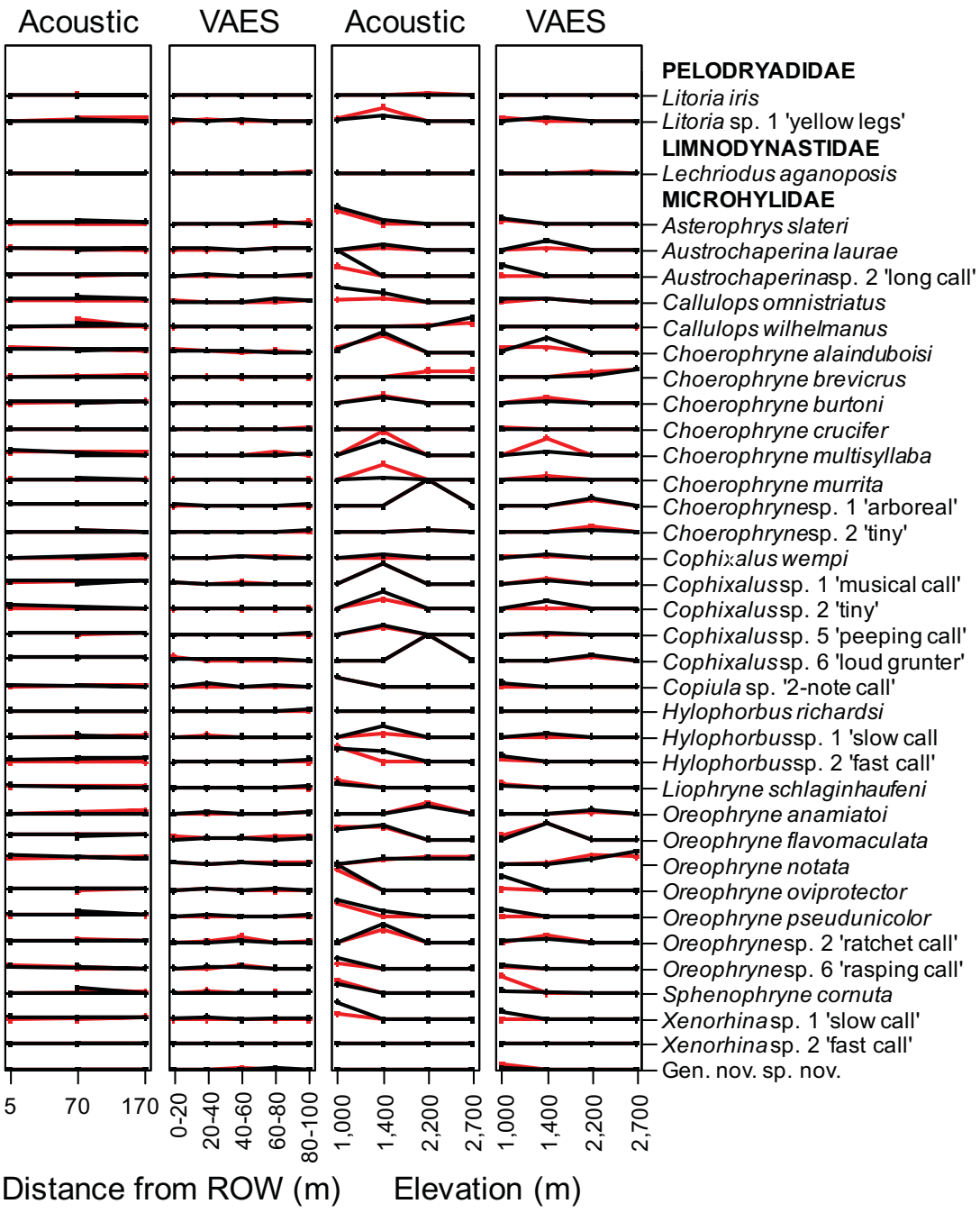

Figure 2.7. Summary of trends in Indicator Species indices for increasing distances (m) from linear infrastructure based on data from VAES transects and acoustic recordings in 2015 (red) and 2017 (black).

The Indicator Species index for each species at different elevations highlighted the difference in frog diversity between low and high elevations, for both the acoustic recording and VAES survey methods (Figure 2.7). For example, Indicator Species indices were greatest at 1,000 m for *Asterophrys slateri*, *Copiula* sp. '2-note call', and all *Oreophryne* species apart from *O. notata*, There was some difference between years that is probably an artefact of either sampling effects or natural variation in population demographics, including a slightly greater relative abundance of *Austrochaperina* sp. 2 'long call' and *Xenorhina* sp. 1 'slow call' in 2017. A better understanding of natural variation over time will come from surveys in coming years. Other species were clearly more common at 1,400 m, such as *Choerophryne multisyllaba* and *Cophixalus* sp. 2 'tiny'. Given that diversity was lower at elevations above 2,000 m only *Choerophryne brevicrus* and *Oreophryne notata* had increasing Indicator Species indices with increasing elevation. Some differences between the two methods was apparent, with *Choerophryne* sp. 1 'arboreal' and *Cophixalus* sp. 6 'loud grunter' having a relatively high Indicator Species index at 2,200 m based on acoustic recordings, but somewhat less so for the VAES method, and the opposite trend for *Choerophryne brevicrus*.

In contrast to the patterns of frog diversity at different elevations, an inspection of the trends of Indicator Species indices with increasing distance from the ROW do not show any obvious trends. The signal will be somewhat dampened in these trend lines because not every species is found at all elevations, but we might have expected some slight inflations if species had been particularly common at the edge of the transects. The two species identified as possible 'Indicator Species' based on 2015 data, *Choerophryne burtoni* and *Liophryne sclaginhaufeni*, were recorded with insufficient frequency during 2017 to be useful indicators. Another potentially sensitive species, the high-elevation microhylid frog *Callulops wilhelmanus*, was infrequently encountered on transects using either survey method and appears to occur at low density in the forest. However during both survey periods it occurred at extremely high densities on the rocky verges of the clearing. Most members of this genus occupy small tunnels and gaps between rocks and roots on steep slopes, and on Hides Ridge *C. wilhelmanus* appears to be continuing to benefit from structurally similar habitat created during construction of the road and pipeline ROW.

Comments on efficacy of the two survey methods

Because the activity levels and calling behaviour of each frog species is influenced differently by changes in temperature, humidity and rainfall, climatic factors introduce a potential element of stochasticity into datasets of the kind reported here. To maximise species detection rates and minimise the impact of stochastic factors on frog detectability, we used two quantitative field methods, VAES and Acoustic Recorders for this PMA3 frog monitoring program.

Of the 108 species-by-transect detection events from both survey methods, 60 (55.5%) were detected by both survey methods, 26 (24.1%) were detected only by Acoustic Recorders and 22 (20.4%) were detected only by VAES. These results are extremely similar to those from 2015 (Richards and Armstrong 2017). Of particular interest is that overall 30 of the 34 species (88%) were detected at least once by both survey methods and just four species (12%) were detected only by VAES. No species were detected on automated sound recordings that were not also encountered during VAES transect surveys.

Despite some small differences in the particular species detected by each of the two methods, it is clear from both the statistical results and the patterns observed in the summary boxplots and NMDS plots (Figures 2.1–2.6) that the two methods detected the same general patterns within the frog fauna, most notably the influence of elevation on species diversity, and the absence of major shifts in species diversity or community composition associated with linear infrastructure impacts. In this regard, it is possible that either method alone might be adequate for detecting future changes in the overall frog community. This question is directly relevant for future monitoring because VAES methodology may become logistically less feasible during future surveys.

A more detailed assessment of the future use of VAES transects should be made after the 2019 survey.

Observations on damage to vegetation adjacent to Project infrastructure

During the two years between the 2015 and 2017 PMA3 surveys several trees were removed by members of the local communities from the vicinity of monitoring transects, for use as construction materials and other purposes. Tree felling, and associated disturbance of surrounding vegetation was documented on or adjacent to three survey transects during the 2017 survey; one at the forest edge (0 m) at Transect H2 in BAA 1, one at the forest edge (0 m) at Transect M2 in BAA 2 and one c 200 m inside the forest adjacent to Transect M4 at Arakubi in BAA 2. Removal of the trees at H2 and M2 directly impacted the forest cover at the starting point of these two transects, shifting the forest edge approximately 5 m further into the forest from its previous location. Insufficient data are currently available to detect whether these new disturbance events have had an impact on frogs at those sites, and this will be assessed following the collection of additional data during future survey programs.

Conclusions

1. The forests at Hides Ridge in BAA 1 and on the Agogo Range near Moro in BAA 2 continue to support a high diversity of frog species. Diversity on transects at these sites was slightly lower in 2017 than in 2015, but this mainly reflected taxonomic reassignments and failure to detect two species previously recorded at low densities. In contrast two species not detected during 2015 were added to the known fauna in 2017.

2. These results suggest that no major declines or losses have been experienced within these communities.

3. Five species of frogs recorded from the two BAAs have been formally described since the 2015 survey.

4. Quantitative surveys of frog communities at different elevations within the two BAAs revealed differences in community composition at different elevations, and a statistically significant effect of elevation on species diversity.

5. However a Generalised Linear Mixed Model statistical analysis of frog communities at different distances from linear infrastructure during this survey found no evidence for shifts in species diversity with increasing distance from the forest edge.

6. Overall, the results from the second monitoring survey suggest that, in relation to frogs, the biodiversity values of the Upstream Project Area have been retained to date.

Recommendations

1. This survey provided quantitative and repeatable data that are suitable for long-term documentation of frog communities in BAA 1 and BAA 2 and we recommend that frog monitoring be continued biennially for the duration of the PMA3 program.

2. Because most species were encountered by both methods, and Audio Recorders produced the most statistically robust data, we recommend that the use of VAES transects be reassessed after the 2019 survey due to the logistical difficulties associated with conducting field work at night. It may be possible in future to rely on Acoustic Recorders as the sole survey method.

3. The 2019 survey should continue to target collection of data that will allow association of unidentified calls with relevant frog species; and collection of sufficient voucher material to permit the establishment of a resource for ensuring consistent identification of frog species across surveys. This material can also be used to contribute to formal descriptions of new species and to provide a broader genetic framework for frogs in the Upstream Project Area.

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Plate 1

Figure 2.8. *Austrochaperina* sp. 2 'long call'

Figure 2.9. *Callulops omnistriatus*

Figure 2.10. *Choerophryne brevicrus*

Figure 2.11. *Choerophryne* sp. 1 'arboreal'

Figure 2.12. *Cophixalus wempi*

Figure 2.13. *Cophixalus* sp. 5 'peeping call'

Plate 2

Figure 2.14. *Cophixalus* sp. 6 'loud grunter'

Figure 2.15. *Copiula* sp. '2-note call'

Figure 2.16. *Hylophorbus* sp. 2 'fast call'

Figure 2.17. *Liophryne schlaginhaufeni*

Figure 2.18. *Oreophryne pseudunicolor*

Figure 2.19. *Sphenophryne cornuta*

Appendix 2.1 Start and finish points for the ten 100 m VAES frog survey transects in Baa 1 and BAA 2.

BAA 1	**Start**	**Finish**
H1	S5.97242 E142.75320	S5.97304 E142.75284
H2	S5.96907 E142.75124	S5.96914 E142.75045
H3	S5.94380 E142.74182	S5.94459 E142.74188
H4	S5.91842 E142.69533	S5.91919 E142.69496
H5	S5.91627 E142.69284	S5.91652 E142.69208
BAA 2		
M1	S6.44025 E143.22417	S6.44025 E143.22339
M2	S6.44063 E143.22559	S6.44130 E143.22540
M3	S6.44166 E143.22717	S6.44231 E143.22658
M4	S6.46203 E143.25664	S6.46181 E143.25580
FT5*	S6.46179 E143.25532	S6.46154 E143.25457

*FT5 is a replacement transect for M5 which could not be accessed at night.

Appendix 2.2. Frog recording site locations in BAA 1 on Hides Ridge and BAA 2 on the Agogo Range near Moro. Coordinates in WGS84 datum.

Elevation category	Transect	Site	Latitude	Longitude	Elevation (m asl)
1,000	M4	M4_005	S6.462013	E143.256616	1,017
1,000		M4_070	S6.461926	E143.256018	1,030
1,000		M4_170	S6.461667	E143.255006	1,041
1,000	M5	M5_005	S6.461944	E143.250132	1,052
1,000		M5_070	S6.462124	E143.250560	1,057
1,000		M5_170	S6.461528	E143.251531	1,056
1,400	M1	M1_005	S6.440230	E143.224085	1,403
1,400		M1_070	S6.440240	E143.223590	1,398
1,400		M1_170	S6.440079	E143.222562	1,408
1,400	M2	M2_005	S6.440718	E143.225566	1,395
1,400		M2_070	S6.441409	E143.225425	1,378
1,400		M2_170	S6.442099	E143.224895	1,391
1,400	M3	M3_005	S6.441778	E143.227103	1,379
1,400		M3_070	S6.442142	E143.226678	1,375
1,400		M3_170	S6.443061	E143.226314	1,392
2,200	H1	H1_005	S5.972520	E142.753279	2,163
2,200		H1_070	S5.972856	E142.752890	2,155
2,200		H1_170	S5.973729	E142.752471	2,151
2,200	H2	H2_005	S5.969087	E142.751274	2,167
2,200		H2_070	S5.969068	E142.750669	2,187
2,200		H2_170	S5.969126	E142.749804	2,217
2,200	H3	H3_005	S5.943807	E142.741784	2,289
2,200		H3_070	S5.944572	E142.741865	2,284
2,200		H3_170	S5.945233	E142.741622	2,322
2,700	H4	H4_005	S5.918423	E142.695320	2,695
2,700		H4_070	S5.919144	E142.694951	2,702
2,700		H4_170	S5.919827	E142.694924	2,692
2,700	H5	H5_005	S5.916343	E142.692853	2,751
2,700		H5_070	S5.916471	E142.692311	2,749
2,700		H5_170	S5.916749	E142.691230	2,731
2,700	H6	H6_005	S5.913796	E142.690169	2,733
2,700		H6_070	S5.914176	E142.689647	2,737
2,700		H6_170	S5.914911	E142.688983	2,729

Appendix 2.3. Summary of species detections for all frogs encountered on each VAES transect. The sequence of circles is increasing distance from the road (0 to 100 m, left to right in 20 m increments), with a black circle indicating a detection of that species, and an open circle an apparent absence.

Elevation	**BAA 2**					**BAA 1**				
	1,000	1,000	1,400	1,400	1,400	2,200	2,200	2,200	2,700	2,700
Transect	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5
PELODRYADIDAE										
Litoria iris	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Litoria sp. 1 'yellow legs'	oo●oo	ooooo	●●oo●	oo●●o	●ooo●	ooooo	ooooo	ooooo	ooooo	ooooo
LIMNODYNASTIDAE										
Lechriodus aganoposis	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
MICROHYLIDAE										
Asterophrys slateri	ooo●o	o●o●●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Austrochaperina laurae	ooooo	ooooo	o●o●●	●●●o●	o●o●o	ooooo	ooooo	ooooo	ooooo	ooooo
*Austrochaperin*a sp. 2 'long call'	oooo●	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Callulops omnistriatus	ooooo	●oo●●	oo●oo	ooo●o	ooo●●	ooooo	ooooo	ooooo	ooooo	ooooo
Callulops wilhelmanus	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	●oooo
Choerophryne alainduboisi	o●ooo	ooo●o	●●●●o	●●●●●	●●●oo	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne brevicrus	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooo●●	oo●o●	●●●●●	o●●o●
Choerophryne burtoni	ooooo	ooooo	ooooo	oo●o●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne crucifer	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne multisyllaba	ooooo	ooooo	oooo●	ooo●●	oo●oo	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne murrita	ooooo	ooooo	ooo●●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne sp. 1 'arboreal'	ooooo	ooooo	ooooo	ooooo	ooooo	●●●o●	●ooo●	o●o●●	ooooo	ooooo
Choerophryne sp. 2 'tiny'	ooooo	ooooo	ooooo	ooooo	ooooo	oooo●	ooooo	oooo●	ooooo	ooooo
Cophixalus wempi	ooooo	ooooo	●o●oo	oooo●	o●●oo	ooooo	ooooo	ooooo	ooooo	ooooo
Cophixalus sp. 1 'musical call'	ooooo	ooooo	ooooo	●oo●o	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo
Cophixalus sp. 2 'tiny'	ooooo	ooooo	ooooo	●o●●o	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo
Cophixalus sp. 5 'peeping call'	ooooo	ooooo	ooooo	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Cophixalus sp. 6 'loud grunter'	ooooo	ooooo	ooooo	ooooo	ooooo	●oooo	o●●●o	ooooo	ooooo	ooooo
Copiula sp. '2-note call'	o●ooo	o●o●o	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Hylophorbus richardsi	ooooo	ooooo	ooooo	ooooo	ooooo	oooo●	ooooo	ooooo	ooooo	ooooo
Hylophorbus sp. 1 'slow call'	ooooo	ooooo	ooooo	ooo●●	oo●oo	ooooo	ooooo	ooooo	ooooo	ooooo
Hylophorbus sp. 2 'fast call'	●ooo●	o●o●●	ooooo	ooooo	ooo●●	ooooo	ooooo	ooooo	ooooo	ooooo
Liophryne schlaginhaufeni	ooooo	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne anamiatoi	ooooo	ooooo	ooooo	ooooo	ooooo	oooo●	●●ooo	ooooo	ooooo	ooooo
Oreophryne flavomaculata	ooooo	ooooo	o●●●●	●●●o●	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne notata	ooooo	ooooo	●●ooo	●o●o●	ooooo	●●●●●	oo●●●	●●●●o	●●●●●	●●●●●
Oreophryne oviprotector	o●o●o	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne pseudunicolor	●●ooo	o●o●●	ooooo	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne sp. 2 'ratchet call'	ooooo	oo●oo	o●●●o	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne sp. 6 'rasping call'	ooooo	o●●oo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Sphenophryne cornuta	oooo●	oo●oo	o●ooo	ooooo	●oooo	ooooo	ooooo	ooooo	ooooo	ooooo
Xenorhina sp. 1 'slow call'	o●ooo	●●o●●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Xenorhina sp. 2 'fast call'	ooooo	ooooo	ooooo	oo●oo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Gen. nov. sp. nov.	ooooo	ooo●o	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo

Appendix 2.4. Summary of species detections for all calls detected at each acoustic recording site on transects perpendicular to the linear infrastructure. The sequence of circles is increasing distance from the road (5, 70 and 100 m, left to right), with a black circle indicating a detection of that species, and an open circle an apparent absence.

Elevation	**BAA 2**					**BAA 1**					
	1,000	1,000	1,400	1,400	1,400	2,200	2,200	2,200	2,700	2,700	2,700
Transect	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5	H6
PELODRYADIDAE											
Litoria iris	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Litoria sp. 1 'yellow legs'	ooo	●oo	●●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
LIMNODYNASTIDAE											
Lechriodus aganoposis	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
MICROHYLIDAE											
Asterophrys slateri	●●●	●●●	●o●	●●o	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Austrochaperina laurae	ooo	ooo	ooo	o●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Austrochaperina sp. 2 'long call'	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Callulops omnistriatus	●●●	●●●	●●o	●o●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Callulops wilhelmanus	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	●oo	●●o	ooo
Choerophryne alainduboisi	ooo	o●●	●●●	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne brevicrus	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne burtoni	ooo	ooo	o●o	oo●	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne crucifer	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne multisyllaba	ooo	ooo	o●●	oo●	●o●	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne murrita	ooo	ooo	ooo	ooo	●oo	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne sp. 1 'arboreal'	ooo	ooo	ooo	ooo	ooo	●●●	●●●	●●●	ooo	ooo	ooo
Choerophryne sp. 2 'tiny'	ooo	ooo	ooo	ooo	ooo	ooo	ooo	●oo	ooo	ooo	ooo
Cophixalus wempi	ooo	ooo	ooo	ooo	o●o	ooo	ooo	ooo	ooo	ooo	ooo
Cophixalus sp. 1 'musical call'	ooo	ooo	o●●	●●●	o●●	ooo	ooo	ooo	ooo	ooo	ooo
Cophixalus sp. 2 'tiny'	ooo	ooo	oo●	o●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Cophixalus sp. 5 'peeping call'	ooo	ooo	oo●	●●o	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Cophixalus sp. 6 'loud grunter'	ooo	ooo	ooo	ooo	ooo	●●●	●●●	●●●	ooo	ooo	ooo
Copiula sp. '2-note call'	ooo	●o●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Hylophorbus richardsi	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Hylophorbus sp. 1 'slow call'	ooo	ooo	●oo	●oo	o●●	ooo	ooo	ooo	ooo	ooo	ooo
Hylophorbus sp. 2 'fast call'	●●●	●●●	●●●	●●o	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Liophryne schlaginhaufeni	ooo	oo●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne anamiatoi	ooo	ooo	ooo	ooo	ooo	ooo	●●●	ooo	ooo	ooo	ooo
Oreophryne flavomaculata	o●●	●●●	●●●	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne notata	oo●	●o●	●●●	●●●	●●●	●●●	●●●	●●●	●●●	●●●	●●●
Oreophryne oviprotector	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne pseudunicolor	●●●	●●●	●oo	●o●	●●o	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne sp. 2 'ratchet call'	ooo	ooo	o●●	●●●	●oo	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne sp. 6 'rasping call'	oo●	●oo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Sphenophryne cornuta	●oo	●oo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Xenorhina sp. 1 'slow call'	oo●	●●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Xenorhina sp. 2 'fast call'	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Gen. nov. sp. nov.	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo

Appendix 2.5. Summary of taxonomic changes to frog names since 2015 that are incorporated into this report.

Name used in 2015	New name	Reference or comment
Austrochaperina sp. 1 'short call'	*Austrochaperina laurae*	This species has now been tentatively identified as *A. laurae* pending further studies.
Callulops sp.	*Callulops omnistriatus*	Now identified as *C. omnistriatus*, a species described from near Moro by Kraus and Allison (2009).
Choerophryne sp. 3 'buzz call'	*Choerophryne alainduboisi*	Formally described from Iagifu Ridge as a new species by Günther and Richards (2018)
Choerophryne sp. 4 'montane clicker'	*Choerophryne multisyllaba*	Formally described from Iagifu Ridge as a new species by Günther and Richards (2017)
Choerophryne sp. 5 'lowland clicker'	*Choerophryne crucifer*	Formally described from Iagifu Ridge as a new species by Günther and Richards (2017)
Cophixalus sp. 4 'rasping call'	*Oreophryne* sp. 6 'rasping call'	Still undescribed, but now known to belong in the genus *Oreophryne*.
Hylophorbus sp. 1 'small'	*Hylophorbus* sp. 1 'slow call'	Additional specimens observed during the 2017 survey indicate that size differences between these species may be slight or non-existent – but calls are distinct so the species label has been modified accordingly.
Hylophorbus sp. 2 'large'	*Hylophorbus* sp. 2 'fast call'	
Metamagnusia slateri	*Asterophrys slateri*	Rivera et al. (2017) demonstrated that this species belongs in the genus *Asterophrys*.
Oreophryne sp. 3 'slow peeper'	*Oreophryne pseudunicolor*	Formally described from the Kikori basin as a new species by Günther and Richards (2016).
Oreophryne sp. 4 'yellow spots'	*Oreophryne flavomaculata*	Formally described from Iagifu and Gobe Ridges as a new species by Günther and Richards (2016).
Oreophryne? sp. 5 'loud grunter'	*Cophixalus* sp. 6 'loud grunter'	A single specimen of this difficult to capture species was obtained at Hides Ridge in 2017. Morphological examination and DNA barcoding reveal it to be an undescribed *Cophixalus* species.

Chapter 3 – Camera trap monitoring of terrestrial mammals and birds

Iain A. Woxvold and Leo Legra

The IUCN Near Threatened Small Dorcopsis (*Dorcopsulus* cf. *vanheurni*)

Summary

Background and aims

Terrestrial mammals and birds are suitable for monitoring because they include a variety of species that are targeted by hunters, are sensitive to forest disturbance or to invasive species impacts, or are otherwise indicative of ecosystem health (for example top-order predators). Wildlife most at risk in Papua New Guinea (PNG) include a variety of 'charismatic' species such as wallabies, cassowaries and tree kangaroos, a number of which are listed by the IUCN as Threatened or Near Threatened with extinction. While many of these are large, they often occur at naturally low densities and are difficult to detect due to their avoidance of humans.

Camera traps are increasingly used to monitor terrestrial wildlife populations, and as a non-invasive, continuous sampling tool they provide a practical and unbiased method for sampling rare and elusive species. Here we present the results of a camera trap study conducted in May–August 2017 to meet the following objectives:

1. To improve our understanding of mammal and bird diversity within the PNG LNG Upstream Project Area.

2. To monitor trends (increase/decrease) in the activity rates of wildlife populations in two Biodiversity Assessment Areas (BAAs) established on Hides Ridge (BAA 1) and on the Agogo Range near Moro (BAA 2).

Major results

Eighty camera traps were deployed at four sites in BAA 1 and BAA 2 for a period of 90–102 days. At each site, to test for potential edge effects four cameras were positioned in each of five parallel 'bands' of increasing distance from the nearest clearing: 0–50 m; 50–100 m; 100–200 m; 200–300 m; 300+ m.

From 71 functioning cameras (nine cameras were lost or malfunctioned), more than 80 species were documented in 5,506 independent photographic events recorded over 6,551 sampling days. Animals photographed include 13 species not previously recorded in the BAAs, a number of which were not previously known from the broader Kikori basin. Nine conservation listed species were camera trapped, including five IUCN Threatened species – the Eastern Long-beaked Echidna (*Zaglossus bartoni*), Pademelon (*Thylogale* sp.), Goodfellow's Tree Kangaroo (*Dendrolagus goodfellowi*), Western Montane Tree Kangaroo (*D. notatus*) and Papuan Eagle (*Harpyopsis novaeguineae*) – three Near Threatened species and one Data Deficient species. The Near Threatened Small Dorcopsis (*Dorcopsulus* cf. *vanheurni*) was the most frequently camera trapped of all species with more than 950 photographic events recorded across all sites.

Multi-model comparisons (using Akaike information criterion (AIC_c)) and model averaging revealed a notable correlation between animal activity rates and distance from infrastructure (roads or clearings) in six species. Most species demonstrated higher activity rates further from infrastructure clearings at the BAA 2 sites, and a reverse pattern at Hides High (BAA 1) with higher activity nearer to clearings. Two widespread species – Raffray's Bandicoot (*Peroryctes raffrayana*) and Small Dorcopsis – shifted the direction of their response to distance from clearings across the BAAs. Terrain effects offer an alternative and parsimonious explanation—steeper terrain is present closer to clearings at BAA 2 and further from clearings at BAA 1, so that most observed patterns can be explained by animals avoiding the steepest ground. In remaining cases, the null model was either among the best-ranked models ($\Delta AIC_c < 2$: *Echymipera* sp. at Arakubi) or could not readily be discounted ($2 < \Delta AIC_c < 6$: dasyurids, all sites).

The highest number of forest incursions by humans and dogs, and the lowest photographic event rates for hunting-sensitive species, were recorded at the BAA 1 sites. Hunting-sensitive species were rarest at Hides Low, where pooled activity rates of widespread (study area-wide) taxa were significantly lower than at all other sites.

Conclusions and recommendations

The 2017 camera trap study represents the first full year of sampling using this efficient and effective monitoring tool. The value of camera traps in detecting elusive species is demonstrated, with multiple rare and Threatened taxa recorded in the BAAs for the first time. The majority of terrestrial bird and mammal taxa expected to occur in the study area have been recorded, and the deployment period of 90–102 days was sufficient to collect statistically useful datasets for 31 of the more common species and genera.

There was no unequivocal evidence that edge effects negatively influence the presence or behaviour of any species. Terrain steepness (local relief) offers a viable alternative explanation to most correlations between animal activity and distance from infrastructure, and it is not possible to conclusively disentangle the influence of terrain and edge effects with the current dataset.

Available evidence suggests that hunting pressure is highest on Hides Ridge. Hunting pressure is difficult to quantify, and impacts on local wildlife populations are best measured by monitoring population trends over time. The 2017 dataset provides a useful baseline against which to measure future changes.

Sampling in subsequent years will improve the resolution of the available dataset, and allow for: (1) improved confidence in ranking the influence of various predictor variables; (2) detailed analysis of additional taxa for which statistically useful datasets are not yet available, and; (3) monitoring of population trends in hunting-sensitive species within sites over time.

We recommend that the camera trapping program continue in 2019 and in subsequent survey years. Data acquired to date provide detailed insights into the distribution and behaviour of a suite of poorly known endemic New Guinean fauna, and additional data collected over subsequent years will improve our understanding of the potential influence of Project-related impacts on these and other taxa.

In future surveys, we will aim to collect additional information on fine-scale vegetation variables for consideration in the modelling. A relevant sampling protocol has already been developed, and we recommend adding one more member to the camera trapping team to assist with this data collection during the 2019 survey.

Finally, we recommend that funds be made available to work with a biostatistician to help develop the R script to enable analysis of data over multiple years and to facilitate separate modelling of occupancy (ψ) and detectability (*p*) patterns.

Introduction

As a remotely operated, static sampling tool camera traps bring many advantages to wildlife monitoring studies—they run continuously for long periods without maintenance; they are effective at sampling rare and elusive species; they are non-invasive and result in minimal environmental disturbance; and they provide quantitative data suitable for statistical analysis (O'Connell et al. 2011; Swann and Perkins 2015; Rovero and Zimmerman 2016a). Because of these benefits, camera traps are increasingly used as an efficient and effective tool for monitoring terrestrial animal populations. For example, camera trap studies have been used to examine the influence of roads or edge effects on animal behaviour and abundance (Srbek-Araujo and Chiarello 2013), to compare use of different habitats (Pettorelli et al. 2010), to examine the impacts of hunting and disturbance (Datta et al. 2008; Jenks et al. 2011), to monitor feral animal populations (Bengsen et al. 2011a, b), to test the effectiveness of wildlife corridors (Gregory et al. 2014), and to detect the presence of rare and elusive species (Beirne et al. 2017).

Large and medium-bodied terrestrial birds and mammals, particularly those that are hunted, are an excellent candidate monitoring group because changes in hunting pressure and the impacts of invasive species (including dogs) are among

the most important processes to be considered during impact assessment for any major development in PNG forest environments. Species most at risk include a variety of 'charismatic' terrestrial birds and mammals, a number of which are listed as Threatened or Near Threatened on the IUCN *Red List of Threatened Species* (IUCN 2018). Additionally, large-bodied vertebrates are often considered a useful indicator of ecosystem health and habitat connectivity (Crooks et al. 2011; Peters et al. 2015). Despite their size, such animals often occur at naturally low densities and/or are difficult to detect due to their avoidance of humans. Examples present within the PNG LNG Upstream Project Area include IUCN Endangered tree kangaroos (*Dendrolagus* spp.), IUCN Vulnerable Eastern Long-beaked Echidna (*Zaglossus bartoni*) and Pademelon (*Thylogale*) wallaby, the Near Threatened Small Dorcopsis (*Dorcopsulus* cf. *vanheurni*) and cassowaries (*Casuarius* spp.).

Smaller birds and mammals that are not specifically targeted by hunters may also be sensitive to the impacts of invasive species or disturbance. For example, in other tropical regions insectivorous birds of the forest understorey are known to be sensitive to habitat degradation and fragmentation (Lambert 1992; Johns 1996; Peh et al. 2005; Edwards et al. 2009). Though not well studied in New Guinea, many terrestrial birds found in the PNG LNG Upstream Project Area feed mainly on invertebrates and may be similarly susceptible to changes in the forest environment, for example via edge effects. In 2015 a pilot study was conducted to test the effectiveness of camera traps in monitoring terrestrial wildlife populations within the PNG LNG Upstream Project Area (Woxvold and Aplin 2017). Based on the results of the pilot study, the camera trapping program was expanded for the 2017 monitoring year. Camera trap arrays were deployed to meet two main objectives:

1. To improve our understanding of bird and mammal diversity present in sampling areas—at the simplest level we anticipate that camera trapping will detect a number of rare and elusive species that are typically missed during rapid assessment biodiversity surveys.

2. Second, to monitor changes in the presence and behaviour of target species, via trends in photographic capture rates, over time and space, with observed patterns interpreted in relation to potential Project-related impacts.

Terrestrial fauna are susceptible to a variety of impact processes, each of which may influence a distinct group of taxa and be measurable over different spatial and temporal scales. For example, 'edge effects' associated with forest clearance and infrastructure development may measurably influence animal activity from tens to a few hundred metres into the forest (Laurance and Bierregaard 1997). Edge effects may occur via changes to vegetation structure and floristics associated with microclimate change near the forest edge (Pohlman et al. 2007), and/or traffic-associated disturbance along roads (Andrews et al. 2015; van der Ree et al. 2015). Conversely, hunting pressure may affect a select group of preferred target species with population declines observable over tens or even hundreds of square kilometres.

Camera trap data collected within the study area in 2017 and during subsequent survey years will be used to examine the potential influence of (1) edge effects over limited spatial areas and (2) hunting pressure over time. Here we describe the results of the 2017 camera trapping study.

Methods

Study area

The study was conducted within two Biodiversity Assessment Areas (BAAs) located in upland sectors of the PNG LNG Upstream Project Area—on Hides Ridge (BAA 1) in Hela Province, located approximately 25 km west-southwest of Tari township; and on the Agogo Range in the Moro area (BAA 2), Southern Highlands Province, approximately 9 km southwest of Lake Kutubu (see Figure 1 in Report Summary). Camera traps were deployed at two sites within each BAA:

- Within BAA 1—at 'Hides Low' immediately northwest of Wellpad D, and at 'Hides High' between Wellpad E and Wellpad G, their camera arrays separated by 4.6 km at their closest point.

- Within BAA 2—at 'Arakubi' around Arakubi Quarry and east of the pipeline right-of-way (ROW), and at 'KP107' in the vicinity of kilometre-point 107 along the pipeline ROW, their camera arrays separated by 2.7 km at their closest point.

Each site differs in elevation, with all camera positions spanning an elevational range of approximately 1,800 m (range: 922–2,731 m above sea level (asl); Table 3.1).

All sites are located on polygonal karst. The terrain in most areas is rugged and characterised by a series of sub-parallel and networking ridgelines interspersed with numerous dolines and valleys. The overlying vegetation is described in detail in Venter and Ona (2017). Most sites are characterised by evergreen lower montane forest, with *Nothofagus* dominant in the canopies at BAA 1 and *Nothofagus–Papuacedrus–Alaeocarpus–Cryptocarya* at KP107. At Arakubi, lower montane forest is mixed with upper hill forest with *Nothofagus* stands restricted largely to the ridgelines. The regional landscape is well forested with all sites connected by continuous tracts of natural forest habitat. Rainfall throughout the region is continuously heavy (little seasonality; McAlpine et al. 1983), averaging approximately 4 m per year at BAA 1 and more than 4 m per year at BAA 2 (Bryan and Shearman 2008). Despite the high rainfall, no watercourses or wetlands are present at the surveyed sites due to the porous limestone substrate.

Sampling design and effort

In order to test for potential edge effects, a sampling design was developed to examine differences in activity rates of terrestrial bird and mammal species at increasing distances from impacted areas. Twenty white-flash digital camera traps (Reconyx PC850) were deployed at each site, with four cameras positioned in each of five parallel 'bands' of increasing distance from the nearest clearing: 0–50 m; 50–100 m; 100–200 m; 200–300 m; 300+ m. Cameras were set at variable distances apart due to terrain and habitat conditions, with distances to the nearest camera ranging from 25–365 m. The position of functioning camera traps at each site is shown in Figures 3.1–3.2 (see below for summary of camera losses and malfunctions). This design is similar to those used to test project-related impacts in other tropical regions (T. Gregory and A. Alonso, unpublished data) and was developed in consultation with a biostatistician (Arthur Rylah Institute (ARI), Department of the environment, Land, Water and Planning (DELWP), Victoria, Australia).

Camera traps operated 24 hours/day, were programmed to maximum detection sensitivity and to take three photographs on each 'trigger event' with the minimum amount of rest time between triggers (<2 seconds). Each camera was fixed to a tree or freshly cut wooden pole and directed along an animal trail or towards a confluence of trails in an area of flat or gently sloping ground. Cameras were positioned 15–25 cm above the ground in order to capture images of small as well as medium-sized and large animals. Site disturbance was kept to a minimum, with low vegetation (herbs, ferns, etc.) removed from 2–3 m directly in front of the camera. Most camera sites were located on ridges/spurs or on gentle hill-slope terraces; valley floors and gullies were avoided as these were often difficult to reach in the terrain and in order to minimise variability in detectability associated with local topographic effects. Camera sites were unbaited and fruiting trees were avoided to minimise the influence of natural attractants. Once set, camera traps were left to operate undisturbed until collection.

Camera traps were deployed from 10 May to 30 August 2017. Table 3.1 summarises the trapping effort at each site. Of 80 cameras deployed, seven were lost (from Hides Low) and two malfunctioned soon after deployment yielding no results (one each at Arakubi and KP107). Of 71 functioning cameras, 61 (85.9%) operated for the full deployment period of 90–102 days. Of the remaining 10 cameras, five malfunctioned during deployment but provided results for more than two months of survey (65–77 days), and five provided partial datasets (28–62 days) before the camera view was obscured by falling vegetation (two cameras) or mud from heavy rainfall (one camera), or because the site was converted to a garden (two cameras at Arakubi). The overall trapping effort across all sites was 6,551 camera days.

Table 3.1. Elevational range and camera trapping effort at each site.

Site	Elevation (m asl)	No. operating cameras	Camera days		
			Total	Mean	Range
BAA 1					
Hides Low	2,192–2,389	13	1,199	92.23	77–98
Hides High	2,645–2,731	20	1,848	92.40	65–99
BAA 2					
Arakubi	922–1,052	19	1,748	92.00	36–102
KP107	1,297–1,398	19	1,756	92.42	28–102
Total		**71**	**6,551**	**92.27**	**28–102**

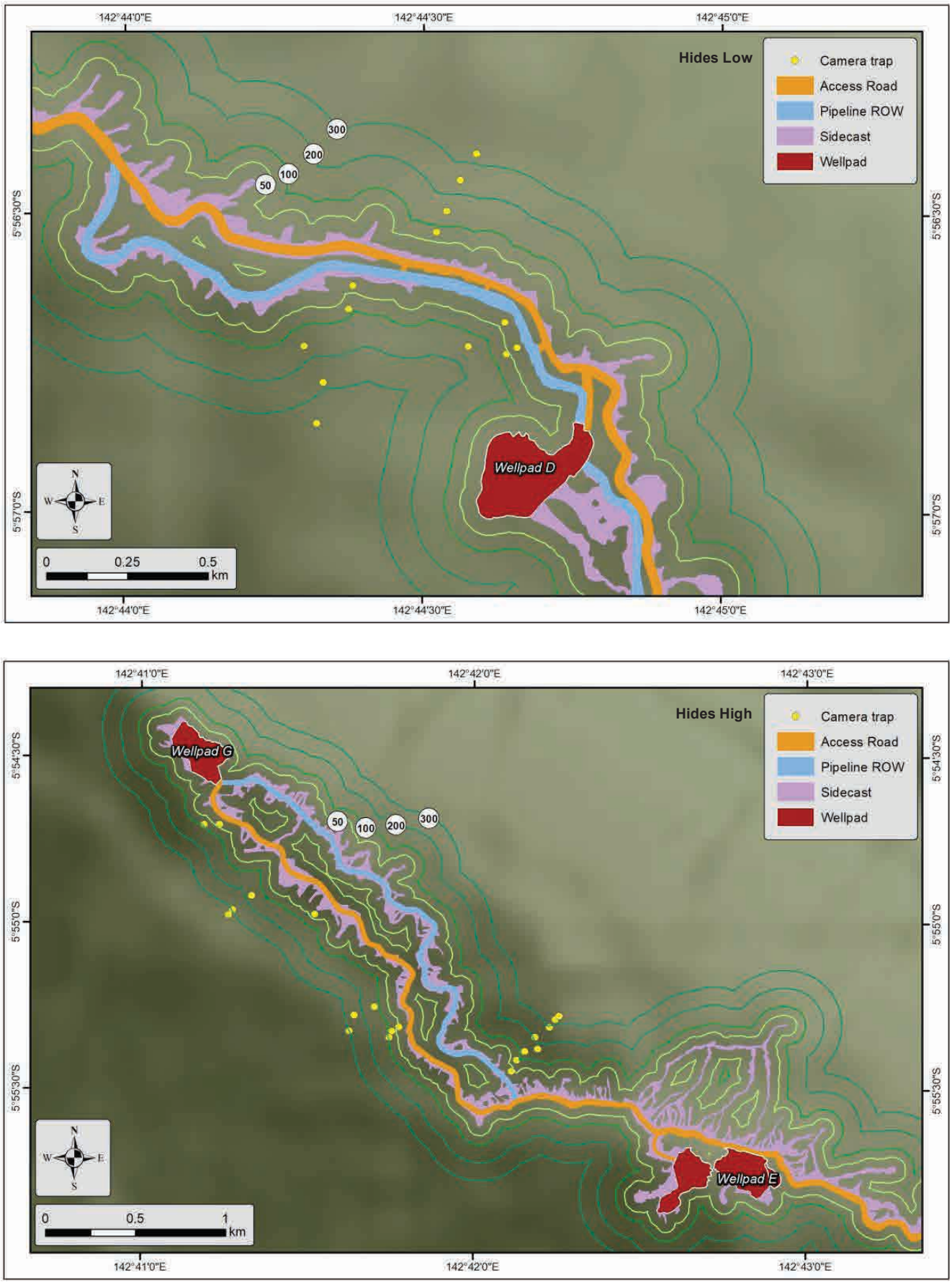

Figure 3.1. Camera trap positions and distance bands (numbered in metres) at Hides Low and Hides High in BAA 1.

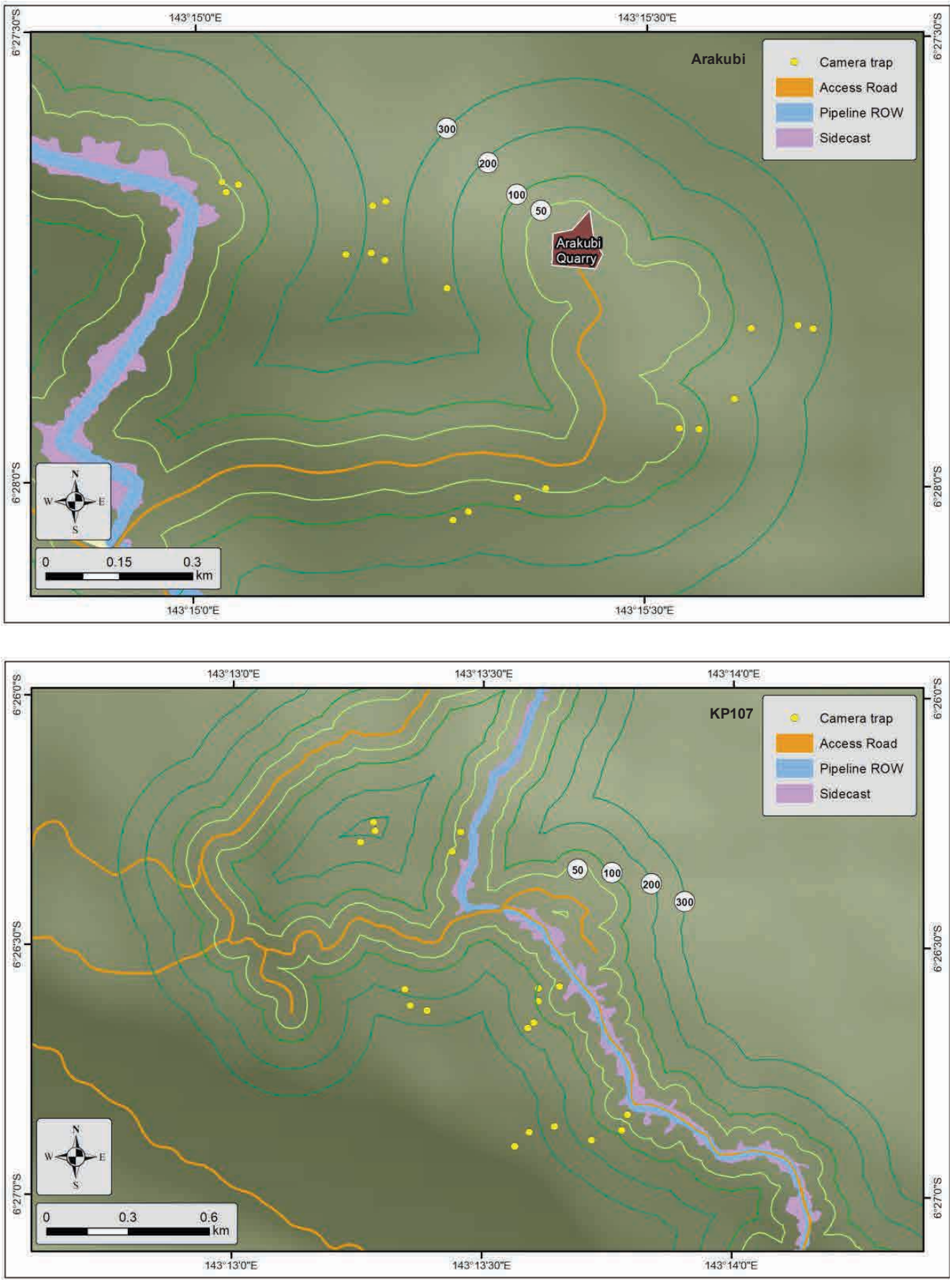

Figure 3.2. Camera trap positions and distance bands (numbered in metres) at Arakubi and KP107 in BAA 2.

Analysis

Data organisation

Images were sorted into taxa with birds identified by IW and mammals by IW and Ken Aplin. Photographs of animals of uncertain identity were set aside and excluded from subsequent analysis. Images and associated metadata were managed for analysis using the 'camtrapR' package (Niedballa et al. 2016).

For each taxon of interest, activity rates were calculated on a per-camera basis as the daily rate of independent photographic events. For most taxa, following numerous prior examples (Burton et al. 2015), within-camera events were considered independent where consecutive pictures of the same species were taken more than 60 minutes apart. Multiple events were scored within 60-minute periods where more than one individual was seen in a single photograph or sequence. Humans and dogs were tallied differently, as in most cases they were individually recognisable and in order to accurately document interior forest incursions including hunting forays. Events for these species were scored on a per-site/day basis, with recognisable individuals tallied once per day regardless of the number of cameras on which they appeared. Anthropogenic events leading to the loss of cameras (at Hides Low) or garden construction (at Arakubi) were not included.

Naïve occupancy (ψ) was calculated for each taxon as the proportion of cameras at each site at which it was detected.

Examining edge effects

In order to examine potential edge effects, Generalised Linear Mixed Models (GLMMs) were used to explore the relationship between animal activity rates and distance from infrastructure clearings while controlling for select environmental covariates. Site and camera position were treated as random effects.
Five measures of distance from infrastructure and associated clearings were assessed:

- Distance from the nearest clearing (road, pipeline ROW, wellpad, quarry or sidecast):
  1. As a continuous measure (DClr).
  2. As a comparison of activity at <50 m and >50 m distance (LT50).
  3. As a comparison of activity at <100 m and >100 m distance classes (LT100).

- Distance from the nearest road:
  1. As a continuous measure (DRd).
  2. As a comparison of activity at <100 m and >100 m distance (LT100Rd) (there were insufficient data to compare activity rates at <50 m and >50 m from roads).

Distance from the nearest settlement was not assessed as it was positively correlated with elevation (Pearson correlation coefficient = 0.929, $P<0.0001$).

Among environmental variables, we assessed elevation (m asl) (Elev), canopy cover (%) (CC), topographic position (ridge/spur or slope terrace) (TP) and local relief (difference between the highest and lowest elevations) at the 20 m, 50 m and 100 m radius scales (R20, LR50, LR100). Elevation data were taken from 5 m LiDAR Digital Elevation Model (DEM). Canopy cover was measured from digital hemispherical photographs taken with a fish-eye lens and analysed using the DHPT 1.0 software package (Loffredo et al. 2016).

Collinearity among variables was examined using Pearson correlation coefficient (PCC) and associated *P*-value matrices and by running overall multicollinearity diagnostics using the 'mctest' R package. Collinearity tests were run for all variable-pairs across the whole study area (all sites) and separately for each site and BAA. For each site/group of sites, the list of collinear and near-collinear variable-pairs excluded from consideration within the same models is

provided in Appendix 3.1. Different variable-pairs were collinear at different spatial scales. In most cases, the various distance measures were significantly correlated so that only one of each was used in each model. At Arakubi, however, most distance from clearing and distance from road measures were strongly non-collinear, so that for taxa analysed separately at this site it was possible to test for the different effects of these measures in the same model.

The activity patterns of terrestrial taxa were modelled across their distribution where sufficient data were available (1–4 sites where ≥16–20 events per site; models for taxa with fewer events typically fail to converge: this study; Martin et al. 2015; Oberosler et al. 2017). Most taxa were analysed at the species level. Data from marsupial carnivores (Dasyuridae) were sufficient to analyse activity only at the family level.

Models were initially built using the dredge function in the 'MuMIn' R package (Bartoń 2015). We used a common set of models for all taxa of interest at each site/group of sites, as determined by all possible combinations of explanatory variables excluding collinear pairs. Models were ranked using Second-order Akaike Information Criterion (AIC_c) and their associated Akaike weights (w_i). Because this information theoretic (IT)-AIC approach compares multiple competing models at once, it is useful in exploring the influence of a range of variables that may be associated with particular traits or behaviours (Symonds and Moussalli 2011). As a general rule, models that differ from the best-ranked model by an AIC_c value of less than two ($\Delta AIC_c<2$) are considered equally as good as the best model, while models with $\Delta AIC_c>6$ may be readily discounted (Richards 2005; Symonds and Moussalli 2011).

Analysis of most taxa revealed high model uncertainty, with multiple top-ranked models having a similar AIC_c score. Thus, for each taxon we examined the influence of various predictor variables from within a candidate set of models with $\Delta AIC_c<6$ using the model averaging function available in 'MuMIn'. For each variable, its 'relative importance' was calculated by summing the Akaike weights for all models in which it appeared and its coefficient point estimate and standard error were obtained by full model averaging (Grueber et al. 2011; Symonds and Moussalli 2011).

Within the initial full-model sets, collinear distance and terrain measures often compete with one another for weight among the best-ranked models. Because of this, for each taxon of interest a reduced-model set was subsequently analysed by including only the best-performing collinear distance and terrain measures as previously determined by their relative importance in the full-model set. Summary statistics presented in the Results (including best-ranked models, Akaike weights, model averaged coefficient point estimates and relative importance) are those of the reduced-model sets.

For taxa distributed across multiple sites, the potential for wildlife to respond differently to infrastructure at different sites was examined by modelling interactions between distance measures and elevation. In cases where the relative importance of the interaction term was higher than 0.2 in the reduced-model set, and where sufficient data were available, analyses were re-run at the site level.

Finally, after comparing the best-ranked models in reduced-model sets, the influence of top-performing variables of interest was examined by running the best-ranked models (GLMMs).

All analyses were performed in R (R Development Core Team 2015).

Examining hunting pressure

Compared to edge effects, impacts from hunting may penetrate many kilometres into the forest. Hunting-sensitive species include those medium to large-bodied animals that are known to be targeted by subsistence hunters in New Guinea. Ten hunting-sensitive species recorded in 2017 were selected for analysis—the Eastern Long-beaked Echidna (*Zaglossus bartoni*), Short-beaked Echidna (*Tachyglossus aculeatus*), Small Dorcopsis (*Dorcopsulus* cf. *vanheurni*), Pademelon (*Thylogale* sp.), Goodfellow's Tree Kangaroo (*Dendrolagus goodfellowi*), Western Montane Tree Kangaroo

(*Dendrolagus notatus*), Dwarf Cassowary (*Casuarius bennetti*), Wattled Brushturkey (*Aepypodius arfakianus*), Collared Brushturkey (*Talegalla jobiensis*) and New Guinea Scrubfowl (*Megapodius decollatus*).

The strongest inferences will be made by comparing results within sites across survey years, with the 2017 dataset providing a detailed baseline. In this report we summarise the baseline data and, for species whose elevational range spans all sites, compare activity rates across BAAs.

Conventions

Where species are referred to in the text, the scientific name appears with the English name on first mention. For species whose identity and taxonomy are certain, only the English name is used in the text thereafter. The scientific name is used persistently in photographs and tables, and in the text for species whose identity or taxonomy are not well known (for example because photographs are insufficient to identify an animal to species level or where their relationship with closely related taxa is still under investigation).

Results

Recorded diversity

A total of 5,506 independent photographic events was recorded during the 2017 sampling period of 6,551 camera days. More than 80 species were documented including 48 bird species, 30 mammal taxa and two reptile species. All taxa camera trapped are listed in Appendix 3.2 along with their conservation status, the number of independent photographic events and naïve occupancy level recorded at each site. A selection of taxa is shown in Figures 3.12–3.47. The total number of photographed species is considered to be more than 80 since a number of the mammal taxa are only identifiable to genus level in the images. For example, across all four sites it is known that multiple species of *Murexia* (Figure 3.15) and of the native rodents *Paramelomys* and *Rattus* are present (Aplin and Opiang 2017) and, given the recorded shift in community structure across elevations within the study area, more than one member of each of these genera is believed to have been photographed.

Thirteen species camera trapped in 2017 have not previously been recorded in the BAAs (Aplin and Opiang 2017; Woxvold and Legra 2017; Table 3.2). They include three IUCN Threatened mammal species and two notable bird discoveries (see *Species of conservation significance*).

Table 3.2. Species camera trapped in 2017 and not previously recorded from the BAAs.

Scientific Name	English Name	Status	Arakubi	KP107	Hides Low	Hides High
Mammals						
Zaglossus bartoni	Eastern Long-beaked Echidna	VU, P	X			X
Phascolosorex dorsalis	Narrow-striped Dasyure				X	X
Phalanger gymnotis	Ground Cuscus		X	X	X	X
Dactylopsila palpator	Long-fingered Striped Possum				X	X
Thylogale sp.	Pademelon	VU	X	X		
Dendrolagus goodfellowi	Goodfellow's Tree Kangaroo	EN, P	X			
Sus scrofa	Feral Pig		X	X		
Felis catus	Domestic Cat				X	
Birds						
Chalcophaps stephani	Stephan's Emerald Dove		X			
Alopecoenas jobiensis	White-breasted Ground Dove				X	
Ailuroedus stonii	Ochre-breasted Catbird		X			
Ptilorrhoa sp.				X		
Amalocichla sclateriana	Greater Ground Robin					X

Appendix 3.2 includes 56 taxa with predominantly or entirely terrestrial habits (hereafter 'terrestrial'). One terrestrial species camera trapped during the 2015 pilot study was not recorded in 2017—the Waterside Rat (*Parahydromys asper*) (Woxvold and Aplin 2017). Terrestrial species are the most suitable for monitoring under the current approach, since lower image rates result from incidental trapping of predominantly arboreal species. Figure 3.3 shows the number of independent photographic events taken for various terrestrial mammal and bird taxa in 2017.

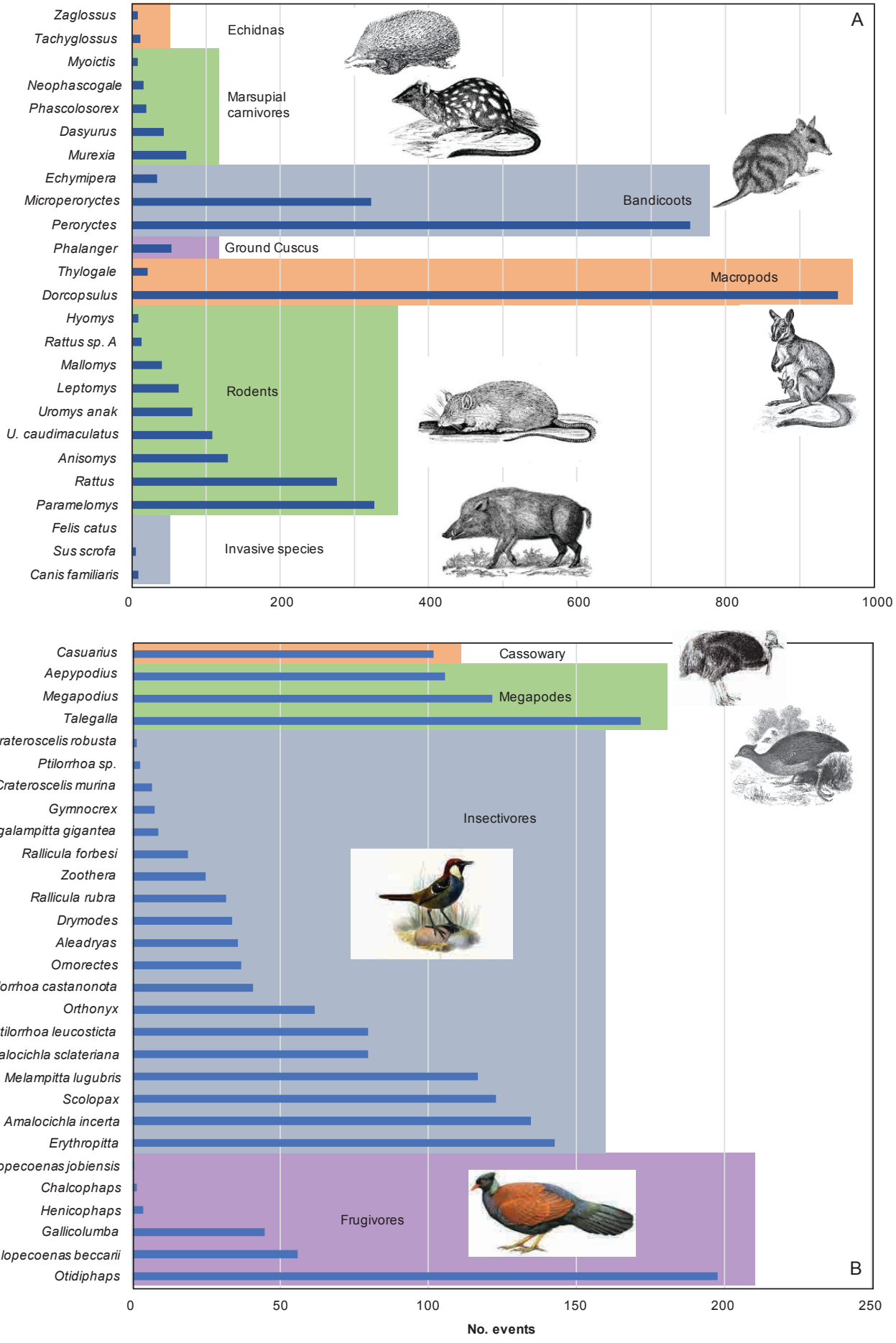

Figure 3.3. Number of independent photographic events for major groups of terrestrial (A) mammals and (B) birds.

Species of conservation significance

Species of conservation significance here include (1) conservation listed species and (2) rare endemics that have small known population size and/or geographic range.

Conservation listed species

Nine conservation listed species were camera trapped (Table 3.3), including five IUCN Threatened species, three Near Threatened species and one Data Deficient species. Four IUCN Threatened species are also protected under Papua New Guinean law.

Five of the conservation listed species are terrestrial. The two Endangered tree kangaroo species are predominantly arboreal but do occasionally come to ground (Eldridge and Coulson 2015). Brief accounts follow (in taxonomic order) for each conservation listed species.

Table 3.3. Conservation listed species camera trapped in 2017, their conservation status and the number of independent photographic events recorded at each site. Conservation status indicates those species listed in the IUCN *Red List of Threatened Species* (IUCN 2018) as Threatened (Endangered (EN), Vulnerable (VU)), Near Threatened (NT) or Data Deficient (DD) and those Protected (P) under the *PNG Fauna (Protection and Control) Act 1966***.** Terrestrial species (Terr. = Y) include those with predominantly or entirely terrestrial habits.

Scientific Name	English Name	Status	Terr.	Arakubi	KP107	Hides Low	Hides High	Total
Mammals								
Zaglossus bartoni	Eastern Long-beaked Echidna	VU, P	Y	6			3	9
Dasyurus albopunctatus	New Guinea Quoll	NT	Y	13	9	6	16	44
Myoictis leucura	Woolley's Three-striped Dasyure	DD	Y	4	5			9
Dorcopsulus cf. *vanheurni*	Small Dorcopsis	NT	Y	279	335	128	210	952
Thylogale sp.	Pademelon	VU	Y	6	16			22
Dendrolagus goodfellowi	Goodfellow's Tree Kangaroo	EN, P		4				4
Dendrolagus notatus	Western Montane Tree Kangaroo	EN, P		3	3		2	8
Birds								
Harpyopsis novaeguineae	Papuan Eagle	VU, P		1				1
Archboldia papuensis	Archbold's Bowerbird	NT					1	1

Eastern Long-beaked Echidna (*Zaglossus bartoni*) (VU, P) (Figures 3.12 & 3.29)

A heavy (4–9 kg), slow-moving mammal of the forest floor with a long snout and harsh spines concealed within dark fur. It is endemic to New Guinea where it has been recorded from near sea level (at least historically) to the highest mountains in a variety of habitats including hill forest, montane forest and sub-alpine grassland and scrub (Flannery 1995; Nicol 2015).

Long-beaked echidnas are prized as game and are particularly vulnerable to hunting with dogs. Long-lived and slow maturing, they are highly susceptible to overhunting and are generally extirpated from areas near human settlement, though they can be fairly common in areas inaccessible to humans (Nicol 2015; Leary et al. 2016). They are susceptible also to habitat disturbance where this reduces food availability (worms and grubs) via effects on surface soil.

This Vulnerable species is regionally widespread. At lower elevations in the Kikori basin it has been reported by locals from Wassi Falls, Mt Kemenagi, Darai Plateau and the Lake Kutubu area (Seri et al. 1995; Leary 1998, 2004), and it is present in the Gobe operations area where it was recorded by Leary (1999).

Not previously recorded in the BAAs, in 2017 multiple images were obtained from each of the Arakubi and Hides High sites.

New Guinea Quoll (*Dasyurus albopunctatus*) (NT) (Figure 3.14)

A medium-sized (to 0.7 kg) marsupial carnivore, brown with white spots. It is endemic to New Guinea where it occurs from sea level to highest elevations, mostly above 1,000 m, in diverse habitats including primary and secondary forest and gardens and subalpine heath (Flannery 1995; Baker 2015). As a top-order predator, it is generally uncommon. This Near Threatened species is susceptible to forest loss and habitat degradation (Woolley et al. 2008) and to poisoning by cane toads. It is too small and uncommon to be a specific hunting target, though it is taken opportunistically with snares and the use of dogs.

The New Guinea Quoll is regionally widespread (e.g. Seri et al. 1995; Leary 1999, 2004) and has been recorded previously in both BAAs (Woxvold and Aplin 2017). In 2017 it was recorded at all sites and was the most frequently camera trapped of all dasyurids identifiable to species level (Appendix 3.2).

Woolley's Three-striped Dasyure (*Myoictis leucura*) (DD) (Figure 3.16)

A small (200–230 g), brightly coloured, diurnal marsupial carnivore with bold longitudinal dorsal stripes and a reddish tail with a white tip. It is endemic to PNG where known from scattered localities in alluvial, hill and lower montane forest on the southern slopes of the central cordillera from the Mt Bosavi–Mt Sisa area east to Central Province (Namo 2004; Baker 2015; Woxvold and Aplin 2017; Woxvold, unpublished data). In 2017, images were obtained from multiple cameras at Arakubi and KP107.

Small Dorcopsis (*Dorcopsulus* cf. *vanheurni*) (NT) (Figure 3.22)

A small (1.5–2.3 kg), delicately built forest wallaby, dark brown on the back and usually paler below. It is endemic to New Guinea where it is found throughout the central ranges at 800–3,100 m asl (Eldridge and Coulson 2015). Mainly nocturnal and solitary, it is rarely seen other than as a glimpse as they disappear into dense cover. *Dorcopsulus* wallabies are threatened mainly by subsistence hunting and to some degree by habitat modification, with clear declines and localised extinctions recorded in some lower montane areas where human population densities are highest (Leary et al. 2016; Eldridge and Coulson 2015).

The Small Dorcopsis is widespread and locally common in upland forests of the Kikori basin (Seri et al. 1995; Leary 1999; Kale et al. 2018a). In 2017 it was the most frequently camera trapped of all species with more than 950 photographic events recorded across all sites.

Pademelon (*Thylogale* sp.) (VU) (Figure 3.23)

Pademelons (*Thylogale* spp.) are medium-sized (2.5–10 kg) wallabies with short faces, brown fur and variable patterning of pale markings on the face and flanks. The ecology of the New Guinean taxa is poorly known—they occupy a variety of habitats including closed rainforest and open and disturbed environments and, as with their Australian congeners, their diet is believed to include grass as well as herbs and browse (Eldridge and Coulson 2015). All New Guinean pademelon species are susceptible to hunting, especially with dogs, and to forest degradation and conversion; all are listed as Threatened on the *IUCN Red List* (Endangered or Vulnerable).

In 2017, pademelons were photographed on 22 occasions on 11 cameras at Arakubi and KP107. These are the first *Thylogale* records from the Kikori basin (Namo 2004). It is unclear which taxon is present. The New Guinea Pademelon

(*Thylogale browni*) is reported to occupy rainforest below 2,100 m asl in northern New Guinea and on the southern slopes of the cordillera in areas north of the Gulf of Papua (Eldridge and Coulson 2015; Leary e al. 2016). The Dusky Pademelon (*T. brunii*) is usually mapped as having three disjunct populations—on the Aru Islands, in the Trans-Fly region and on the southeast peninsula near Port Moresby (possibly extinct) (Eldridge and Coulson 2015; Leary e al. 2016); however, there is another possible population on the Karimui Plateau (listed as '*Thylogale* cf. *bruni*' in Hide et al. 1984) and a specimen was collected by K. P. Aplin in 1984 from near Haia village in the Purari basin (held in the Australian Museum, Sydney (AMS)). Recent molecular studies do not support the distinction of these two species (Eldridge and Coulson 2015), and as both are listed as IUCN Vulnerable the BAA 2 record is here reported at genus level.

Goodfellow's Tree Kangaroo (*Dendrolagus goodfellowi*) (EN, P) (Figure 3.24)
A large (up to 9.5 kg) predominantly arboreal kangaroo with bright chestnut fur, yellow lower limbs, a yellow banded tail and twin yellow stripes on the lower back. It is endemic to PNG where there are reliable historical records from near sea level to 2,860 m asl, though its current range is fragmented with most surviving populations above 1,000 m (Flannery 1995; Eldridge and Coulson 2015; Leary et al. 2016). All tree kangaroos are threatened by a combination of subsistence hunting, especially with dogs, and habitat modification. They appear sensitive to disturbance and are rarely found close to human habitation (George 1978).

This Endangered species is regionally widespread. It has been recorded previously at Gobe (Leary 1999), reported by local informants from the Darai Plateau (Leary 2004) and trophy skins have been observed at Babeo (Veiru) village (Kale et al. 2018b). In 2017 it was photographed on four occasions at Arakubi.

Western Montane Tree Kangaroo (*Dendrolagus notatus*) (EN, P) (Figure 3.25)
A large (up to 9.5 kg) predominantly arboreal kangaroo, dark brown with paler yellowish tail-base. This species is endemic to the central range of PNG, east from the Star Mountains to the base of the southeast peninsula, at 900–3,100 m asl (Eldridge and Coulson 2015; Leary et al. 2016). As for the previous species, it is threatened by subsistence hunting, especially with dogs, and by habitat modification. It is generally rare and present at low densities with localised extinctions reported in some settled areas.

The Western Montane Tree Kangaroo is regionally widespread. Within the Kikori basin it has been recorded previously at Mt Kemenagi (Seri et al. 1995) and at Gobe (Leary 1999), and it has been reported by local informants from the Darai Plateau (Leary 2004). In 2015 an individual was camera trapped at the Hides High site (Woxvold and Aplin 2017), and the expanded effort in 2017 yielded multiple photographs from most sites (all except Hides Low) across all elevations. Though not a truly terrestrial animal, this species is reported to spend more time on the ground than Goodfellow's Tree Kangaroo (Eldridge and Coulson 2015) and may therefore be more easily detected by terrestrial camera traps.

Papuan Eagle (*Harpyopsis novaeguineae*) (VU, P)
The island's largest bird of prey, the Papuan Eagle is endemic to New Guinea where it is widespread in forested habitats from sea-level to over 3,000 m asl (Coates 1985). Though not terrestrial, it hunts below the canopy taking mammals and birds from the ground, in trees or from tree hollows (Coates 1985; Watson and Asoyama 2001). It is thus occasionally camera trapped, with single events recorded at Hides Low in 2015 (Woxvold and Aplin 2017) and at Arakubi in 2017.

Archbold's Bowerbird (*Archboldia papuensis*) (NT) (Figure 3.40)
This large (to 37 cm), black bowerbird is a rare endemic of the high mountains of New Guinea (mostly above 2,600 m asl) where it is known from only a few scattered localities along the central cordillera (Beehler and Pratt 2016). It has been recorded locally at Tari Gap and the Karius Range, and its presence on Hides Ridge was confirmed by Leo Legra (bower sighting) during preconstruction surveys (Woxvold and Legra 2017). Normally a canopy dweller, in 2017 a female was camera trapped at Hides Ridge.

Rare endemics with limited geographic range

In addition to conservation listed species, camera trapping has resulted in two notable ornithological discoveries involving rare species with small known population size and/or geographic range.

Greater Ground Robin (*Amalocichla sclateriana*) (Figure 3.46)

The Greater Ground Robin is a large, terrestrial robin endemic to the high mountains of New Guinea. A rare and cryptic species, it is known from three isolated populations located at the extreme east and west of the central cordillera and on the Huon Range (Beehler and Pratt 2016). In 2017 this was among the most frequently camera trapped birds at the Hides High site, with 80 independent events recorded on 70% of the camera positions (14/20). Hides Ridge is situated in the centre of a distributional gap spanning nearly 900 km between previously known populations. Restricted to elevations above 2,600 m asl, the Hides population is isolated from nearby areas of suitable habitat, where despite recent searches the species is yet to be located. It is unknown whether the Hides Ridge population belongs to a known subspecies or represents a new, undescribed taxon.

Jewel-babbler (*Ptilorrhoa* sp.)

A distinctive jewel-babbler (*Ptilorrhoa* sp.) recorded at BAA 2 is unlike any known member of this endemic New Guinean genus. Additional studies are planned to determine its taxonomic status.

Activity rate models

Model summaries

Multi-model analyses were successfully run for 12 mammal taxa (11 species and the family Dasyuridae) and 19 bird species. Statistical models did not converge for the Ground Cuscus (*Phalanger gymnotis*), Chestnut Forest Rail (*Rallicula rubra*) or Spotted Jewel-babbler (*Ptilorrhoa leucosticta*) despite more than 20 independent events recorded at one or more sites for these species.

For all taxa analysed, Appendix 3.3 shows the best-ranked models ($\Delta AIC_c < 2$) emerging from reduced-model sets and the relative position of the null model. Model-averaged coefficient point estimates, their standard errors and the relative importance of predictor variables appearing in all models with $\Delta AIC_c < 6$ are shown in Appendix 3.4.

The evidence for predictor variable effects is summarised for various taxa in Table 3.4, which shows the ranking of null models, and the coefficient point estimate, standard error and relative importance of all variables whose standard error was smaller than the estimate. Standard errors larger than the point estimate include zero within their range; in such cases there is little evidence that the predictor variable affects animal activity rates.

Table 3.4. Null model rank (ΔAIC_c) and the model-averaged coefficient point estimate, standard error and relative importance of variables with standard error smaller than the estimate. Null models with ΔAIC_c>6, shown in bold, may confidently be discounted. Relative importance (Rel. Imp.) is calculated as the sum of Akaike weights over all models in which the term appears; the number of models in which the term is featured is shown (x/y). The P-value – indicating whether the coefficient estimate is significantly different from zero – is shown for near-significant cases (P<0.15) and in bold where P<0.05. Abbreviated candidate model variables: DClr—distance from clearing; LT50/LT100—less/more than 50/100 m from clearing; DRd—distance from road; LR20/LR50/LR100—local relief at the 20, 50 or 100 m radius scales; Elev—elevation; CC—canopy cover; TP—topographic position.

Taxa/sites	Null model ΔAIC_c	Variable	Estimate (SE)	Rel. Imp. (no. models)	*P*
Mammals					
Dasyurids (all) all sites	2.899	DRd	0.002(0.001)	0.73(8/15)	
Dasyurids (all) Arakubi	2.079				
Echymipera Arakubi	1.493	LT100	-0.656(0.610)	0.67(17/30)	
Peroryctes all sites	**8.987**	LR50	-0.023(0.019)	0.67(6/8)	
		CC	0.113(0.112)	0.58(4/8)	
Peroryctes Arakubi	Best				
Peroryctes KP107	**7.813**	LT50	1.073(0.466)	0.96(8)	**0.030**
Peroryctes Hides Low	0.998				
Peroryctes Hides High	2.609	LT100	-0.462(0.394)	0.71(9)	
Microperoryctes BAA1	Best				
Dorcopsulus all sites	4.440	LT50	1.267(1.134)	0.78(6/12)	
Dorcopsulus Arakubi	4.125	LR20	-0.089(0.054)	0.85(16/23)	0.112
Dorcopsulus KP107	Best				
Dorcopsulus Hides Low	**9.076**	LR50	0.039(0.017)	0.87(2/3)	**0.025**
		CC	0.320(0.082)	1.00(3/3)	**0.001**
Dorcopsulus Hides High	Best				
Anisomys KP107	Best				
Anisomys Hides High	0.970				
Mallomys Hides High	Best				
Uromys anak BAA 1	1.075	CC	0.261(0.231)	0.65(10/19)	
U. caudimaculatus BAA 2	2.171				
Leptomys KP107	4.525	LR50	-0.097(0.045)	0.91(6/8)	**0.038**
Paramelomys all sites	**7.712**	LR20	0.072(0.026)	1.00(7/7)	**0.006**
Rattus BAA 1	0.607				
Birds					
Casuarius BAA 2	Best				
Aepypodius KP107	Best				
Aepypodius Hides High	Best				
Talegalla BAA 2	**11.089**	DClr	0.008(0.008)	0.99(8/9)	
Megapodius BAA 2+Hides Low	0.506	LR20	-0.042(0.042)	0.61(12/22)	
Scolopax Hides High	4.603	Elev	-0.043(0.019)	0.95(6/16)	**0.033**
Gallicolumba Arakubi	2.920				
Alopecoenas Hides High	Best				
Otidiphaps BAA 2	3.911				
Erythropitta KP107	0.896				

Taxa/sites	Null model ΔAIC_c	Variable	Estimate (SE)	Rel. Imp. (no. models)	*P*
Orthonyx BAA 1	4.763	LR100	-0.057(0.046)	0.67(12/21)	
Ptilorrhoa castanonota BAA 2	0.199				
Aleadryas BAA 1	0.764				
Ornorectes BAA 2	Best				
Melampitta lugubris Hides High	**10.872**	LT100	-1.700(0.432)	1.00(11/11)	**<0.001**
Heteromyias BAA 1	Best				
Drymodes BAA 2	Best				
Amalocichla sclateriana Hides High	1.798	TP	-0.971(0.921)	0.63(7/16)	
A. incerta Hides Low	3.099	CC	0.621(0.430)	0.79(5/10)	
Zoothera KP107	Best				

The null model was among the best-ranked models (ΔAIC_c<2) in 24 reduced model-sets analysed across 21 species (three species having separate analyses performed for different sites), and was the best-ranked model in 14 model-sets (13 species) (Table 3.4; Appendix 3.3). In such cases there is little evidence for an effect of any investigated predictor variable. The null model was readily discounted (ΔAIC_c>6) from only six model-sets (five species).

Model averaging revealed 20 cases where a predictor variable's coefficient point estimate was larger than the standard error (Table 3.4). In seven of these cases the point estimate was significantly different from zero, and in six of these the null model was readily discounted (ΔAIC_c>6). Most of these cases (5/7) involved environmental (non-distance measure) variables, with terrain (local relief) factors significant in three cases, and canopy cover and within-site elevation each significant in one case (Table 3.4).

The following results and discussion focus on the influence of distance measure variables. A detailed treatment of environmental covariate effects is beyond the scope of this study, and subsequent assessment of environmental variables is limited to cases where this provides context to understanding edge effects.

Evidence for edge effects

There were seven cases (in six species) where a distance measure's point estimate was larger than its standard error (Table 3.4). In two of these cases the coefficient point estimate was significantly different from zero—Raffray's Bandicoot (*Peroryctes raffrayana*; Figure 3.18) at KP107 and Lesser Melampitta (*Melampitta lugubris*; Figure 3.44) at Hides High. In most other cases the null model was either among the best-ranked models (ΔAIC_c<2: *Echymipera* at Arakubi) or could not readily be discounted (2<ΔAIC_c<6: dasyurids, all sites; Raffray's Bandicoot, Hides High; Small Dorcopsis, all sites). In the following accounts, the evidence for edge effects is summarised for each taxon in which a distance measure's point estimate was larger than its standard error. These are further assessed, along with alternative potential explanations, in the Discussion.

***Dasyurids* (all genera)**

Examining marsupial carnivore activity across all sites, distance from the nearest road (DRd) was present in all six best-ranked models (ΔAIC_c<2) and was the most influential variable after model averaging (Table 3.4; Appendix 3.3). Dasyurid activity was significantly higher away from roads, and this effect was consistent when DRd was modelled alone (*P*=0.0082; Figure 3.4) and after controlling for other covariates that featured in the best-ranked models (CC, Elev and TP; Appendix 3.3; DRd—all *P*<0.01). While suggestive of a road-avoidance pattern, the null model was only marginally worse than the best-ranked models (ΔAIC_c=2.899) and is thus not easily rejected.

The interaction term Elev*DRd featured just outside the best-model set (ΔAIC_c=2.76), indicating a possible site-based difference in the influence of this distance measure on dasyurid activity. A site-level test (all site data: GLMM Site*DRd) revealed the DRd effect to be significant only at Arakubi: Arakubi – *P*=0.027, KP107 – *P*>0.35, Hides Low – *P*>0.40, Hides High – *P*>0.11). However, when the Arakubi data were tested separately, model averaging yielded no variables with a point estimate larger than the standard error and, again, the null model was not easily rejected (ΔAIC_c=2.079; Table 3.4). Running the best-ranked models, the DRd effect was marginally non-significant (*P*=0.054) after controlling for the more influential covariate LT100 which showed a non-significant reverse trend toward more dasyurid activity closer to clearings (<100 m; *P*=0.08–0.13 in various models).

Overall, while data from all sites are initially suggestive of an edge effect, the response patterns for this group are as yet unclear.

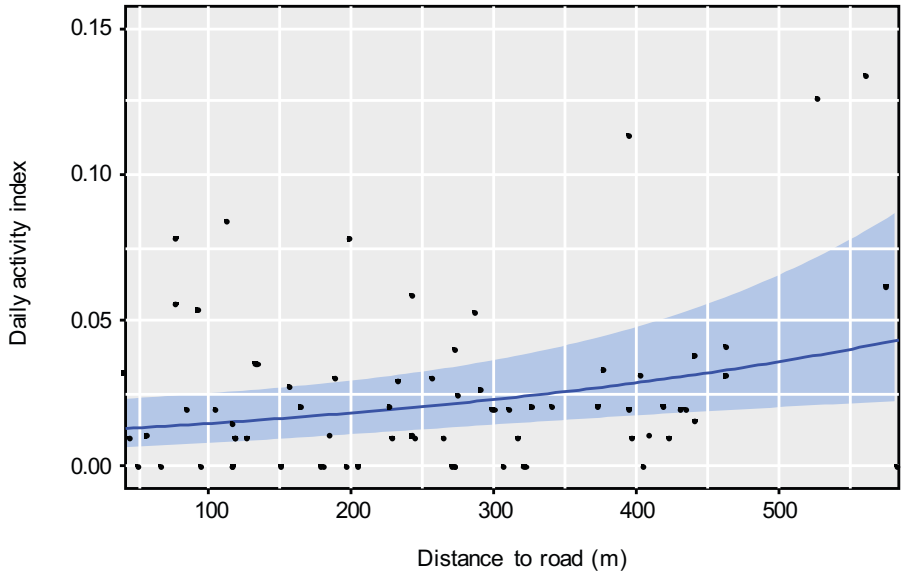

Figure 3.4. The relationship between dasyurid activity (all sites) and distance from the nearest road.

Echymipera* cf. *kalubu

Echymipera data were sufficient for analysis only at Arakubi where there was no evidence of an adverse edge effect on this bandicoot species. The null model was among the best-ranked models (ΔAIC_c=1.493) and the LT100 distance measure, the most important variable after model averaging, showed a non-significant trend toward more activity within 100 m of the nearest clearing (GLMM LT100: *P*=0.057).

Raffray's Bandicoot (*Peroryctes raffrayana*)

Analysing data across sites, distance measures were not among the most important model-averaged predictor variables (Table 3.4). However, support for the interaction term DClr*Elev (present among the two best-ranked models, relative importance = 0.31, null model ΔAIC_c=8.987) suggested a possible difference among sites in the influence of distance measures.

Site-level multi-model comparisons revealed no effect of any predictor variable at Arakubi and Hides Low (Table 3.4). At KP107, LT50 was the most important variable with a point estimate significantly different from zero and significantly higher bandicoot activity at distances more than 50 m from the nearest clearing (GLMM LT50: *P*=0.008; Figure 3.5). The reverse pattern was observed at Hides High where there was more activity within 100 m of clearings (GLMM LT100: *P*=0.032; Figure 3.5). At this site the LT100 measure featured in all 3 best-ranked models, though these were only marginally better than the null model (ΔAIC_c=2.609).

This inconsistent pattern in the response of a single species to infrastructure at different sites may also be explained by terrain effects. This potentially confounding issue is discussed below (Discussion).

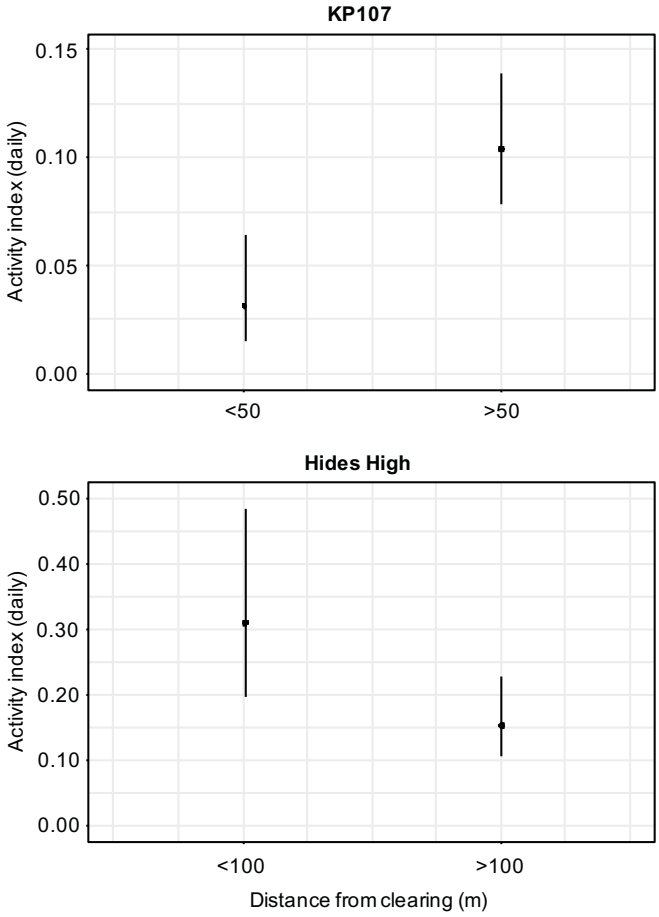

Figure 3.5. Comparison of Raffray's Bandicoot activity at various distances from the nearest clearing at KP107 and at Hides High.

Small Dorcopsis

This IUCN Near Threatened species showed initial evidence of an edge effect across its range (all sites) with the LT50 distance measure present in both best-ranked models and a model-averaged estimate of 1.27 times more activity at distances more than 50 m from the nearest clearing. The interaction between elevation and LT50 was present in both best models (relative importance = 0.51), indicating a site-based difference in the influence of this distance measure. Site-level tests showed the effect to be significant only at Arakubi (GLMM Site*LT50: Arakubi – *P*=0.017, KP107 – *P*=0.119, Hides Low – *P*=0.303, Hides High – *P*=0.344), and a reverse (non-significant) pattern at Hides High where the average activity rate was higher nearer to Project infrastructure (Figure 3.6), explaining the interactive effect.

Site-level multi-model comparisons revealed that different variables were influential at each site (Table 3.4; Appendix 3.3 and 3.4). At Arakubi, the LT50 distance measure was no longer the most influential variable; rather, local relief at the 20 m radius scale showed the strongest effect at this site, with more activity at camera stations located on gentler terrain (GLMM LR20: *P*=0.015). No distance measures were influential at other sites.

Detailed analysis thus shows inconsistent evidence for an edge effect on Small Dorcopsis activity. Terrain effects provide a viable alternative explanation for the observed pattern, and these are discussed below (Discussion).

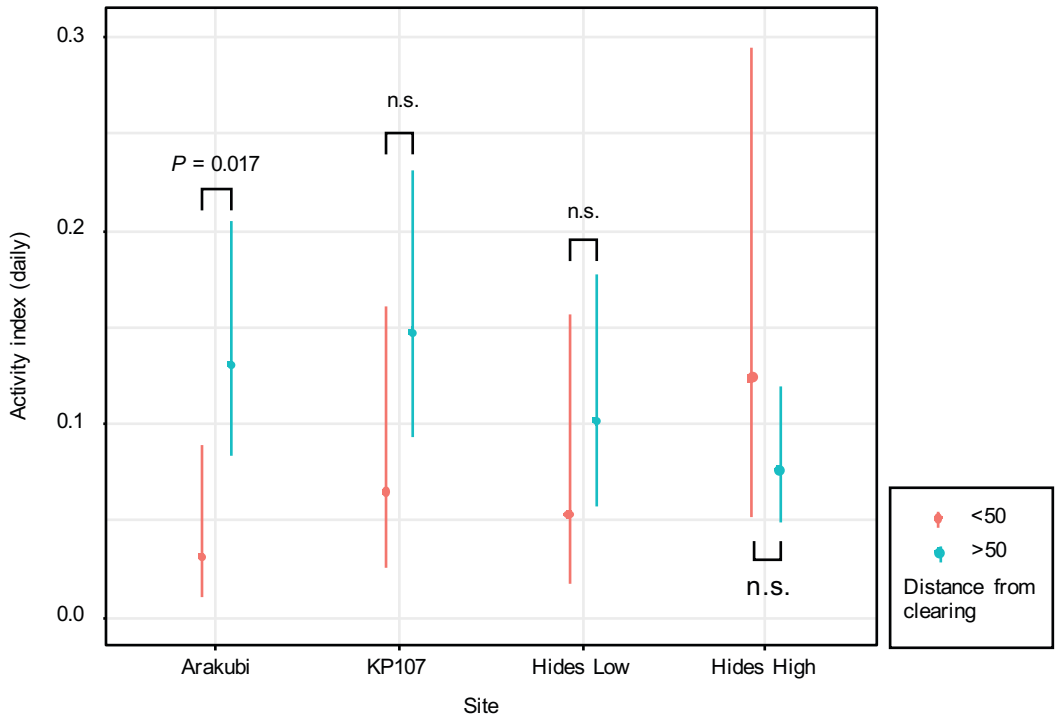

Figure 3.6. Per-site comparison of Small Dorcopsis activity at distances of less than 50 m and more than 50 m from the nearest clearing.

Collared Brushturkey (*Talegalla jobiensis*) (Figure 3.32)

There was some evidence of an edge effect for this megapode with more activity away from clearings at both BAA 2 sites. The DClr distance measure was the most influential variable after model averaging and was present in all five best-ranked models, all of which were clearly better than the null model (Table 3.4; Appendix 3.3). Brushturkey activity rates were significantly higher away from clearings, and this effect was consistent when DClr was modelled alone (P=0.0003; Figure 3.7) and after controlling for other covariates that featured in the best models (Elev and CC; Appendix 3.3; DClr—all GLMMs P<0.001).

The interaction between elevation and DClr was present in the fourth best model (ΔAIC_c=1.89), indicating a possible site-based difference in the influence of this distance measure. However, site-level tests showed the effect to be significant at both sites (GLMM Site*DClr: Arakubi – P=0.002; KP107 – P=0.017).

Despite the consistent performance of the DClr measure, its influence is difficult to disentangle from terrain effects since local relief measures are collinear with distance from clearings at these sites. This potentially confounding issue is discussed below (Discussion).

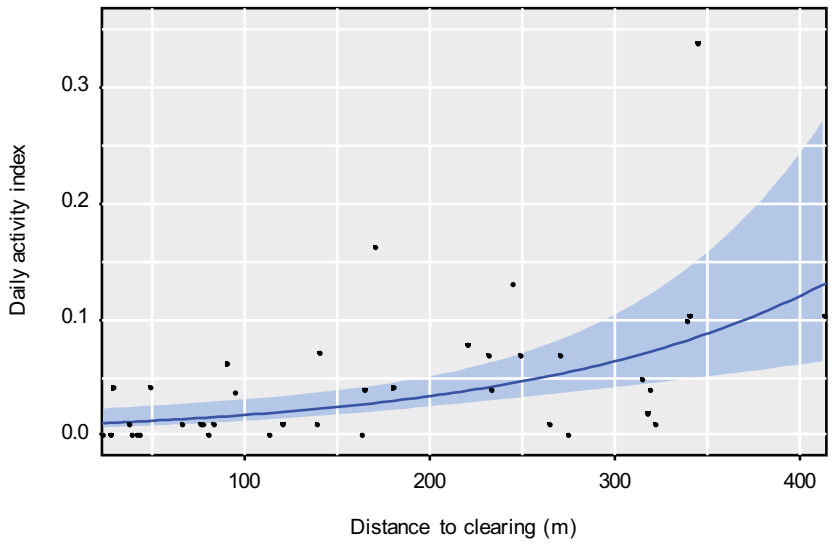

Figure 3.7. The relationship between Brushturkey activity and distance from the nearest clearing at BAA 2.

Lesser Melampitta (*Melampitta lugubris*)

Lesser Melampitta activity showed a reverse edge effect with higher activity rates nearer to infrastructure clearings (within 100 m) at Hides High ($P<0.001$; Figure 3.8). The LT100 distance measure was strongly supported, appearing in all 11 models with $\Delta AIC_c<6$ (relative importance = 1.0), and the null model was readily rejected ($\Delta AIC_c>10$).

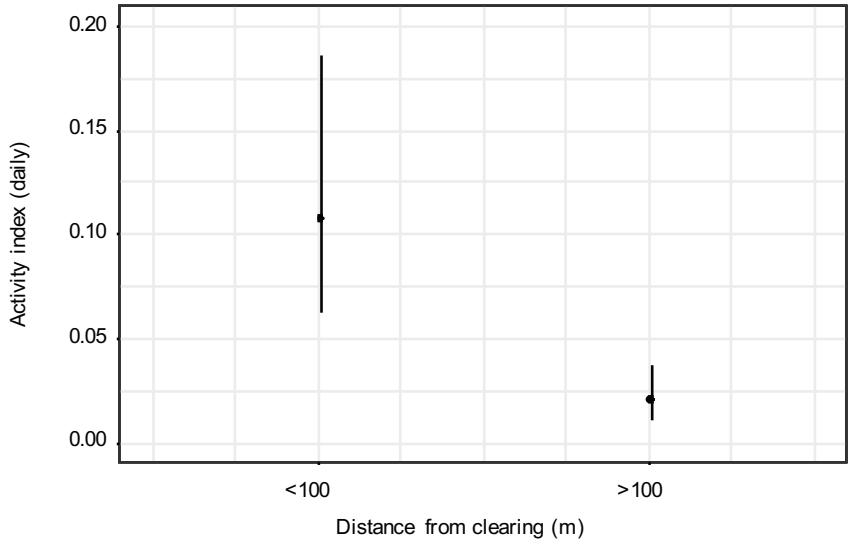

Figure 3.8. Comparison of Lesser Melampitta activity at distances of less than 100 m and more than 100 m from the nearest clearing at Hides High.

Human/dog incursions and evidence for hunting

Event rates for humans and dogs were highest at the BAA 1 sites (Appendix 3.2). Examination of the photographs revealed five recognisable groups of people and/or dogs entering the forest on nine occasions:

- Group A—One man with a bush-knife and two dogs, photographed at Hides Low on 25 May. The same two dogs were photographed at Hides High on 12 June, 26 June and 24 July. This was the most frequently recorded hunting group at BAA 1.

- Group B—Three men with axe and bush-knives and three dogs, recorded at Hides High on 16 August. This group was carrying a freshly killed long-beaked echidna (Figure 3.29).

- Group C—Two young men with a slingshot at Hides Low on 11 July.

- Group D—A distinctive dog photographed alone at Hides Low on 15 June.

- Group E—A distinctive dog photographed alone at Hides Low on 10 and 13 August.

It is unknown whether the dogs of group D and E are feral or are owned by local residents.

Fewer forest incursions were recorded at the BAA 2 sites. At Arakubi, three people were photographed at a single camera position (two groups, separate dates) and the development of a garden near the access road cut short the deployment time of two camera traps. No people were camera trapped at KP107, and no dogs were photographed at either of the BAA 2 sites.

Site-based activity rates are shown for nine-hunting sensitive taxa in Figure 3.9. For most species (5/6) whose distribution spans all sites, average daily activity rates are lower at the BAA 1 sites where a higher rate of human/dog incursions was recorded. The exception is the Small Dorcopsis, the most abundant terrestrial vertebrate across the study area. For the remaining five study area-wide species – the Eastern Long-beaked Echidna, two species of tree kangaroo, Dwarf Cassowary (*Casuarius bennetti*) and Wattled Brushturkey (*Aepypodius arfakianus*) – pooled activity rates are shown in Figure 3.10. Event rates for these species were lowest at Hides Low, and significantly lower there than at all other sites (GLMM Hides Low cf.: Arakubi – P=0.001; KP107 – P=0.003; Hides High – P=0.026) (the loss of the seven cameras from Hides Low does not influence this results as the data are averaged over camera position).

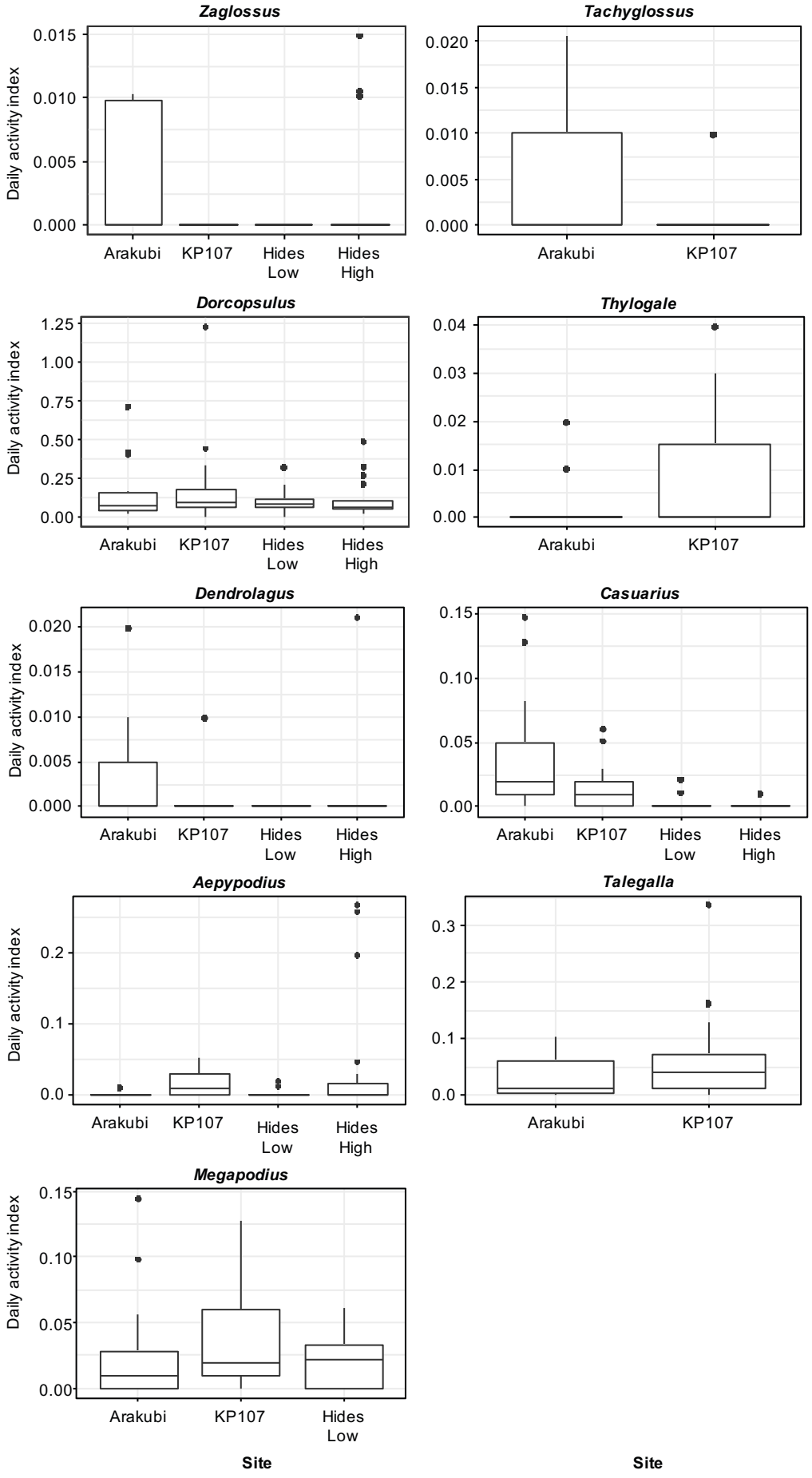

Figure 3.9. Activity rates recorded for nine hunting sensitive taxa at different sites across their elevational range—Eastern Long-beaked Echidna (*Zaglossus*), Short-beaked Echidna (*Tachyglossus*), Small Dorcopsis (*Dorcopsulus*), Pademelon (*Thylogale*), tree kangaroos (*Dendrolagus*, data for two species combined), Dwarf Cassowary (*Casuarius*), Wattled Brushturkey (*Aepypodius*), Collared Brushturkey (*Talegalla*) and New Guinea Scrubfowl (*Megapodius*).

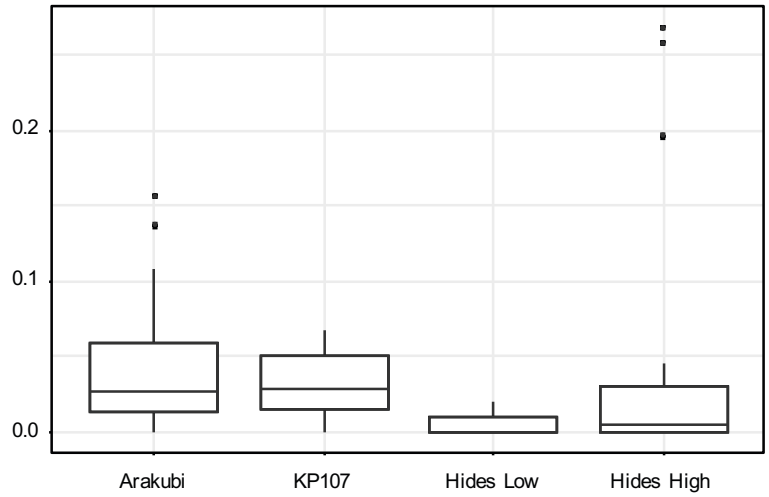

Figure 3.10. Combined site-based activity rates for hunting sensitive species whose distribution spans all sites; Small Dorcopsis data excluded.

Discussion

Species richness

This study provides good coverage of the local diversity of terrestrial birds and medium-to-large terrestrial mammal species as well as useful information on small mammal diversity and a number of arboreal mammal species not previously recorded in the study area. Species photographed in 2015 and 2017 include the majority of terrestrial bird and mammal taxa expected to occur in the study area – only one terrestrial species camera trapped during the 2015 pilot study, the Waterside Rat (*Parahydromys asper*), was not recorded in 2017 (Woxvold and Aplin 2017) – and the 2017 deployment period of 90–102 days was sufficient to collect statistically useful datasets for 31 of the more common taxa.

In terms of unrecorded species, small non-volant mammals are likely to be the most under-represented group. A number of (at least partly) terrestrial, forest-dwelling murid genera that are known to be regionally present are yet to be recorded, such as *Coccymys*, *Macruromys*, *Mammelomys*, *Melomys*, *Microhydromys*, *Pseudohydromys* and *Xenuromys* (Denys et al. 2017). Other predominantly arboreal taxa such as *Abeomelomys* may occasionally be captured on the ground. At least some of these taxa may be recognised in good quality images. Additionally, there is hidden diversity among individuals already photographed, with taxa such as *Murexia* and all of the small murid genera recorded in this study being rather cryptic in appearance so that trapping would be required to accurately determine the number of species represented.

Camera traps are proving increasingly important in the detection and monitoring of rare and elusive terrestrial mammal and bird species (Meek and Fleming 2015; Rovero and Zimmerman 2016b; Beirne et al. 2017), and this study further illustrates the advantage of camera traps in detecting such taxa. Animals photographed in 2017 include 13 species which have not been previously recorded in the BAAs, including three IUCN Threatened species, one of which (Pademelon sp.) was not previously known from the PNG LNG Upstream Project area. Two notable ornithological discoveries, involving previously unknown taxa/populations, are also reported. Included among the most frequently detected species are a number of animals for which few behavioural ecological data are currently available, such as various dasyurids, the IUCN Near Threatened Small Dorcopsis, Woolly Giant Rat (*Mallomys* sp.; Figure 3.27), Black-tailed Giant Rat (*Uromys anak*) and birds such as the New Guinea Woodcock (*Scolopax rosenbergii*; Figure 3.34), Papuan Logrunner (*Orthonyx novaeguineae*; Figure 3.41), Greater Ground Robin (*Amalocichla sclateriana*) and New Guinean populations of the Russet-tailed Thrush (*Zoothera heinei*; Figure 3.47) (Baker 2015; Eldridge and Coulson 2015; Denys et al. 2017; HBW Alive 2018). Sufficient data were available for these species to statistically model activity rates in response to various predictor variables.

Edge effects and confounding factors

Anthropogenic infrastructures have been shown to influence the presence and behaviour of a variety of animal species (Laurance and Bierregaard 1997; Laurance et al. 2004; Leblond et al. 2013; van der Ree et al. 2015), and camera trapping has successfully been used to demonstrate behavioural responses to infrastructure or forest edge in multiple taxa (e.g. Leblond et al. 2013; Martin et al. 2015; Oberosler et al. 2017; da Silva et al. 2018). We have summarised the evidence for edge effects in six species where the results of model averaging showed that a distance measure's point estimate was larger than its standard error. Evidence was strongest for three species/sites in which the null model was readily rejected—Raffray's Bandicoot at KP107, Collared Brushturkey at BAA 2 and Lesser Melampitta at Hides High. The case for edge effects was less compelling where the null model was among the best supported models ($\Delta AIC_c<2$; Echymipera at Arakubi) or where it could not be readily be discounted ($2<\Delta AIC_c<6$; marsupial carnivores (dasyurids) at all sites, Raffray's Bandicoot at Hides High, Small Dorcopsis at all sites).

The direction of effect (positive/negative) associated with proximity to infrastructure varied both among and within species. For five of the taxa modelled above, Figure 3.11 summarises the direction of effect of an increase in distance from the nearest clearing on activity rates at various sites (dasyurid activity is excluded as it was related to distance from the nearest road and the pattern was observable only across all sites). In general, the direction of effect was more consistent within sites than it was within species, with a reverse-effects pattern observed between the two BAAs—in most cases, activity rates were lower nearer to clearings at the BAA 2 sites (Arakubi and KP107, 4/5 cases), while activity rates were higher nearer to clearings at Hides High (3/3 cases). In both species whose distribution spanned both BAAs (Raffray's Bandicoot and Small Dorcopsis), the direction of effect changed between sites.

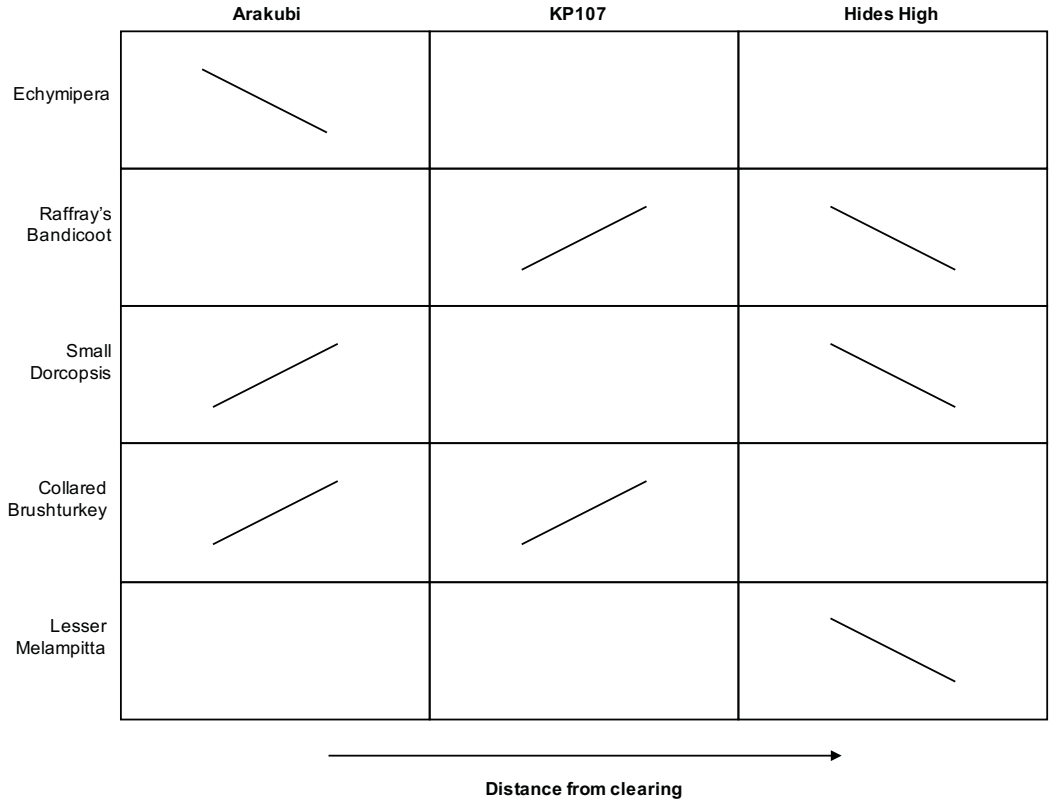

Figure 3.11. Schema of the direction of effect of an increase in distance from the nearest clearing (DClr, LT50, LT100) on animal activity rates. The relative magnitude of effect is not shown.

The observation of higher Echymipera activity near clearings at Arakubi runs counter to this broader trend. It is consistent with the Common Echymipera's preference for open and disturbed habitats (Flannery 1995; Dickman 2015), although with the null model among the best-ranked ($\Delta AIC_c=1.493$), more data are required to confirm this pattern.

For the remaining species depicted in Figure 3.11, the consistent difference in response to infrastructure observed between the BAAs is of some interest and there are a number of possible explanations.

First, the pattern may be anthropogenic if near-edge disturbance levels are higher at the BAA 2 sites. Human disturbance is very difficult to quantify (da Silva et al. 2018), and distance from settlements is sometimes used as a proxy measure (e.g. Oberosler et al. 2017). Across the study area, settlement distance increases with elevation so that the BAA 2 sites are positioned closest to the nearest village (mean straight-line distances from various camera positions: Arakubi—1.7 km, KP107—2.7 km, Hides Low—3.6 km, Hides High—5.7 km). However, the BAA 2 sites yielded the highest photographic event and naïve occupancy rates for a suite of notoriously hunting-sensitive IUCN listed mammals, including the Eastern Long-beaked Echidna, Pademelon, Small Dorcopsis and two species of tree kangaroo. An anthropogenic disturbance-based explanation thus appears not to be well supported.

Second, it is possible that climatic differences between the two BAAs may influence the degree of microclimate change experienced within near-edge forest environments. Hides Ridge receives 'continuously heavy' rainfall with little seasonality (McAlpine et al. 1983), and the persistently wet and cloudy conditions may limit the potential for floristic or structural change to near-edge forest habitats. However, the climate at BAA 2 is similar and receives the same or slightly higher total annual rainfall (Bryan and Shearman 2008). Moreover, preservation of near-edge environments at BAA 1 does not explain the preference for these habitats in some species, particularly where the same taxa show reverse patterns at BAA 2.

An alternative explanation may lie in terrain effects. At all sites, most or all measures of terrain steepness (local relief) were strongly correlated with distance from clearing (Table 3.5). However, the direction of this relationship was reversed across BAAs, with steeper terrain present closer to clearings at BAA 2 and further from clearings at BAA 1. Thus, observations of higher animal activity rates further from clearings at the BAA 2 sites, and reverse patterns at Hides High, may be explained by an aversion to the steepest ground, with animals responding to a natural 'experimental' variation in the relationship between terrain and infrastructure distance across the BAAs.

Table 3.5. The relationship between distance from the nearest clearing and local relief at each BAA and site. Local relief was measured across 20 m (LR20), 50 m (LR50) and 100 m (LR100) radii from each functioning camera position. Numbers show Pearson Correlation Coefficients and associated *P*-values.

BAA/site	LR20	LR50	LR100
BAA 1	**0.48, *P*=0.005**	**0.63, *P*<0.0001**	**0.67, *P*<0.0001**
Hides Low	0.51, *P*=0.076	**0.75, *P*=0.003**	**0.82, *P*<0.001**
Hides High	**0.46, *P*=0.044**	**0.53, *P*=0.016**	**0.53, *P*=0.016**
BAA 2	**-0.46, *P*=0.004**	**-0.46, *P*=0.004**	-0.27, *P*=0.105
Arakubi	-0.44, *P*=0.095	**-0.53, *P*=0.021**	**-0.58, *P*=0.009**
KP107	**-0.49, *P*=0.035**	**-0.47, *P*=0.044**	0.19, *P*>0.4

Steepness of terrain is known to influence the abundance and behaviour of a variety of terrestrial fauna (e.g. Namgail et al 2004; Oberosler et al. 2017). In this study, the case is particularly compelling for Raffray's Bandicoot and Small Dorcopsis, both of which shifted their response to clearing distance across sites while maintaining their relationship with terrain factors. In further support, when Raffray's Bandicoot activity was analysed across all sites, local relief at the 50 m scale proved the most important predictor variable, and when Small Dorcopsis activity at Arakubi was analysed separately, local relief at the 20 m scale was the most important predictor (Table 3.4). For the Collared Brushturkey, while local relief measures did not feature strongly in the model averaged results (Appendix 3.4), separate modelling of terrain factors showed there was significantly less activity on steeper ground at the 20 m scale (GLMM LR20: *P*=0.014). Thus, for all three species in which there is initial evidence for avoidance of forest clearings (shown in Figure 3.11), terrain effects offer a viable, and in some cases statistically preferred, alternative explanation. While in some cases terrain factors were

not included among the best models (for example, Collared Brushturkey), this does not necessarily preclude them as important—it may simply be that the data used to represent these factors (local relief at various scales) is an imprecise measure of the terrain feature to which the animal is responding.

In addition to those species showing an apparent response to infrastructure distance (Figure 3.11), local relief proved the most important predictor of activity rates in a number of other species analysed in this study. The Large Leptomys at KP107, New Guinea Scrubfowl at BAA 2 and Hides Low, and the Papuan Logrunner at BAA 1 all showed higher rates of activity in gentler terrain (Table 3.4).

Rather than responding to distance from clearings, the marsupial carnivore group (dasyurids) showed a reduction in activity rate nearer to roads (data from all sites). The impact of roads on wildlife has been well studied (Andrews et al. 2015; van der Ree et al. 2015) and includes processes not relevant to other linear corridors (for example, a pipeline ROW) such as traffic-related noise, lights and roadkill (Clevenger et al. 2003; Latham and Boutin 2015; Parris 2015). Accordingly, a number of studies have shown that wildlife avoid roads (Trombulak and Frissell 2000; Leblond et al. 2013). In the present study, response patterns of dasyurids are as yet unclear—the full dataset null model was not easily rejected and site-level tests failed to show a clear pattern of avoidance. In this case a genuine avoidance trait may be obscured by a lack of data and/or the pooling of species with different behavioural traits. For example, the New Guinea Quoll and *Murexia* species are predominantly nocturnal, while Woolley's Three-striped Dasyure, Speckled Dasyure (*Neophascogale lorentzi*) and Narrow-striped Dasyure (*Phascolosorex dorsalis*; Figure 3.17) are mostly diurnal (Baker 2015; this study). Individual species may respond differently to various impact processes. For example, with most Project vehicle traffic occurring during the day, diurnal species may be more susceptible to road noise than those active at night (da Silva et al. 2018). The dasyurid behavioural patterns reported here are best considered preliminary, with more data on these uncommon top-level predators required to determine the responses of individual taxa at various sites. As more data become available, the issue of confounding terrain factors will again come into play at the BAA 1 sites (less so at BAA 2), where the distance from roads is positively correlated with local relief (all relief measures $P<0.001$). If dasyurids respond negatively to steep terrain at BAA 1, a real effect of roads may be obscured.

Can infrastructure distance and terrain effects be untangled? In the absence of pre-construction data from these sites, and control data from comparable habitats lacking infrastructure, the task may be difficult. Such data allow a comparison of trajectories in animal behaviour before and after the impacting event, providing for stronger inference of predictor variable effects (Smith 2002; Smokorowski and Randall 2017). Nevertheless, sampling in subsequent years will improve the resolution of the available dataset, and may allow for (1) improved confidence in ranking the influence of various predictor variables for those species whose behavioural patterns have already shown a correlation with infrastructure distance measures, and (2) detailed analysis of additional taxa for which sufficient data are not yet available.

Hunting impacts

Hunting of terrestrial wildlife is a core pursuit in subsistence cultures across New Guinea, and has contributed to the decline of many bird and mammal species, including all of the IUCN Threatened taxa recorded in this study and the Near Threatened Small Dorcopsis (IUCN 2018). Dogs have been implicated in terrestrial wildlife declines in many tropical regions (e.g. Cassano et al. 2014; Lessa et al. 2016) and are often used as a hunting tool by local landowners (pers. obs.; Nicol 2015; Eldridge and Coulson 2015; Leary et al. 2016).

During this study, the highest rates of human/dog forest incursions were recorded at the BAA 1 sites, where a photographic sequence from Hides High confirmed the capture of an Eastern Long-beaked Echidna by a party of three men and three dogs. These results are consistent with lower photographic event rates recorded for hunting-sensitive species at the BAA 1 sites. Sensitive species were rarest at Hides Low, where pooled activity rates of Eastern Long-beaked Echidna, two species of tree kangaroo, Dwarf Cassowary and Wattled Brushturkey were significantly lower than at all other sites, including Hides High.

Permanent settlements are further from BAA 1 than BAA 2. However, all sites are within 6 km of the nearest settlement, well within range of hunting forays, and Hides Ridge is regularly visited by local landowners, as indicated by multiple photographic sequences and the theft of seven cameras from Hides Low. In addition to these incursions, a caretaker permanently stationed at an OilSearch facility near Hides Low owns a number of hunting dogs and has indicated (pers. comm. to IW) that they hunt in the bush there and regularly catch a variety of game. It is possible that this is the hunting 'Group A' (reported above) photographed on multiple occasions and observed at both Hides Low and Hides High.

Hunting pressure is difficult to quantify, and impacts on local wildlife populations are, in most cases, measurable only across a considerable period of time. While the available data are suggestive of an influence of hunting on the Hides Ridge wildlife, especially at Hides Low, without a comparable pre-construction dataset there is no way to accurately quantify the impact that hunting has had to date, or the potential influence of Project development. The 2017 dataset provides a useful baseline against which to measure future changes.

Sampling design and analytical approach

With a variety of infrastructure types present in non-uniform overlapping arrays (roads and pipeline ROW; Figures 3.1–3.2), and accurate measures of disturbance lacking (traffic loads on different roads, hunting pressure, human visitation rates), the interpretation of results across species and sites is difficult. To help tease apart these effects, we have tested a variety of distance measure variables, including a distinction between road and clearing effects, and where data permit, we have modelled effects separately at different sites. Model rankings (using AIC_c) are often used to assess which 'class' of covariate is the most influential (e.g. edge effects, terrain factors, vegetation aspects), and the multi-model comparison and model averaging approach employed here has been used in a number of similar recent studies (e.g. O'Brien and Kinnaird 2008; Rovero et al. 2014; Murphy et al. 2017; Oberosler et al. 2017).

The use of 'relative abundance indices' (RAIs), such as the activity rate response variables examined here, as a surrogate estimate for the population density of unmarked species (whose individuals cannot be told apart on camera trap images) has received a good deal of criticism (e.g. O'Brien 2011; Sollman et al. 2013; Burton et al. 2015). Much of this criticism stems (1) from the assumption that, in order to accurately compare and estimate population densities, detectability (p) – the probability of detection given an animal's presence within the home range – must be constant among species, space and time, and (2) from the difficulty in standardising surveys over time and space to effectively control for unmodelled variations in detectability.

However, the main objective of the present study is not to estimate the population density/abundance of detected species, but rather to examine their distribution and use of habitats over time and space in relation to Project components and associated forest clearings. We acknowledge that changes in photographic rate do not always accurately reflect changes in local abundance (though in a number of cases they have been shown to: e.g. Carbone et al. 2001; O'Brien et al. 2003; Rovero and Marshall 2009), but consider that potentially confounding factors are most influential when comparing activity rates between species and between sites. With repeat sampling from a standardised design, and where analysis is restricted to comparing RAIs within species and within sites, changes in the RAI are considered to provide a reliable indication of the direction of the change (increase, decrease) in a species' local population density (O'Brien 2011). In this study, we have not used activity rates to infer differences in abundance between species, and where site-based effects were suspected, we have modelled activity rates for each site independently where sufficient data are available. Because the close spacing of our sampling positions means that individuals of many (or all) species may be detected on more than one camera, capture rates are used to assess variation in spatial activity patterns rather than changes in actual abundance. Relative abundance indices have been similarly used in other studies to examine species-specific habitat associations (e.g. Martin et al. 2015).

Our sampling strategy employed a mix of systematic deployment design with an opportunistic approach to camera placement while considering terrain and vegetation parameters that may influence the probability of detection among camera stations within sites—by always placing cameras on animal trails and away from other natural attractants (e.g. fruiting trees), and by standardising their position within the local landscape (ridges and broad terraces rather than valley floors and gullies). Within sites, we have further controlled for environmental factors that may influence detectability among camera stations by modelling terrain variability (topographic position, local relief), and by including elevation and canopy cover as surrogates for changes in vegetation characteristics among stations. In future surveys, it is further considered reasonable to compare activity rates over time at the same site as variation in *p* is likely to be small within species and at within sites over time (O'Brien 2011).

Conclusions

1. The 2017 camera trap study represents the first full year of sampling using this efficient and effective monitoring tool. The results have improved our knowledge of vertebrate diversity within the study area and across the broader PNG LNG Upstream Project Area; animals photographed include 13 species not previously recorded in the BAAs, including three IUCN Threatened mammal species – the Eastern Long-beaked Echidna, the Pademelon and Goodfellow's Tree Kangaroo – and two notable bird discoveries.

2. The majority of terrestrial bird and mammal taxa expected to occur in the study area have been recorded, and the deployment period of 90–102 days was sufficient to collect statistically useful datasets for 31 of the more common species and genera. Longer deployment times may increase the number of taxa for which detailed analysis is possible within sampling years.

3. There was no unequivocal evidence that edge effects influence the presence or behaviour of any species. Multi-model comparisons and model averaging revealed a notable correlation between animal activity rates and distance from infrastructure (roads or clearings) in six species. However, in most cases terrain effects offer an alternative and parsimonious explanation, with observed patterns potentially explained by animals avoiding the steepest ground. In these cases it is not possible to conclusively disentangle the influence of terrain and edge effects with the current dataset. In other cases, the null model was either among the best-ranked models or could not readily be discounted.

4. The highest number of forest incursions by humans and dogs was recorded on Hides Ridge (BAA 1), where a photographic sequence confirmed the hunting capture of an Eastern Long-beaked Echidna at Hides High. These results are consistent with lower photographic event rates recorded for hunting-sensitive species at BAA 1. These species were rarest at the Hides Low site, where pooled activity rates of widespread taxa (whose geographic ranges cover all sites/elevations) were significantly lower than at all other sites. Hunting pressure is difficult to quantify, and impacts on local wildlife populations are best measured by monitoring population trends over time. The 2017 dataset provides a useful baseline against which to measure future changes.

5. Sampling in subsequent years will improve the resolution of the available dataset, and allow for: (1) improved confidence in ranking the influence of various predictor variables; (2) detailed analysis of additional taxa for which statistically useful datasets are not yet available, and; (3) monitoring of population trends in hunting-sensitive species within sites over time.

Recomendations

1. We recommend that the camera trapping program continue in 2019 and in subsequent survey years. Additional data will allow for: (1) improved confidence in ranking the influence of various predictor variables; (2) detailed analysis of additional taxa for which statistically useful datasets are not yet available, and; (3) monitoring of population trends in hunting-sensitive species within sites over time.

2. Due to deployment time constraints, few environmental covariate data were collected in 2017, with information on vegetation structure currently restricted to canopy cover. In future surveys, we will aim to collect additional information on fine-scale vegetation variables for consideration in the modelling. A relevant sampling protocol has already been developed (and trialled in other projects). To assist with collection of these data, we recommend adding one more member to the camera trapping team for the 2019 survey. A preferred candidate would be someone from BRC with vegetation sampling experience.

3. Some aspects of the R script used to analyse data in this study were developed in consultation with a biostatistician from the ARI (DELWP). Treatment of future datasets will require expansion of the analytical protocol (1) to compare data across multiple sampling events (years) and (2) to potentially separate the relative abundance index data used in 2017 into modelling of occupancy (ψ) and detectability (p) patterns. We recommend funds be made available for additional time with the ARI biostatistician to help expand the analysis protocol.

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Plate 1

Figure 3.12. Eastern Long-beaked Echidna (*Zaglossus bartoni*)

Figure 3.13. Short-beaked Echidna (*Tachyglossus aculeatus*)

Figure 3.14. New Guinea Quoll (*Dasyurus albopunctatus*)

Figure 3.15. Murexia (*Murexia* sp.)

Figure 3.16. Woolley's Three-striped Dasyure (*Myoictis leucura*)

Figure 3.17. Narrow-striped Dasyure (*Phascolosorex dorsalis*)

Plate 2

Figure 3.18. Raffray's Bandicoot (*Peroryctes raffrayana*)

Figure 3.19. Eastern Striped Bandicoot (*Microperoryctes ornate*)

Figure 3.20. Ground Cuscus (*Phalanger gymnotis*)

Figure 3.21. Long-fingered Striped Possum (*Dactylopsila palpator*)

Figure 3.22. Small Dorcopsis (*Dorcopsulus* cf. *vanheurni*)

Figure 3.23. Pademelon (*Thylogale* sp.)

Plate 3

Figure 3.24. Goodfellow's Tree Kangaroo (*Dendrolagus godfellowi*)

Figure 3.25. Western Montane Tree Kangaroo (*Dendrolagus notatus*)

Figure 3.26. White-eared Giant Rat (*Hyomys* sp.)

Figure 3.27. Woolly Giant Rat (*Mallomys* sp.)

Figure 3.28. Feral Domestic Cat (*Felis catus*)

Figure 3.29. Hunting party with freshly killed echidna.

Plate 4

Figure 3.30. Dwarf Cassowary (*Casuarius bennetti*)

Figure 3.31. Wattled Brushturkey (*Aepypodius arfakianus*)

Figure 3.32. Collared Brushturkey (*Talegalla jobiensis*)

Figure 3.33. Forbes's Forest Rail (*Rallicula forbesi*)

Figure 3.34. New Guinea Woodcock (*Scolopax rosenbergii*)

Figure 3.35. White-breasted Ground Dove (*Alopecoenas jobiensis*)

Plate 5

Figure 3.36. Bronze Ground Dove (*Alopecoenas baccarii*)

Figure 3.37. Pheasant Pigeon (*Otidiphaps nobilis*)

Figure 3.38. Shovel-billed Kookaburra (*Clytoceyx rex*)

Figure 3.39. Papuan Pitta (*Erythropitta macklotii*)

Figure 3.40. Archbold's Bowerbird (*Archboldia papuensis*)

Figure 3.41. Papuan Logrunner (*Orthonyx novaeguineae*)

Plate 6

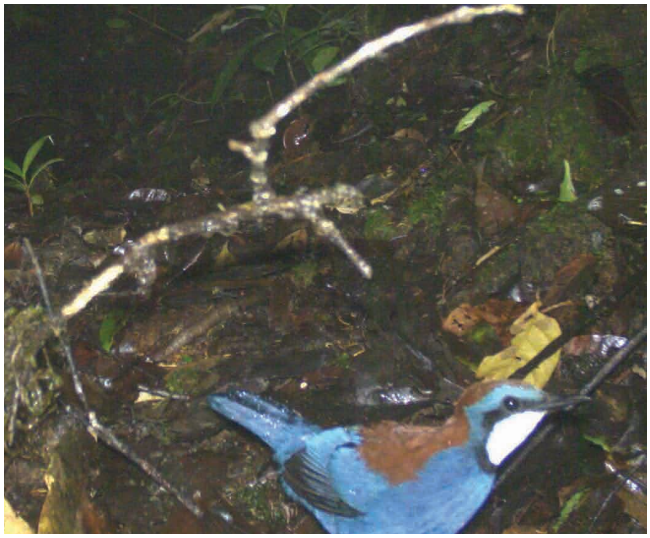

Figure 3.42. Chestnut-backed Jewel-babbler (*Ptilorrhoa castanonota*)

Figure 3.43. Spotted Jewel-babbler (*P. leucosticta*) and Rufous-naped Bellbird (*Aleadryas rufinucha*)

Figure 3.44. Lesser Melampitta (*Melampitta lugubris*)

Figure 3.45. Brown Sicklebill (*Epimachus meyeri*)

Figure 3.46. Greater Ground Robin (*Amalocichla sclateriana*)

Figure 3.47. Russet-tailed Thrush (*Zoothera heinei*)

Appendix 3.1. Variable-pairs not included in the same models due to significant or near-significant collinearity. DClr—distance from clearing; LT50/LT100—less/more than 50/100 m from clearing; DRd—distance from road; LT100Rd—less/more than 100 m from road; LR20/LR50/LR100—local relief at the 20, 50 or 100 m radius scales; Elev—elevation; CC—canopy cover; TP—topographic position. P values show results of Pearson correlation coefficient (PCC) tests.

Variable	All sites	BAA 1	Hides Low	Hides High	BAA 2	Arakubi	KP107	BAA 2 + Hides Low
Distance measures	All correlated	All correlated	Most correlated; LT100Rd not strongly collinear with DClr or DRd (P≈0.1) but not tested together	Most correlated; LT50 and LT100Rd not strongly collinear (P≈0.1) but not tested together	Most correlated; DRd not collinear with LT50 (P>0.5) or LT100 (P≈0.1) but not tested together	Most correlated, but a number of road and clearing measures testable together at this site. See below for non-testable pairs.	Most correlated; DRd not strongly collinear with LT50 (P>0.13) but not tested together	Most correlated; DRd not strongly collinear with LT50 (P≈0.1) but not tested together
DClr	TP	LR20, LR50, LR100	LR50, LR100, TP	LR20, LR50, LR100	LR20, LR50, TP	LT50, LT100, LR20, LR50, LR100, Elev	LR20, LR50, TP	TP
LT50	CC, TP	TP	LR100, TP		LR20	LT100, CC	LR20, LR100	LR20, LR100, TP
LT100		LR50, LR100	LR50, LR100	LR50	LR20	LT100Rd	LR20, TP	TP
DRd	LR20, LR50	LR20, LR50, LR100	LR20, LR50, LR100, TP	LR20, LR50, LR100	LR100	LT100Rd, LR100, Elev	CC	LR50, TP
LT100Rd		LR20, LR50	LR100	LR20, LR50		LR100, Elev	CC	
Relief measures	All correlated	All correlated	All correlated	All correlated				All correlated
LR20	TP		Elev	TP	LR50, TP	LR50	LR50, TP	
LR50	Elev		Elev	TP	LR100, Elev, TP	Elev, TP	LR100, TP	Elev
LR100	Elev		TP	TP	Elev	Elev	CC	Elev
Elevation	CC						CC	CC

Appendix 3.2. Species recorded on camera traps in 2017, their conservation status (Status), the number of independent photographic events (No. events) and naïve occupancy (ψ) at each site. Terrestrial species (Terr. = Y) include those with predominantly or entirely terrestrial habits. Conservation status indicates those species listed in the IUCN Red List of Threatened Species (IUCN 2018) as Endangered (EN), Vulnerable (VU), Near Threatened (NT) or Data Deficient (DD) and those Protected (P) under the PNG Fauna (Protection and Control) Act 1966. Species not given an IUCN category are either Least Concern (most species) or Not Evaluated.

Family	Scientific Name	English Name	Status	Terr.	No. events					Naïve ψ			
					Arakubi	KP107	Hides Low	Hides High	Total	Arakubi	KP107	Hides Low	Hides High
Mammals													
Tachyglossidae	*Zaglossus bartoni*	Eastern Long-beaked Echidna	VU, P	Y	6			3	9	0.316			0.150
Tachyglossidae	*Tachyglossus aculeatus*	Short-beaked Echidna		Y	10	2			12	0.421	0.105		
Dasyuridae	*Dasyurus albopunctatus*	New Guinea Quoll	NT	Y	13	9	6	16	44	0.474	0.421	0.308	0.600
Dasyuridae	*Murexia* spp.	Multiple *Murexia* spp.		Y	19	17	25	13	74	0.316	0.579	0.615	0.250
Dasyuridae	*Myoictis leucura*	Woolley's Three-striped Dasyure	DD	Y	4	5			9	0.211	0.211		
Dasyuridae	*Neophascogale lorentzi*	Speckled Dasyure		Y			8	9	17			0.154	0.300
Dasyuridae	*Phascolosorex dorsalis*	Narrow-striped Dasyure		Y			18	2	20			0.615	0.100
Peramelidae	*Echymipera* cf. *kalubu*	An Echymipera		Y	30	5			35	0.632	0.158		
Peramelidae	*Peroryctes raffrayana*	Raffray's Bandicoot		Y	31	167	98	457	753	0.632	0.947	0.769	1.000
Peramelidae	*Microperoryctes ornata*	Eastern Striped Bandicoot		Y		7	146	170	323		0.158	1.000	0.950
Peramelidae		Unidentified bandicoot		Y	1	10	3	3	17				
Phalangeridae	*Phalanger gymnotis*	Ground Cuscus		Y	21	14	14	5	54	0.421	0.421	0.538	0.150
Pseudocheiridae	*Pseudochirops* sp.	A Ring-tailed Possum					1	4	5				
Petauridae	*Dactylopsila palpator*	Long-fingered Striped Possum					1	3	4				
Macropodidae	*Dorcopsulus* cf. *vanheurni*	Small Dorcopsis	NT	Y	279	335	128	210	952	1.000	0.947	0.923	1.000
Macropodidae	*Thylogale* sp.	Pademelon	VU	Y	6	16			22	0.211	0.368		
Macropodidae	*Dorcopsulus/ Thylogale* sp.	Dorcopsis/ Pademelon	NT/ VU	Y	2	1			3				
Macropodidae	*Dendrolagus goodfellowi*	Goodfellow's Tree Kangaroo	EN, P		4				4	0.105			

Family	Scientific Name	English Name	Status	Terr.	No. events					Naïve ψ			
					Arakubi	KP107	Hides Low	Hides High	Total	Arakubi	KP107	Hides Low	Hides High
Macropodidae	*Dendrolagus notatus*	Western Montane Tree Kangaroo	EN, P		3	3		2	8	0.158	0.158		0.050
Muridae	*Anisomys imitator*	Uneven-toothed Rat		Y		49	14	67	130		0.737	0.538	1.000
Muridae	*Hyomys* sp.	White-eared giant rat		Y			2	8	10			0.154	0.250
Muridae	*Mallomys* sp.	Woolly Giant Rat		Y		5	9	27	41		0.158	0.308	0.500
Muridae	*Uromys anak*	Black-tailed Giant Rat		Y	4	10	26	42	82	0.211	0.316	0.538	0.800
Muridae	*Uromys caudimaculatus*	White-tailed Giant Rat		Y	82	27			109	0.895	0.526		
Muridae		Unidentified large murids			5	16	9	13	43				
Muridae	*Leptomys elegans*	Large Leptomys		Y	16	48			64	0.158	0.632		
Muridae	*Paramelomys* spp.	Multiple *Paramelomys* species		Y	108	81	90	49	328	0.632	0.737	0.769	0.700
Muridae	*Rattus* spp.	Multiple *Rattus* species		Y	21	2	44	210	277	0.368	0.053	0.846	0.850
Muridae	*Rattus* sp. A	A distinctive large *Rattus*		Y	14				14	0.263			
Muridae		Unidentified small murids			19	18	37	37	111				
Suidae	*Sus scrofa*	Feral Pig		Y	2	4			6	0.105	0.158		
Canidae	*Canis familiaris*	Domestic Dog		Y			5	9	14			0.462	0.150
Felidae	*Felis catus*	Domestic Cat		Y			1		1			0.077	
Hominidae	*Homo sapiens*	Human		Y	3		3	3	9	0.053		0.462	0.100
Birds									0				
Casuariidae	*Casuarius bennetti*	Dwarf Cassowary		Y	70	28	3	1	102	0.842	0.632	0.154	0.050
Megapodiidae	*Aepypodius arfakianus*	Wattled Brushturkey		Y	2	24	3	77	106	0.105	0.579	0.154	0.300
Megapodiidae	*Talegalla jobiensis*	Collared Brushturkey		Y	59	113			172	0.737	0.789		
Megapodiidae	*Megapodius decollatus*	New Guinea Scrubfowl		Y	41	56	25		122	0.579	0.789	0.615	
Accipitridae	*Harpyopsis novaeguineae*	Papuan Eagle	VU, P		1				1				
Accipitridae	*Accipiter poliocephalus*	Grey-headed Goshawk			1				1				
Rallidae	*Rallicula rubra*	Chestnut Forest Rail		Y				32	32				0.500
Rallidae	*Rallicula forbesi*	Forbes's Forest Rail		Y		5	14		19		0.158	0.538	

Family	Scientific Name	English Name	Status	Terr.	No. events					Naïve ψ			
					Arakubi	KP107	Hides Low	Hides High	Total	Arakubi	KP107	Hides Low	Hides High
Rallidae	*Gymnocrex plumbeiventris*	Bare-eyed Rail		Y		8			8		0.158		
Scolopacidae	*Scolopax rosenbergii*	New Guinea Woodcock		Y				123	123				0.550
Columbidae	*Chalcophaps stephani*	Stephan's Emerald Dove		Y	2				2	0.053			
Columbidae	*Henicophaps albifrons*	New Guinea Bronzewing		Y	1	3			4	0.053	0.158		
Columbidae	*Gallicolumba rufigula*	Cinnamon Ground Dove		Y	38	7			45	0.632	0.263		
Columbidae	*Alopecoenas jobiensis*	White-breasted Ground Dove		Y			1		1			0.077	
Columbidae	*Alopecoenas beccarii*	Bronze Ground Dove		Y			10	46	56			0.385	0.750
Columbidae	*Otidiphaps nobilis*	Pheasant Pigeon		Y	155	40	3		198	0.842	0.737	0.154	
Columbidae	*Gymnophaps albertisii*	Papuan Mountain Pigeon						1	1				
Alcedinidae	*Clytoceyx rex*	Shovel-billed Kookaburra					3		3				
Pittidae	*Erythropitta macklotii*	Papuan Pitta		Y	4	139			143	0.211	0.526		
Ptilonorhynchidae	*Ailuroedus stonii*	Ochre-breasted Catbird			3				3				
Ptilonorhynchidae	*Ailuroedus melanotis*	Black-eared Catbird				6			6				
Ptilonorhynchidae	*Archboldia papuensis*	Archbold's Bowerbird	NT					1	1				
Ptilonorhynchidae	*Amblyornis macgregoriae*	MacGregor's Bowerbird						2	2				
Meliphagidae	*Melilestes megarhynchus*	Long-billed Honeyeater			1				1				
Acanthizidae	*Crateroscelis murina*	Rusty Mouse-warbler		Y	7				7	0.158			
Acanthizidae	*Crateroscelis robusta*	Mountain Mouse-warbler		Y			1	1	2			0.385	0.050
Acanthizidae	*Sericornis nouhuysi*	Large Scrubwren						1	1				
Orthonychidae	*Orthonyx novaeguineae*	Papuan Logrunner		Y			34	28	62			0.462	0.450
Cnemophilidae	*Cnemophilus macgregorii*	Crested Satinbird						3	3				
Psophodidae	*Ptilorrhoa leucosticta*	Spotted Jewel-babbler		Y			62	18	80			0.923	0.200
Psophodidae	*Ptilorrhoa castanonota*	Chestnut-backed Jewel-babbler		Y	21	20			41	0.632	0.316		
Psophodidae	*Ptilorrhoa* sp.			Y		3			3		0.105		

Family	Scientific Name	English Name	Status	Terr.	No. events					Naïve ψ			
					Arakubi	KP107	Hides Low	Hides High	Total	Arakubi	KP107	Hides Low	Hides High
Oreoicidae	*Aleadryas rufinucha*	Rufous-naped Bellbird		Y			19	17	36			0.538	0.500
Oreoicidae	*Ornorectes cristatus*	Piping Bellbird		Y	17	20			37	0.316	0.474		
Pachycephalidae	*Pachycephala soror*	Sclater's Whistler					1		1				
Oriolidae	*Pitohui dichrous*	Hooded Pitohui				1			1				
Rhipiduridae	*Rhipidura atra*	Black Fantail					1		1				
Melampittidae	*Melampitta lugubris*	Lesser Melampitta		Y			1	116	117			0.077	0.900
Melampittidae	*Megalampitta gigantea*	Greater Melampitta		Y	2	7			9	0.105	0.158		
Paradisaeidae	*Parotia carolae*	Queen Carola's Parotia				4			4				
Paradisaeidae	*Epimachus meyeri*	Brown Sicklebill					3	18	21				
Petroicidae	*Heteromyias albispecularis*	Ashy Robin					19	16	35				
Petroicidae	*Peneothello cyanus*	Slaty Robin					1		1				
Petroicidae	*Pachycephalopsis poliosoma*	White-eyed Robin				3			3				
Petroicidae	*Drymodes beccarii*	Papuan Scrub Robin		Y	16	18			34	0.474	0.263		
Petroicidae	*Amalocichla sclateriana*	Greater Ground Robin		Y				80	80				0.700
Petroicidae	*Amalocichla incerta*	Lesser Ground Robin		Y			135		135			0.692	
Turdidae	*Zoothera heinei*	Russet-tailed Thrush		Y	2	23			25	0.105	0.421		
Reptiles									0				
Varanidae	*Varanus indicus*-group	Monitor species			7	1			8				
Scincidae	cf. *Emoia* sp.	Skink species		Y	4				4				

Appendix 3.3. The best-ranked models (ΔAICc<2), and the relative position of the null model (regardless of rank, in bold), emerging from reduced-model sets (see Analysis) for terrestrial mammals and birds. For each model the degrees of freedom (df), AICc score, ΔAICc, Akaike weight (wi) and cumulative Akaike weight (acc wi) are shown. Abbreviated candidate model variables: DClr—distance from clearing; LT50/LT100—less/more than 50/100 m from clearing; DRd—distance from road; LT100Rd—less/more than 100 m from road; LR20/LR50/LR100—local relief at the 20, 50 or 100 m radius scales; Elev—elevation; CC—canopy cover; TP—topographic position. Interactions between variables are denoted by an asterisk (*).

Taxa/sites/model rank	Candidate models	df	AICc	ΔAICc	*wi*	acc *wi*
Mammals						
Dasyurids (all) all sites						
1	DRd+CC	5	208.607		0.155	0.155
2	DRd	4	208.647	0.040	0.152	0.307
3	DRd+Elev	5	209.193	0.586	0.116	0.422
4	DRd+TP	5	209.658	1.051	0.092	0.514
5	DRd+CC+TP	6	209.697	1.090	0.090	0.604
6	DRd+Elev+TP	6	210.454	1.846	0.062	0.665
12	**Null**	**3**	**211.506**	**2.899**	**0.036**	
Dasyurids (all) Arakubi						
1	LT100+DRd	4	60.541		0.137	0.137
2	LT100+LR100	4	61.313	0.772	0.093	0.230
3	LT100	4	61.610	1.069	0.080	0.310
4	DRd	3	62.165	1.625	0.061	0.370
5	LT100+Elev	3	62.456	1.915	0.052	0.423
6	**Null**	**2**	**62.620**	**2.079**	**0.048**	
Echymipera Arakubi						
1	LT100	3	61.616		0.128	0.128
2	LT100+Elev	4	61.884	0.269	0.112	0.239
3	DRd+LT100	4	61.901	0.286	0.111	0.350
4	LT100+LR100	4	63.091	1.475	0.061	0.411
5	**Null**	**2**	**63.109**	**1.493**	**0.060**	**0.471**
6	LR100	3	63.138	1.523	0.060	0.531
Peroryctes all sites						
1	CC+LR50	5	204.119		0.323	0.323
2	DClr*Elev	6	204.316	0.197	0.293	0.616
14	**Null**	**3**	**213.107**	**8.987**	**0.004**	
Peroryctes Arakubi						
1	**Null**	**2**	**58.536**		**0.142**	**0.142**
2	LR50	3	58.756	0.219	0.128	0.270
3	LT50	3	59.583	1.047	0.084	0.354
4	Elev	3	59.690	1.153	0.080	0.434
5	CC	3	60.322	1.786	0.058	0.493

Taxa/sites/model rank	Candidate models	df	AICc	ΔAICc	*wi*	acc *wi*
Peroryctes KP107						
1	LT50	3	43.943		0.313	0.313
2	LT50+CC	4	45.194	1.251	0.167	0.480
3	LT50+TP	4	45.757	1.814	0.126	0.607
14	**Null**	**2**	**51.756**	**7.813**	**0.006**	
Peroryctes Hides Low						
1	CC	3	47.251		0.195	0.195
2	DClr	3	48.098	0.847	0.128	0.323
3	DClr+LR20+CC	5	48.122	0.871	0.126	0.449
4	DClr+CC	4	48.146	0.895	0.125	0.573
5	**Null**	**2**	**48.249**	**0.998**	**0.118**	**0.692**
6	DClr+LR20	4	48.427	1.176	0.108	0.800
Peroryctes Hides High						
1	LT100	3	47.613		0.228	0.228
2	LT100+TP	4	48.625	1.013	0.138	0.366
3	LT100+LR100	4	48.833	1.220	0.124	0.490
5	**Null**	**2**	**50.222**	**2.609**	**0.062**	
Microperoryctes BAA 1						
1	**Null**	**3**	**87.696**		**0.207**	**0.097**
2	CC	4	88.762	1.066	0.121	0.218
3	LR20	4	89.448	1.753	0.086	0.304
Dorcopsulus all sites						
1	LT50*Elev	6	195.600		0.354	0.354
2	LT50*Elev+LR20	7	197.495	1.895	0.137	0.491
9	**Null**	**3**	**200.040**	**4.440**	**0.038**	
Dorcopsulus Arakubi						
1	LR20	3	56.933	0.000	0.125	0.125
2	Elev+LR20	4	57.141	0.209	0.113	0.238
3	LT50+LR20+LR100	5	57.151	0.218	0.112	0.350
4	LT50+LR20	4	57.276	0.343	0.105	0.455
5	LR20+LR100	4	57.996	1.063	0.074	0.529
6	LR20+CC	4	58.510	1.577	0.057	0.586
7	LT50+Elev+LR20	5	58.557	1.624	0.056	0.641
8	LT50	3	58.792	1.859	0.049	0.691
9	Elev+LR20+CC	5	58.846	1.914	0.048	0.739
16	**Null**	**2**	**61.057**	**4.125**	**0.016**	
Dorcopsulus KP107						
1	**Null**	**2**	**57.377**		**0.234**	**0.234**
2	LT50	3	57.563	0.186	0.213	0.448
3	LR50	3	59.131	1.754	0.097	0.545
Dorcopsulus Hides Low						
1	LR50+CC	4	26.461		0.726	0.726
7	**Null**	**2**	**35.537**	**9.076**	**0.008**	
Dorcopsulus Hides High						
1	**Null**	**2**	**54.115**		**0.295**	**0.295**
2	LT50	3	55.906	1.791	0.121	0.416

Taxa/sites/model rank	Candidate models	df	AICc	ΔAICc	*wi*	acc *wi*
Anisomys KP107						
1	**Null**	**2**	**61.000**		**0.218**	**0.218**
2	LT50	3	61.848	0.848	0.143	0.361
3	LR20	3	62.280	1.280	0.115	0.476
Anisomys Hides High						
1	CC	3	45.268		0.242	0.242
2	**Null**	**2**	**46.238**	**0.970**	**0.149**	**0.390**
3	LR20	3	47.215	1.947	0.091	0.482
Mallomys Hides High						
1	**Null**	**2**	**73.561**		**0.335**	**0.335**
Uromys anak BAA 1						
1	CC	4	105.098		0.210	0.210
2	CC+LR50	5	106.092	0.994	0.128	0.337
3	**Null**	**3**	**106.172**	**1.075**	**0.123**	**0.460**
U. caudimaculatus BAA 2						
1	DRd+LR20	5	113.730	0.000	0.144	0.144
2	DRd+Elev+LR20	6	114.251	0.520	0.111	0.255
3	LR20	4	114.805	1.075	0.084	0.340
4	DRd+Elev	5	114.905	1.175	0.080	0.420
5	DRd	4	115.518	1.787	0.059	0.479
6	Elev+LR20	5	115.625	1.895	0.056	0.535
7	LR20+LR100	5	115.720	1.990	0.053	0.588
8	**Null**	**3**	**115.901**	**2.171**	**0.049**	**0.637**
Leptomys KP107						
1	LT100+LR50	4	64.063		0.361	0.361
2	LR50	3	65.145	1.082	0.210	0.571
8	**Null**	**2**	**68.587**	**4.525**	**0.038**	
Paramelomys all sites						
1	DClr+LR20	5	246.926		0.334	0.334
2	LR20	4	248.176	1.249	0.179	0.514
3	DClr+LR20+CC	6	248.516	1.589	0.151	0.665
9	**Null**	**3**	**254.638**	**7.712**	**0.007**	
Rattus BAA 1						
1	Elev	4	115.756		0.173	0.173
2	**Null**	**3**	**116.363**	**0.607**	**0.128**	**0.301**
3	Elev+TP	5	116.779	1.023	0.104	0.405
4	LT100Rd+Elev	5	117.538	1.782	0.071	0.476
Birds						
Casuarius BAA 2						
1	**Null**	**3**	**121.286**		**0.132**	**0.132**
2	DRd	4	121.340	0.054	0.129	0.261
3	Elev	4	122.251	0.964	0.082	0.343
4	DRd+Elev	5	122.631	1.345	0.068	0.410
5	DRd*Elev	6	122.786	1.500	0.062	0.473

Taxa/sites/model rank	Candidate models	df	AICc	ΔAICc	*wi*	acc *wi*
Aepypodius KP107						
1	**Null**	**2**	**63.579**		**0.244**	**0.244**
2	Elev	3	64.121	0.543	0.186	0.431
3	LT100	3	65.521	1.942	0.093	0.523
Aepypodius Hides High						
1	**Null**	**2**	**97.709**		**0.505**	**0.505**
2	DClr	3	99.608	1.899	0.195	0.700
Talegalla BAA 2						
1	DClr+Elev	5	120.411	0.000	0.254	0.254
2	DClr	4	120.712	0.301	0.219	0.473
3	DClr+CC+Elev	6	122.223	1.812	0.103	0.576
4	DClr*Elev	6	122.304	1.893	0.099	0.675
5	DClr+CC	5	122.403	1.992	0.094	0.769
66	**Null**	**3**	**131.500**	**11.089**	**0.001**	
Megapodius BAA 2+Hides Low						
1	LR20	4	176.690	0.000	0.158	0.158
2	**Null**	**3**	**177.196**	**0.506**	**0.122**	**0.280**
3	LR20+TP	5	177.398	0.708	0.111	0.391
Scolopax Hides High						
1	Elev	3	85.767		0.476	0.476
6	**Null**	**2**	**90.370**	**4.603**	**0.048**	
Gallicolumba Arakubi						
1	DRd+TP	4	67.931		0.162	0.162
2	LR100+TP	4	68.656	0.725	0.113	0.275
3	DRd+LR20	4	69.114	1.184	0.090	0.365
4	DRd	3	69.139	1.208	0.089	0.453
5	LR20+LR100	4	69.497	1.566	0.074	0.527
6	LR100	3	69.883	1.952	0.061	0.588
8	**Null**	**2**	**70.851**	**2.920**	**0.038**	
Alopecoenas Hides High						
1	**Null**	**2**	**61.232**		**0.341**	**0.341**
Otidiphaps BAA 2						
1	DClr+Elev	5	125.448		0.199	0.199
2	DClr*Elev	6	126.319	0.871	0.129	0.327
3	Elev+TP	5	126.773	1.325	0.102	0.430
11	**Null**	**3**	**129.359**	**3.911**	**0.028**	
Erythropitta KP107						
1	LT100Rd	3	87.012		0.367	0.200
2	**Null**	**2**	**87.908**	**0.896**	**0.234**	**0.434**
Orthonyx BAA 1						
1	LT100Rd + LR100	5	126.930		0.185	0.185
2	LR100	4	127.833	0.903	0.118	0.302
3	LT100Rd	4	128.259	1.329	0.095	0.397
4	Elev + LT100Rd + LR100	6	128.299	1.369	0.093	0.490
5	Elev + LT100Rd	5	128.763	1.833	0.074	0.564
16	**Null**	**2**	**131.692**	**4.763**	**0.017**	

Taxa/sites/model rank	Candidate models	df	AICc	ΔAICc	*wi*	acc *wi*
Ptilorrhoa castanonota BAA 2						
1	CC	4	140.040		0.182	0.182
2	**Null**	**3**	**140.238**	**0.199**	**0.165**	**0.347**
3	LR50	4	141.193	1.154	0.102	0.450
4	CC + LR50	5	141.748	1.708	0.078	0.527
5	LT100	4	141.917	1.877	0.071	0.599
Aleadryas BAA 1						
1	LT100Rd	4	112.372		0.176	0.176
2	**Null**	**3**	**113.137**	**0.764**	**0.120**	**0.297**
3	Elev + LT100Rd	5	113.682	1.309	0.092	0.388
4	Elev	4	114.063	1.690	0.076	0.464
Ornorectes BAA 2						
1	**Null**	**3**	**140.228**		**0.200**	**0.200**
2	LR20	4	141.755	1.527	0.093	0.293
3	LT100Rd	4	142.093	1.865	0.079	0.372
4	CC	4	142.106	1.878	0.078	0.450
Melampitta lugubris Hides High						
1	LT100	3	58.252		0.327	0.327
2	LT100+LR20	4	59.315	1.063	0.192	0.519
13	**Null**	**2**	**69.125**	**10.872**	**0.001**	
Heteromyias BAA 1						
1	**Null**	**3**	**133.654**		**0.286**	**0.286**
2	LT50	4	135.490	1.836	0.114	0.400
Drymodes BAA 2						
1	**Null**	**3**	**148.094**		**0.314**	**0.314**
2	LR50	4	149.187	1.092	0.182	0.495
Amalocichla sclateriana Hides High						
1	TP	3	72.759		0.225	0.225
2	Elev+TP	4	73.826	1.067	0.132	0.357
3	LT100+TP	4	74.282	1.522	0.105	0.462
4	**Null**	**2**	**74.558**	**1.798**	**0.092**	**0.554**
A. incerta Hides Low						
1	CC+LR20	4	53.832		0.270	0.270
2	CC	3	53.931	0.099	0.257	0.527
3	CC+Elev	4	54.967	1.135	0.153	0.680
5	**Null**	**2**	**56.931**	**3.099**	**0.057**	
Zoothera KP107						
1	**Null**	**2**	**74.945**		**0.226**	**0.226**
2	DRd	3	75.149	0.204	0.204	0.430
3	LR50	3	75.637	0.692	0.160	0.589
4	DRd + LR50	4	76.748	1.803	0.092	0.681

Appendix 3.4. Model-averaged coefficient point estimates, standard errors and the relative importance of each variable present in the ΔAICc<6 candidate set, and the number of models in which each variable appears. Cases where the estimate is larger than the standard error are shown in bold. Abbreviated variables: DClr—distance from clearing; LT50/LT100—less/more than 50/100 m from clearing; DRd—distance from road; LT100Rd—less/more than 100 m from road; LR20/LR50/LR100—local relief at the 20, 50 or 100 m radius scales; Elev—elevation; CC—canopy cover; TP—topographic position. Interactions between elevation and various distance measures are shown (Elev*DM).

Taxa/sites (no. models ΔAICc<6)	**DClr**	**LT50**	**LT100**	**DRd**	**LT100Rd**	**LR20**	**LR50**	**LR100**	**CC**	**TP**	**Elev**	**Elev*DM**
Mammals												
Dasyurids, all sites (15)												*DRd
Estimate (SE)				**0.002 (0.001)**		0.004 (0.013)			-0.038 (0.071)	0.063 (0.176)	0.000 (0.000)	0.000 (0.000)
Rel. Imp. (no. models)				0.73(8)		0.14(3)			0.35(5)	0.30(7)	0.31(7)	0.06(2)
Dasyurids, Arakubi (31)												
Estimate (SE)			-0.543 (0.613)	0.001 (0.002)		0.011 (0.036)		-0.006 (0.016)	-0.026 (0.111)	-0.236 (0.671)	0.002 (0.004)	
Rel. Imp. (no. models)			0.61(15)	0.32(7)		0.18(10)		0.16(4)	0.17(9)	0.15(9)	0.18(8)	
***Echymipera*, Arakubi (30)**												
Estimate (SE)			**-0.656 (0.610)**	-0.001 (0.001)		0.002 (0.014)	0.000 (0.010)	0.006 (0.015)	-0.020 (0.093)	-0.024 (0.247)	-0.002 (0.005)	
Rel. Imp. (no. models)			0.67(17)	0.25(9)		0.05(4)	0.10(6)	0.19(6)	0.08(5)	0.12(7)	0.19(5)	
***Peroryctes*, all sites (8)**												*DClr
Estimate (SE)	0.003 (0.004)						**-0.023 (0.019)**		**0.113 (0.112)**	-0.007 (0.088)	0.001 (0.001)	0.000 (0.000)
Rel. Imp. (no. models)	0.43(3)						0.67(6)		0.58(4)	0.14(2)	0.31(1)	0.31(1)
***Peroryctes*, Arakubi (23)**												
Estimate (SE)		0.280 (0.655)		0.000 (0.001)			-0.013 (0.027)	-0.004 (0.012)	0.060 (0.153)	-0.013 (0.205)	0.002 (0.004)	
Rel. Imp. (no. models)		0.23(6)		0.11(5)			0.26(5)	0.12(5)	0.19(6)	0.11(6)	0.19(4)	
***Peroryctes*, KP107 (10)**												
Estimate (SE)		**1.073 (0.466)**					-0.004 (0.012)		0.068 (0.112)	-0.098 (0.254)	0.000 (0.001)	
Rel. Imp. (no. models)		0.96(8)					0.19(3)		0.37(5)	0.25(4)	0.09(2)	

Taxa/sites (no. models ΔAICc<6)	**DClr**	**LT50**	**LT100**	**DRd**	**LT100Rd**	**LR20**	**LR50**	**LR100**	**CC**	**TP**	**Elev**	**Elev*DM**
***Peroryctes*, Hides Low (10)**												
Estimate (SE)	-0.003 (0.003)					0.021 (0.043)			0.320 (0.350)	0098 (0.340)		
Rel. Imp. (no. models)	0.50(4)					0.30(4)			0.56(5)	0.12(2)		
***Peroryctes*, Hides High (18)**												
Estimate (SE)			**-0.462 (0.394)**					-0.006 (0.013)	0.002 (0.043)	-0.137 (0.277)	0.000 (0.003)	
Rel. Imp. (no. models)			0.71(9)					0.27(6)	0.14(6)	0.29(6)	0.16(6)	
***Microperoryctes*, BAA 1 (19)**												*LT100Rd
Estimate (SE)					0.580 (2.531)	0.007 (0.017)			0.044 (0.088)	-0.026 (0.136)	0.000 (0.001)	0.000 (0.001)
Rel. Imp. (no. models)					0.19(6)	0.25(6)			0.35(8)	0.17(6)	0.25(8)	0.06(2)
***Dorcopsulus*, all sites (12)**												*LT50
Estimate (SE)		**1.267 (1.134)**				-0.007 (0.015)			0.011 (0.042)		0.000 (0.000)	0.000 (0.001)
Rel. Imp. (no. models)		0.78(6)				0.35(6)			0.09(2)		0.67(6)	0.51(2)
***Dorcopsulus*, Arakubi (23)**												
Estimate (SE)		0.498 (0.709)				**-0.089 (0.054)**		0.007 (0.014)	0.038 (0.116)	0.015 (0.224)	-0.002 (0.004)	
Rel. Imp. (no. models)		0.44(11)				0.85(16)		0.28(7)	0.16(5)	0.13(9)	0.27(6)	
***Dorcopsulus*, KP107 (13)**												
Estimate (SE)		0.338 (0.536)					-0.006 (0.018)		-0.002 (0.055)	-0.012 (0.193)	0.000 (0.003)	
Rel. Imp. (no. models)		0.42(5)					0.20(4)		0.13(3)	0.12(3)	0.14(4)	
***Dorcopsulus*, Hides Low (3)**												
Estimate (SE)				0.001 (0.001)			**0.039 (0.017)**		**0.320 (0.082)**	-0.010 (0.072)		
Rel. Imp. (no. models)				0.013(1)			0.87(2)		1.00(3)	0.06(1)		
***Dorcopsulus*, Hides High (15)**												
Estimate (SE)		-0.116 (0.318)						0.048 (0.205)	0.000 (0.003)	0.003 (0.010)	0.006 (0.060)	
Rel. Imp. (no. models)		0.24(5)						0.17(4)	0.16(5)	0.17(4)	0.16(5)	
***Anisomys*, KP107 (18)**												
Estimate (SE)		0.188 (0.461)				-0.010 (0.027)		0.003 (0.019)	0.013 (0.071)	-0.076 (0.302)	0.000 (0.003)	
Rel. Imp. (no. models)		0.26(5)				0.21(4)		0.16(5)	0.12(4)	0.14(5)	0.15(5)	

Taxa/sites (no. models ΔAICc<6)	DClr	LT50	LT100	DRd	LT100Rd	LR20	LR50	LR100	CC	TP	Elev	Elev*DM
***Anisomys*, Hides High (15)**												
Estimate (SE)					-0.032 (0.196)	0.008 (0.021)			-0.107 (0.128)	0.005 (0.117)	0.001 (0.004)	
Rel. Imp. (no. models)					0.16(5)	0.24(5)			0.50(6)	0.11(3)	0.19(5)	
***Mallomys*, Hides High (13)**												
Estimate (SE)	0.000 (0.001)						0.007 (0.025)		-0.033 (0.119)	-0.068 (0.343)	0.001 (0.006)	
Rel. Imp. (no. models)	0.16(4)						0.17(3)		0.15(4)	0.19(4)	0.15(4)	
***Uromys anak*, BAA 1 (19)**												
Estimate (SE)		0.055 (0.260)					0.007 (0.015)		**0.261 (0.231)**	-0.015 (0.157)	0.000 (0.001)	
Rel. Imp. (no. models)		0.19(6)					0.32(8)		0.65(10)	0.14(5)	0.18(7)	
***U. caudimac-ulatus*, BAA 2 (27)**												*DRd
Estimate (SE)				0.001 (0.003)		0.027 (0.031)		-0.002 (0.008)	0.015 (0.062)	-0.021 (0.137)	-0.001 (0.002)	0.000 (0.000)
Rel. Imp. (no. models)				0.56(12)		0.57(11)		0.11(5)	0.16(10)	0.08(5)	0.43(12)	0.03(2)
***Leptomys*, KP107 (8)**												
Estimate (SE)			-0.702 (0.719)				**-0.097 (0.045)**		0.031 (0.101)		-0.001 (0.005)	
Rel. Imp. (no. models)			0.57(3)				0.91(6)		0.18(2)		0.17(3)	
***Paramelomys*, all sites (7)**												*DClr
Estimate (SE)	0.002 (0.002)					**0.072 (0.026)**			-0.016 (0.057)		0.000 (0.000)	0.000 (0.000)
Rel. Imp. (no. models)	0.67(4)					1.00(7)			0.24(2)		0.22(3)	0.06(1)
***Rattus*, BAA 1 (21)**												*LT100Rd
Estimate (SE)					-0.127 (0.906)	0.003 (0.016)			-0.002 (0.070)	0.150 (0.334)	0.001 (0.001)	0.000 (0.000)
Rel. Imp. (no. models)					0.24(7)	0.15(6)			0.18(8)	0.31(8)	0.58(11)	0.02(1)
BIRDS												
***Casuarius*, BAA 2 (28)**												*DRd
Estimate (SE)				0.003 (0.007)		-0.001 (0.013)		-0.001 (0.006)	0.007 (0.060)	0.008 (0.186)	0.000 (0.002)	0.000 (0.000)
Rel. Imp. (no. models)				0.50(14)		0.16(8)		0.08(4)	0.19(10)	0.17(8)	0.39(12)	0.11(4)
***Aepypodius*, KP107 (15)**												
Estimate (SE)			0.175 (0.483)			0.001 (0.016)		0.000 (0.019)	0.009 (0.062)	-0.067 (0.307)	0.005 (0.008)	
Rel. Imp. (no. models)			0.16(4)			0.12(3)		0.14(5)	0.07(2)	0.13(3)	0.34(5)	

Taxa/sites (no. models ΔAICc<6)	**DClr**	**LT50**	**LT100**	**DRd**	**LT100Rd**	**LR20**	**LR50**	**LR100**	**CC**	**TP**	**Elev**	**Elev*DM**
***Aepypodius*, Hides High (5)**												
Estimate (SE)	-0.002 (0.005)							-0.005 (0.027)		0.159 (0.636)		
Rel. Imp. (no. models)	0.24(2)							0.14(1)		0.16(2)		
***Talegalla*, BAA 2 (9)**												*DClr
Estimate (SE)	**0.008 (0.008)**					-0.001 (0.009)		-0.004 (0.011)	0.048 (0.105)		0.001 (0.002)	0.000 (0.000)
Rel. Imp. (no. models)	0.99(8)					0.01(1)		0.16(3)	0.31(5)		0.51(4)	0.14(2)
***Megapodius*, BAA 2+Hides Low (22)**												
Estimate (SE)					-0.124 (0.342)	**-0.042 (0.042)**			0.002 (0.053)	0.184 (0.350)	0.000 (0.000)	
Rel. Imp. (no. models)					0.25(10)	0.61(12)			0.17(7)	0.36(10)	0.21(7)	
***Scolopax*, Hides High (16)**												
Estimate (SE)		0.178 (0.666)						-0.001 (0.014)	0.061 (0.208)	-0.045 (0.319)	**-0.043 (0.019)**	
Rel. Imp. (no. models)		0.11(2)						0.10(1)	0.12(2)	0.11(1)	0.95(6)	
***Gallicolumba*, Arakubi (23)**												
Estimate (SE)				-0.002 (0.003)		-0.033 (0.057)		-0.017 (0.027)	-0.019 (0.109)	-0.942 (1.227)	-0.001 (0.005)	
Rel. Imp. (no. models)				0.47(7)		0.35(10)		0.33(7)	0.15(8)	0.45(9)	0.07(3)	
***Alopecoenas*, Hides High (16)**												
Estimate (SE)		0.039 (0.280)						0.003 (0.012)	0.003 (0.072)	-0.009 (0.202)	0.001 (0.005)	
Rel. Imp. (no. models)		0.17(5)						0.16(4)	0.17(5)	0.15(4)	0.18(5)	
***Otidiphaps*, BAA 2 (9)**												*DClr
Estimate (SE)	0.005 (0.009)					0.001 (0.009)		-0.007 (0.016)	0.005 (0.059)	-0.200 (0.436)	-0.002 (0.002)	0.000 (0.000)
Rel. Imp. (no. models)	0.55(7)					0.05(3)		0.18(5)	0.16(7)	0.23(5)	0.64(9)	0.16(2)
***Erythropitta*, KP107 (7)**												
Estimate (SE)					-1.474 (1.693)		-0.004 (0.027)		-0.019 (0.111)	0.027 (0.443)		
Rel. Imp. (no. models)					0.55(3)		0.16(2)		0.09(1)	0.14(2)		
***Orthonyx*, BAA 1 (21)**												*LT100Rd
Estimate (SE)					-0.970 (1.633)			**-0.057 (0.046)**	0.041 (0.144)	-0.095 (0.328)	-0.001 (0.001)	0.000 (0.001)
Rel. Imp. (no. models)					0.73(14)			0.67(12)	0.10(5)	0.18(6)	0.38(11)	0.04(2)

Taxa/sites (no. models ΔAICc<6)	DClr	LT50	LT100	DRd	LT100Rd	LR20	LR50	LR100	CC	TP	Elev	Elev*DM
***Ptilorrhoa castanonota*, BAA 2 (18)**												
Estimate (SE)			-0.187 (0.409)				-0.007 (0.018)		-0.186 (0.232)	-0.249 (0.677)	-0.000 (0.001)	
Rel. Imp. (no. models)			0.27(8)				0.27(4)		0.46(9)	0.15(6)	0.12(6)	
***Aleadryas*, BAA 1 (22)**												*LT100Rd
Estimate (SE)					-0.584 (1.105)			-0.10 (0.021)	-0.014 (0.076)	-0.032 (0.214)	-0.001 (0.001)	0.000 (0.000)
Rel. Imp. (no. models)					0.51(10)			0.21(8)	0.16(7)	0.18(7)	0.39(11)	0.03(1)
***Ornorectes*, BAA 2 (20)**												
Estimate (SE)					0.150 (0.516)	-0.011 (0.029)		-0.002 (0.010)	0.063 (0.144)	-0.032 (0.240)	0.000 (0.001)	
Rel. Imp. (no. models)					0.21(6)	0.22(5)		0.15(5)	0.22(6)	0.15(5)	0.15(5)	
***Melampitta lugubris*, Hides High (11)**												
Estimate (SE)			**-1.700 (0.432)**			0.015 (0.030)			0.024 (0.084)	-0.032 (0.184)	0.002 (0.005)	
Rel. Imp. (no. models)			1.00(11)			0.32(4)			0.21(5)	0.12(3)	0.24(5)	
***Heteromyias*, BAA 1 (15)**												
Estimate (SE)		-0.085 (0.395)				0.010 (0.032)			0.022 (0.125)	0.070 (0.320)	0.000 (0.001)	
Rel. Imp. (no. models)		0.21(4)				0.18(5)			0.20(5)	0.18(4)	0.14(5)	
***Drymodes*, BAA 2 (11)**												
Estimate (SE)				0.000 (0.001)			-0.021 (0.035)		0.007 (0.097)	-0.056 (0.386)	0.000 (0.001)	
Rel. Imp. (no. models)				0.20(4)			0.31(3)		0.20(4)	0.03(1)	0.12(3)	
***Amalocichla sclateriana*, Hides High (16)**												
Estimate (SE)			-0.179 (0.428)				-0.005 (0.020)		0.034 (0.120)	**-0.971 (0.921)**	0.004 (0.009)	
Rel. Imp. (no. models)			0.28(6)				0.09(3)		0.19(6)	0.63(7)	0.28(6)	
***A. incerta*, Hides Low (10)**												
Estimate (SE)			0.141 (0.518)			-0.055 (0.075)			**0.621 (0.430)**		-0.003 (0.006)	
Rel. Imp. (no. models)			0.15(4)			0.43(4)			0.79(5)		0.20(2)	
***Zoothera*, KP107 (11)**												
Estimate (SE)				0.004 (0.006)			-0.036 (0.061)		0.025 (0.126)	-0.021 (0.337)	0.002 (0.006)	
Rel. Imp. (no. models)				0.34(3)			0.35(4)		0.07(2)	0.10(3)	0.15(3)	

Chapter 4 – Small non-volant mammals (Rodents)

Kyle N . Armstrong, Enock Kale and Pita Amick

A Large Leptomys, *Leptomys elegans*, trapped at KP107

Summary

Background and aims

Rodents are good targets for monitoring because they often respond rapidly to changes in their habitat, by either declining or becoming more common due to changes in the availability or quality of a local resource. In 2015 rodents were documented, along with other small non-volant mammals, using a variety of survey techniques including camera trapping. The 2017 mammal survey departed slightly from the format taken in 2015 by excluding camera trapping data and focusing on live-trapping along 11 permanent transects at two elevations above 2,000 m on Hides Ridge (BAA 1) and two elevations below 2,000 m on the Agogo Range near Moro (BAA 2). The live-trapping of medium-sized rats in two main groups: the murine tribe Hydromyini (dominated by *Paramelomys* in this study area) and the tribe Rattini (dominated by *Rattus* in this study area) is the sole focus of the present report.

The foundation of all analyses conducted is a genetics-based identification system. The previous 2015 survey used mitochondrial DNA barcoding (with the cytochrome-*b* gene) to establish a comparative identification framework, and to improve on this and resolve several outstanding issues, the 2017 survey introduced a more powerful genomics-based set of genetic markers that provide greater clarity around the species boundaries of closely-related taxa encountered on the survey (Single Nucleotide Polymorphisms; SNPs). The new comparative genetic framework is the most comprehensive ever created for New Guinea (for the genera of particular focus).

The overall aim of this study is to document and interpret observed changes in rodent species diversity and abundance in order to provide informed advice about potential project-related impacts.

Major results

Total captures of small rodents in the Hydromyini and Rattini on the 2017 survey were around two and a half times lower than in 2015 (53 versus 133 novel captures), but Species Richness and total captures were not significantly different amongst the treatment levels of distance from the ROW, elevation and survey year. Despite the lower capture success in 2017, capture rates are relatively high compared to other studies we have been involved in where close to zero or nil capture rates have been reported. Four additional rodent species were detected on the 2017 survey, bringing the total Species Richness to 14. One of the additional species detected was the Black Rat, *Rattus rattus*, which is a commensal and a pest species. One animal was captured at 2,200 m at the edge of transect H2, which suggests this species moves along the ROW. No other potential influences of the ROW were associated with any observation made on the survey. No further introduced *Rattus exulans* were captured at KP107.

The introduction of the genome-scale SNP-based identification system, which incorporated all samples sequenced previously, as well as samples collected from all novel captures in 2017, provided even greater clarity than the cytochrome-b marker. It confirmed the species identities of all morphological-based identifications, was particularly useful for identifying species boundaries between the most closely related taxa, and pointed to several misidentifications that were records of new taxa in the study. The system also confirmed that two species new to science have only been recorded from the BAAs—one species of *Paramelomys* (sp. cf. *rubex* type 'B') and one species of *Rattus* (sp. cf. *niobe* type 'D'); plus several others that are part of species complexes that are still to be fully resolved.

Conclusions and recommendations

Although variability in capture numbers at different treatment levels and the relatively low sample sizes overall have probably influenced some statistical tests, the statistical power of these tests will improve with successive surveys. Rather than pointing to a reduced value of this survey component, the lower capture rate recorded in 2017 demonstrates the value of long-term studies. The lower capture rate is unlikely to be related to an influence of the ROW, but instead is likely to reflect natural patterns of variation that need to be understood more fully from future work.

The detection of an additional four species of rodent during the 2017 survey has improved our understanding of rodent diversity within the BAAs and it is likely that additional species will be encountered during future surveys. Genetics-based identification has been the foundation of reliable comparisons between sites, survey years and investigators in this study; and the results (that have included at least two new species not seen elsewhere) are testament to a likely high, under-estimated level of rodent diversity across New Guinea.

There is evidence that linear infrastructure is being used by introduced commensal mammals which have the potential to increase rates of predation, competitive exclusion and the probability of exposure of naïve native rodent species to novel pathogens. However, the source of these introduced agents varies, with evidence that dogs originate from local villages, and non-native *Rattus* come from the transport of plant and equipment to mining operations and their subsequent movement along new linear infrastructure corridors.

It is recommended that the rodent live-trapping component of the study continue, and that the recommendations of Aplin and Opiang (2017; internal version that includes the recommendations) be revisited, especially:

- Further consideration be given to ensuring that quarantine efforts and rodent pest control are being maintained at the Hides Gas Conditioning Plant in particular. A wider study around the HGCP would provide further context on how common species such as *R. rattus* and *R. exulans* are.

- Establish a second trapping line at Arakubi Quarry, and ensure sufficient personnel are available to service all trapping lines.

Introduction

Small non-volant mammals, particularly rodents, are good targets for monitoring because they often respond rapidly to changes in their habitat, including in areas subject to 'edge effects', by either declining or becoming more common due to changes in the availability or quality of a local resource.

The diversity of non-volant mammals along linear infrastructure in the two BAAs was determined during the 2015 survey using a combination of several methods, including camera trapping, live trapping with two sizes of box traps set out on transect lines, the analysis of owl pellets and opportunistic observations of scats and remains. A significant component of this study was the inclusion of a genetics-based field identification verification system using mitochondrial DNA barcoding, which helped standardise comparisons amongst treatment sites by ensuring that identifications were not confounded by inaccurate identification or the presence of morphologically cryptic species. A novel comparative genetic framework was generated using the extensive resources of the collections in the South Australian Museum, resulting in the first comprehensive genetics-based identification system for New Guinea rodents used in an industry project.

Having established a comprehensive baseline level of species presence in the study areas from the broad combination of methods, the 2017 mammal survey departed somewhat from this format by splitting the camera trapping component into a stand-alone section that identified the presence of birds and all non-volant mammals at new standardised site placements (Chapter 3). This method is effective for detecting larger animals that do not enter small box traps, and particularly so for marsupials that are more easily identified from photographs than small native rodents. We focused instead on the continuation of live trapping with box traps set along the 11 permanent, standardised survey transects established in 2015. This live-trapping component is reported on here, and focuses mainly on medium-sized rats (i.e. rats the size of the introduced Black Rat *Rattus rattus*) that in the study area are dominated by the genera *Paramelomys* and *Rattus*.

Aims

The overall aim of this study is to document and interpret observed changes in non-volant mammal species diversity and abundance in order to provide informed advice about potential project-related impacts. To achieve this aim the study has six major objectives:

1. To document small mammal diversity (the simple tally of different species, also called Species Richness) and abundances within each of the BAAs.

2. To identify non-volant mammal species of conservation significance (including new or undescribed species) within each of the BAAs and, where practicable, determine their special sensitivities.

3. To monitor the status of exotic mammal species in each of the BAAs.

4. To contribute to knowledge of the local ecology of exotic non-volant mammals within each of the BAAs, and, where practicable, determine their potential vulnerabilities.

5. To monitor the specific impact of the linear right-of-way (ROW) infrastructure on the non-volant mammal communities, as an indicator of more general ROW impacts.

6. To assess the usefulness of non-volant mammal communities more broadly as potential indicators of change in habitat quality in each of the BAAs.

Methods

Overview of methods in 2017

Two main sets of methods are described: those pertaining to making robust identifications using advanced genetic markers, and those used in the ecological analysis of the trapping data.

Prior to ecological and statistical analysis of live trapping data, it was first essential to ensure that any comparisons across sites and treatments were made on the basis of accurate species identifications (review in Armstrong and Aplin 2017). Despite authoritative compilations such as the 'Mammals of New Guinea' by Flannery (1995), and even the more recent contribution of Denys et al. (2017) in the 'Handbook of the mammals of the world', there is still an incomplete understanding and an underestimate of murine rodent species diversity in New Guinea where modern methods of taxonomy have not been applied in a comprehensive way. The 2015 survey used mitochondrial DNA barcoding (with the cytochrome-*b* gene) to establish a comparative identification framework, which prompted recognition of a greater number of taxa than morphological-based identifications made in the field, plus several issues that have the potential to confound both field identifications and mitochondrial barcoding approaches to identification. Thus, in 2017, we introduced a more powerful genomics-based set of genetic markers that provide greater clarity around the species boundaries of closely-related taxa encountered on the survey. The new comparative genetic framework is the most comprehensive ever created for New Guinea (for the genera of particular focus), and avoids confounded identifications that result from genetic processes such as introgression, pseudogenisation of mitochondrial genes and mitochondrial capture, as well as common biases in mitochondrial DNA-based barcoding (review in Collins and Cruikshank 2012).

The second suite of analytical methods summarises two aspects of rodent diversity from the box trapping transects—species richness, and abundance. Species composition (the relative mix of each species at different sites) was not examined with multivariate ordinations as was undertaken for the bat and frog groups because rodent richness was lower, and the patterns are clear from tabulated results. Based on the 2015 survey, Aplin and Opiang (2017) provided a range of outputs to establish a baseline understanding of local rodent diversity. Our analyses are similar to those

conducted for frogs and bats that examined the patterns of diversity with increasing distance from the ROW and at increasing elevation, but they incorporate additional sampling effort within 20 m of the forest edge to detect exotic rodents that are potentially migrating along the linear infrastructure.

Genomics-based identification

A 'reduced representation' genome sequencing approach was used, which generates many thousands of single variable sites (Single Nucleotide Polymorphisms: SNPs) from random locations across the entire chromosome area. The specific DNA sequencing method chosen is called 'DArTseq' (Kilian et al. 2003; Grewe et al. 2015), which is the commercial equivalent of an identical widely-used technique called 'RADseq' (restriction site-associated DNA sequencing; Peterson et al. 2012). In this technique the entire DNA content in a sample is cut randomly with two enzymes, the resulting fragments ligated with indexed adapters, and the indexed fragments are then sequenced to 75 base pairs in length on an Illumina sequencing platform. The same DNA extracts used to establish the mitochondrial DNA comparative framework from captures in 2015 and other 'context' samples from elsewhere in New Guinea (for comparison; provided by the South Australian Museum) were included in the sequencing effort, as well as the fresh tissues collected mostly non-lethally in the 2017 trapping effort. All DNA extracts and biopsy tissues were put into 96-well plates and sent to a commercial service for library-making and DNA fragment sequencing (Diversity Arrays Pty Ltd, Canberra).

A custom-written [R] language analysis script was used to tidy and filter the genotype matrix supplied after bioinformatic processing conducted by the commercial service. Individuals and loci that had insufficient coverage were removed. One of the simplest ways to illustrate the results is to produce an ordination plot derived from Principle Coordinates (PCoA) analysis of the genotypes (several thousand SNP loci that are homozygous for either of two (only) alternative alleles (nucleotide bases) or the heterozygote. The PCoA plot shows a pattern where individual samples cluster together in terms of their overall genetic similarity at the several thousand SNP loci. These clusters represent discrete gene pools, which are interpreted to represent distinct species (because species do not share gene pools, unless reproductive isolation is not quite complete). The identification of individuals that are the result of occasional hybridisation between two discrete gene pools present in one locality are straightforward to identify because they generally occupy a position between two clusters in the ordination. The geographic origin of each individual sample was coded in PCoA plots so that a species list could be created for each sampling site (transect). Names of genetic clusters were guided by the groundwork established by Aplin and Opiang (2017) as well as information associated with context samples that was available from the Australian Biological Tissue Database (South Australian Museum).

Field sampling

The May 2017 survey used the same 11 trapping transects that were established in 2015 by Aplin and Opiang (2017) on Hides Ridge (BAA 1); and on the Agogo Range near Moro (BAA 2). Metal tags attached to trees that identified trap positions were relocated (and replaced where necessary) along each transect. Box traps (medium-sized: 37 x 10 x 10 cm; and large-sized: 15 x 15 x 46 cm) were then laid out along the transect in the same format used in 2015 (Figure 4.1). Transects were operated for at least five nights in each case (Table 4.1). The total number of trapping nights was 2,653 (one trap set for one night = one trap-night).

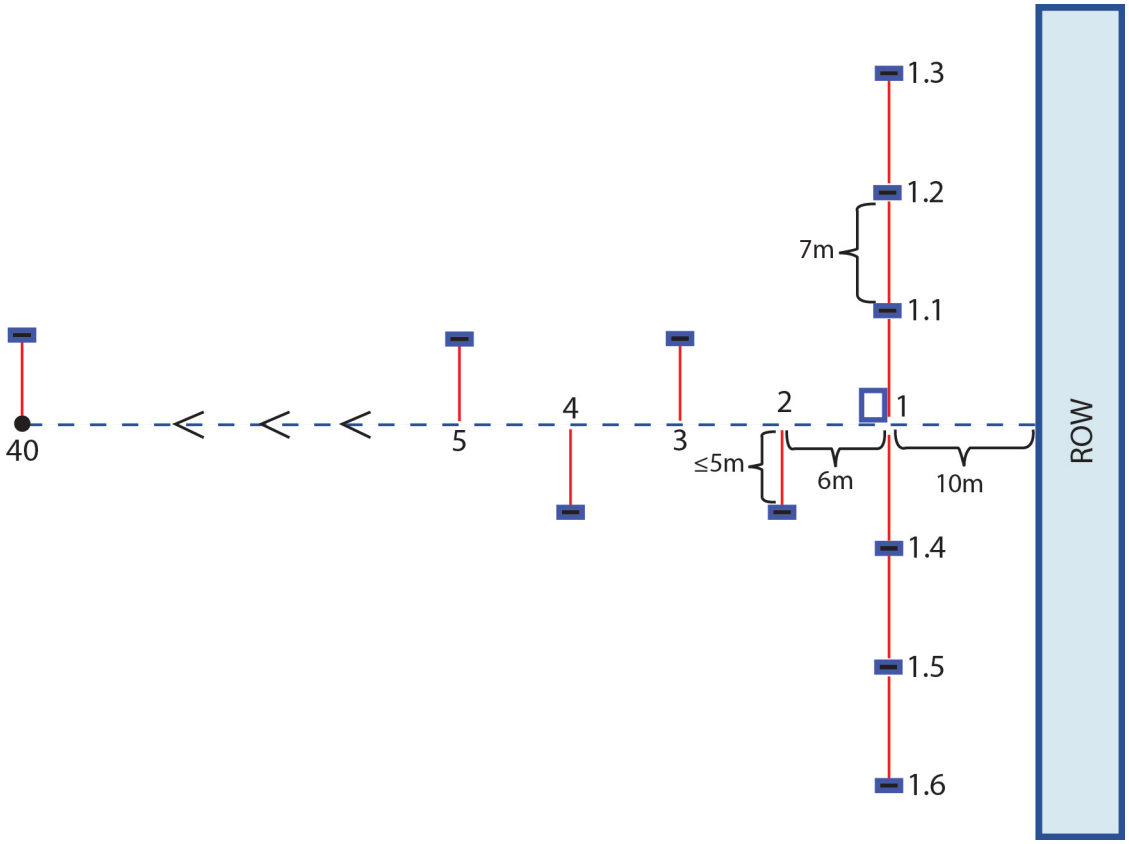

Figure 4.1. Standard design of a transect trap-line. ROW = right of way/road; open rectangle = large Elliott trap; closed rectangle = medium-sized 'Elliott' box trap. The central access path is represented by the dashed line. Trap positions are located at 6 m intervals along the transect access path. Traps are placed on alternate sides of the access path, and no more than 5 m to the right or left. Large box traps are placed at positions 1, 11, 21 and 31. Medium-sized box traps are placed at all other positions. Six medium-sized box traps are placed parallel to the ROW to provide additional sampling of the most heavily impacted 'edge' habitat.

Table 4.1. Summary of box trap deployments in 2017 (total number of traps is given as the number of medium-sized traps + number of large-sized traps).

Elevation	Transect	No. traps	Open date	Close date	Total nights	Total Trap nights	Elevation totals
1,000	M4	66 (62+4)	2017-05-11	2017-05-11	8	528	**528**
1,000	M5	—	—	—	—	—	
1,400	M1	41 (37+4)	2017-05-12	2017-05-20	8	328	
1,400	M2	39 (35+4)	2017-05-14	2017-05-20	6	234	
1,400	M3	41 (37+4)	2017-05-11	2017-05-20	9	369	**931**
2,200	H1	39 (35+4)	2017-05-24	2017-05-29	6	234	
2,200	H2	41 (37+4)	2017-05-26	2017-05-30	5	205	
2,200	H3	39 (35+4)	2017-05-24	2017-05-29	6	234	**673**
2,700	H4	—	—	—	—	—	
2,700	H5	41 (37+4)	2017-05-24	2017-05-30	7	287	
2,700	H6	39 (35+4)	2017-05-25	2017-05-30	6	234	**521**
						Overall	**2653**

Trapping results depend heavily on trap condition and placement, and the status of bait. Given that the investigators in the 2017 survey were different, it was particularly relevant to ensure that the trapping lines were run with similar diligence as in 2015 (Aplin and Opiang 2017; see their Appendix 5.2). Of paramount importance was ensuring that trigger sensitivity of the floor treadle was sufficient for successful operation, and that bait (local sweet potato) was always present, which required daily attention. Cleaned traps were placed off the main transect by c. 5 metres as per the transect design, and arranged against features where rodents had a greater chance of encountering them. The shiny trap surface was covered with leaf litter (Figure 4.14).

Captured animals ('novel' or first-time captures) were processed on-site and then released at point of capture. Seven individuals were kept as voucher specimens when it was deemed that a whole animal was required for confirmation of identity (Appendix 4.1). Each individual was sexed, weighed, measured (lengths of the head-body, tail and pes) and assessed for age and reproductive condition. The tip of the tail (<0.5 cm) was removed with clean scissors and placed into 95% ethanol for later genetic analysis. Barcoded vials (with a human-readable 'MEL-number') were used to minimise the likelihood of sample mix-ups. Recaptured animals (but not actual individuals) encountered on subsequent trapping nights were recognised on the basis of their freshly-snipped tail tips, and re-released near the point of capture.

Ecological analysis

A summary of basic trapping results included total number of novel and recaptured individuals for each species on each transect, as well as 'trapping success' (total number of captures per trap-night on each transect). The overall percentage of recaptures (calculated as the number of recaptures divided by the number of released individuals; i.e. excluding the small number removed from the trap-lines for vouchering purposes) was also calculated.

The trapping results matrix used in statistical analyses consisted of elevation, transect name, trap position (see Figure 4.1), capture night date, field identification, capture type (novel/recapture), plus the survey year. Following genetic analysis, the 'final identification' was added, and the matrix was restructured to reflect the updated identification. The 2015 data were also appended (available in the Appendix 5.4 of Aplin and Opiang 2017), and the 2015 field identifications were also joined by the final genetics-based identification. All statistical analyses and plotting were conducted after recaptures had been removed from the matrix. All statistical tests and plots were generated in a custom-written [R] language (R Core Development Team 2016) statistical computing script, which contains a record of all manipulations of the cleaned raw dataset, and all analyses and plot instructions for transparency.

Trapping data were pooled into six distance categories, each of which included eight trapping positions. The categories are defined as representing the immediate edge of the forest adjacent to the ROW ('0-22 metres': one large box trap at position 1, two medium-sized box traps at positions 2 and 3, and the six medium-sized traps extending in parallel with the ROW either side of position 1); and five distance categories of around 50 metres ('22-70 metres': positions 4–11; '70-120 metres': positions 12–19; '120-170 metres': positions 20–27; '170-220 metres': positions 28–35; '220-270 metres': positions 36-43; '270+ metres': positions 43-48). Abundance values in each category were adjusted according to survey effort in statistical tests (trapping nights and number of trapping positions).

Statistical analyses used Generalised Linear Mixed Models to examine the difference in two main dependent variables: Diversity as 'Species Richness' (total number of species) and 'abundance' (total number of captures from all rodent species; total captures of all Hydromyini rodents combined [genera: *Leptomys, Paramelomys, Uromys*], and total captures of all Rattini rodents combined [genus: *Rattus*]); with three fixed factors: increasing distance from the ROW, elevation category, and survey year; with transect as a random factor. Recapture rates were too low to include this parameter in the models.

Usage of scientific names

The naming scheme of Aplin and Opiang (2017) is followed for undescribed or taxonomically ambiguous taxa. We use 'sp. cf.' to refer to individuals that resemble certain species, but where the identification cannot be confirmed because of issues in the current understanding of the taxonomy of that species. When there is more than one such taxon, they are given a sequential letter code. The codes used follow exactly Aplin and Opiang (2017) to allow correspondence between the two genetic datasets.

Results

Genetics-based identification

Prior to summarising trapping results and conducting statistical analyses, the identification of each novel capture needed to be resolved using the new genome-scale genetics-based identification system. A total of 14 distinct rodent species was identified as being present in the BAA study areas, 12 of which were captured in 2017.

A complete correspondence between field identifications, mitochondrial DNA barcode-based identification and SNP-based identification is summarised in Appendix 4.2. From an inspection of this list, it is clear that the newer SNP-based identification framework resolved the following cases:

- Ambiguity within *Paramelomys mollis*-group animals;
- The species-level affinity of 'spiny' *Rattus* as *R. verecundus*-group;
- The status of one individual with morphological features typical of *Rattus 'niobe'* and a mitochondrial DNA barcode typical of *R. steini* as being *Rattus* sp. cf. *niobe* D;
- Ambiguous identifications of captures later identified as *Rattus rattus* and *R. steini*;
- Detected some mis-identifications from the field for the species *Paramelomys lorentzii*, *P. intermedius* and *P.* sp. cf. *mollis* AD.

It also allowed confirmation of the following:

Hydromyini (Figures 4.2–4.5):

- *Paramelomys* sp. cf. *rubex* A and B types are closely related but distinct species; and that type A is found only on Hides Ridge (though also elsewhere in PNG), and type B has only ever been collected near Moro (BAA 2) at lower elevations below 2,000 m;
- *Paramelomys intermedius* ('2') was detected for the first time in 2017, on Hides Ridge, and could be distinct at the species level from other '*intermedius*' at locations further afield in PNG;
- Likewise, *Paramelomys lorentzii* ('1') that was detected in both survey years in BAA 2 may also be distinct at the species level from other '*lorentzii*' at locations further afield in PNG;
- *Paramelomys* sp. cf. *mollis* mitochondrial types A and D are the same species, and are found on Hides Ridge, and elsewhere in PNG;
- *Paramelomys* in the '*platyops*' group were found near Moro in BAA 2, and are found elsewhere in PNG as well.

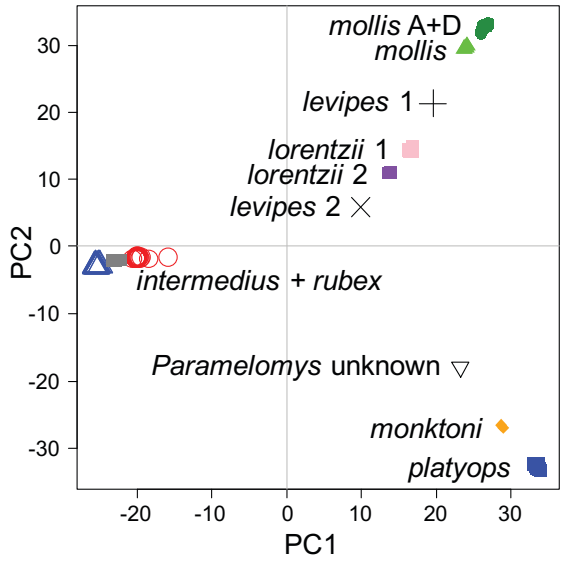

Figure 4.2. Principle Coordinates Analysis (PCoA) of New Guinea *Paramelomys* species (PC1 versus PC2), showing some of the main genetic clusters that correspond to species and species complexes.

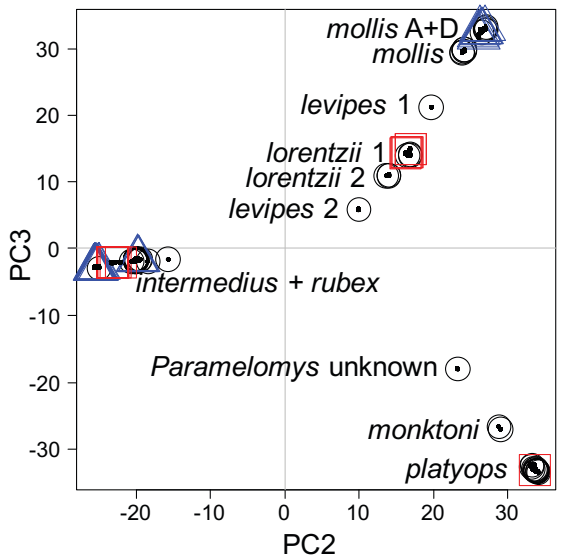

Figure 4.3. Principle Coordinates Analysis of New Guinea Paramelomys species (PC1 versus PC2; all samples have small black dots), highlighting those samples from Hides Ridge (BAA 1; blue triangles), near Moro (BAA 2; red squares), and further afield in PNG (black circles).

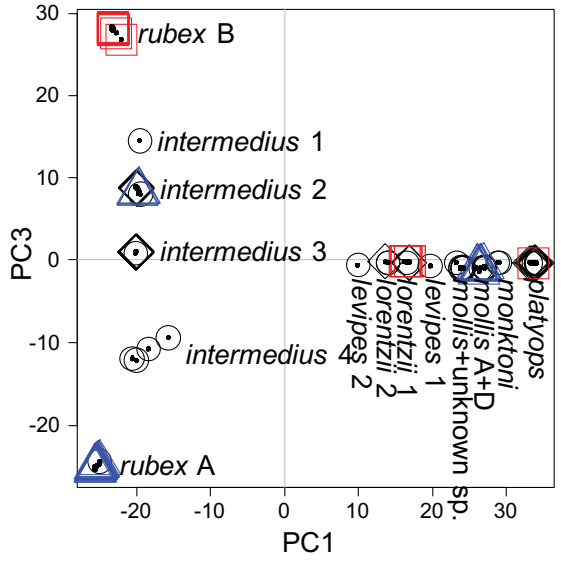

Figure 4.4. Principle Coordinates Analysis of New Guinea *Paramelomys* species (PC1 versus PC3; all samples have small black dots), highlighting those samples from Hides Ridge (BAA 1; blue triangles), near Moro (BAA 2; red squares), and further afield in PNG (black circles); and illustrating the diversity within the '*rubex*' and '*intermedius*' animals.

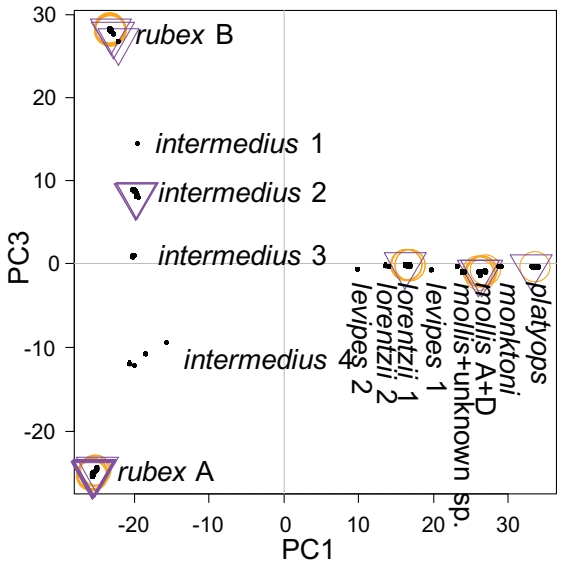

Figure 4.5. Principle Coordinates Analysis of New Guinea *Paramelomys* species (PC1 versus PC3; all samples have small black dots), highlighting those species detected in 2015 (orange circles) and 2017 (purple triangles).

Rattini (Figures 4.6–4.9):

- The identification of non-native *Rattus* were confirmed (*R. exulans* in 2015; *R. rattus* in both 2015 [Hides Camp] and 2017 [Hides Ridge at 2,200 m]);
- *Rattus steini* was detected for the first time in 2017 with the SNP-based identification method;
- The method also confirmed that *Rattus* sp. cf. *niobe* types B and D are very different species, and that type B is found only on Hides Ridge, and type D is found only near Moro;
- Furthermore, that *Rattus* sp. cf. *niobe* type D from Moro is similar but probably distinct at the species level from *niobe*-type animals from the P'nyang range, Mueller Range and Sandaun Province;
- The identity of the 'spiny' *Rattus* was allocated to the R. '*verecundus*' group, and its presence was confirmed on transects near Moro, but not on Hides Ridge.

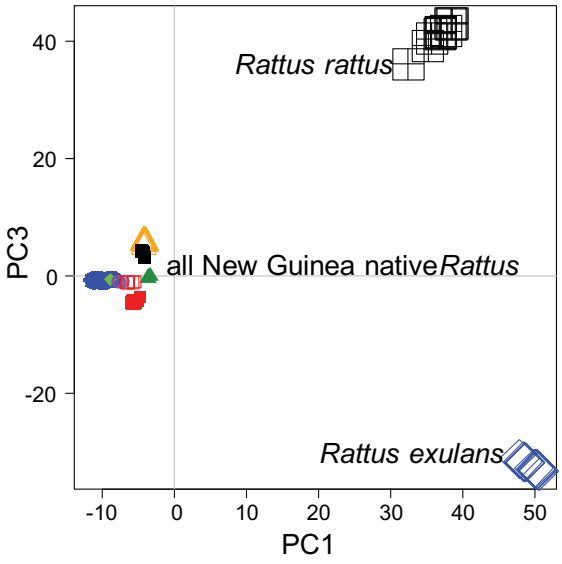

Figure 4.6. Principle Coordinates Analysis (PCoA) illustrating the large genetic differences between native New Guinea *Rattus* species and the introduced species *R. exulans* and *R. rattus*.

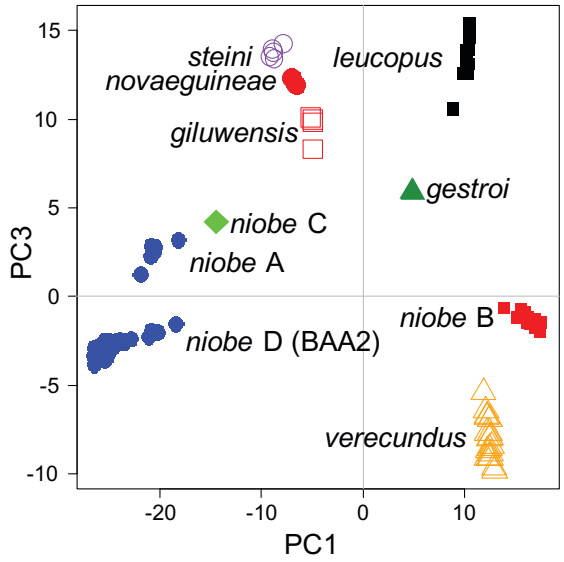

Figure 4.7. Principle Coordinates Analysis (PC1 versus PC3) giving further detail of relationships within New Guinea *Rattus* species.

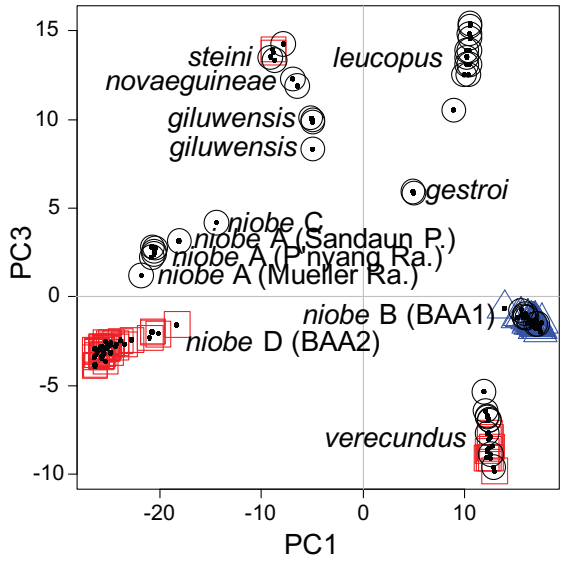

Figure 4.8. Principle Coordinates Analysis of New Guinea Rattus species (PC1 versus PC3; all samples have small black dots), highlighting those samples from Hides Ridge (BAA 1; blue triangles), near Moro (BAA 2; red squares), and further afield in PNG (black circles); and illustrating the diversity within the '*niobe*' animals.

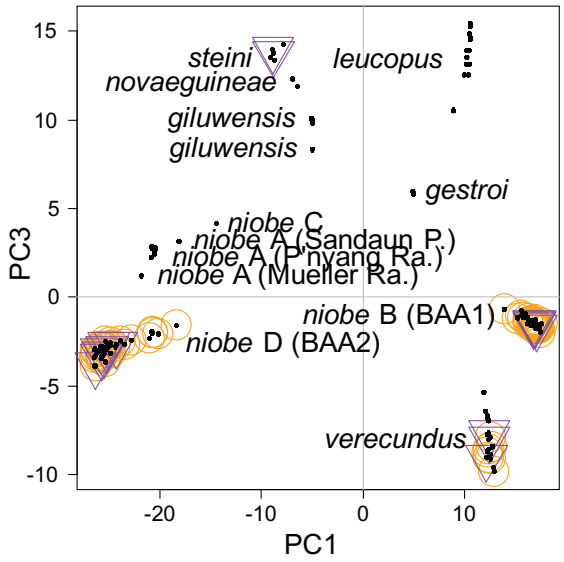

Figure 4.9. Principle Coordinates Analysis of New Guinea *Rattus* species (PC1 versus PC3; all samples have small black dots), highlighting those species detected in 2015 (orange circles) and 2017 (purple triangles).

In summary, the SNP-based identification framework provided the same affiliations as the mitochondrial DNA barcoding-based framework, but provided greater resolution of closely-related taxa, confirmed the species distinctness of all taxa, provided additional species affiliations and views on likely taxonomic breaks with groups further afield, and provided clarity in situations where the mitochondrial genome of one species was present in another. Of greatest importance to the present study, it allowed species identifications across sites, elevations, survey years and investigators to be consistent, and confirmed the presence of species of special significance (invasive species of *Rattus*).

Trapping results summary

A total of 69 rodent captures from 12 species was made on the nine transects (36 captures from BAA 1 and 33 captures from BAA 2), of which 53 (76.8%) were novel (total recapture rate was 25.8% after accounting for seven vouchered individuals) (Table 4.2; Figures 4.15–4.19). There were four species that had the highest captures rates and together accounted for 78.3% of captures: *Paramelomys* sp. cf. *rubex* A (18 captures), *Rattus verecundus* (11 captures), *Rattus* sp. cf. *niobe* B (11 captures), and *Rattus* sp. cf. *niobe* D (14 captures). Overall trapping success was 2.6%, and it ranged from 0 at transect M2 in BAA 2 to 6.1% at transect H1 in BAA 1.

The trapping results in 2017 are lower than the previous survey, with a total of 53 novel captures in 2017 compared with 133 in 2015 (a summary table similar to that of Table 4.2 was recalculated for the 2015 data; Appendix 4.3). Most of the difference between the two survey years is due to a lower abundance of two species—*Rattus* sp. cf. *niobe* B in BAA 1, and *Rattus* sp. cf. *niobe* D in BAA 1 (Table 4.3). However, Species Richness of rodents detected was higher in 2017—12 species compared to 10, with the additional encounters of *Rattus rattus* and *Leptomys elegans*, *Paramelomys intermedius* and *Rattus steini*, and the absence of *Rattus exulans* and *Uromys caudimaculatus*.

Table 4.2. Summary of rodent captures in 2017 (Elev: elevation; Tr: transect; TS: trapping success rates; totals in parentheses are number of novel captures, then number of recaptures; see also Appendix 4.3 to compare with totals from the 2015 survey). Shaded rows show total numbers for each elevation.

				Leptomys elegans	*Paramelomys lorentzii*	*Paramelomys intermedius*	*Paramelomys platyops*	*Paramelomys* sp. cf. *mollis* AD	*Paramelomys* sp. cf. *rubex* A	*Paramelomys* sp. cf. *rubex* B	*Uromys caudimaculatus*	*Rattus exulans*	*Rattus rattus*	*Rattus steini*	*Rattus verecundus*	*Rattus* sp. cf. *niobe* B	*Rattus* sp. cf. *niobe* D	***Total Species Richness***
Elev	**Tr**	**TS%**	**Total**															
BAA2		2.3	**33**															
1,000	M4	2.5	13 (8, 5)	0	0	0	0	0	0	0	0	0	0	1	10	0	2	***3***
1,000		**2.5**	**13**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**1**	**10**	**0**	**2**	***3***
1,400	M1	4.6	15 (11, 4)	1	0	0	1	0	0	1	0	0	0	0	1	0	11	***5***
1,400	M2	0	0															***0***
1,400	M3	1.4	5 (4, 1)	0	1	0	1	0	0	2	0	0	0	0	0	0	1	***4***
1,400		**2.2**	**20**	**1**	**1**	**0**	**2**	**0**	**0**	**3**	**0**	**0**	**0**	**0**	**1**	**0**	**12**	***6***
BAA1		**3.0**	**36**															
2,200	H1	6.0	14 (9, 5)	0	0	4	0	0	10	0	0	0	0	0	0	0	0	***2***
2,200	H2	1.0	2 (2, 0)	0	0	0	0	0	0	0	0	0	1	0	0	1	0	***2***
2,200	H3	2.6	6 (5, 1)	0	0	0	0	2	3	0	0	0	0	0	0	1	0	***3***
2,200		**3.3**	**22**	**0**	**0**	**4**	**0**	**2**	**13**	**0**	**0**	**0**	**1**	**0**	**0**	**2**	**0**	***5***
2,700	H5	3.1	9 (9, 0)	0	0	0	0	0	4	0	0	0	0	0	0	5	0	***2***
2,700	H6	2.1	5 (5, 0)	0	0	0	0	0	1	0	0	0	0	0	0	4	0	***2***
2,700		**2.7**	**14**	**0**	**0**	**0**	**0**	**0**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**9**	**0**	***2***
Total		**2.6**	**69 (53, 16)**	**1**	**1**	**4**	**2**	**2**	**18**	**3**	**0**	**0**	**1**	**1**	**11**	**11**	**14**	***12***

Table 4.3. Summary of captures at each elevation (in each cell the first value is from the 2015 survey, the second value from the 2017 survey; the last column is the total number of novel captures across all elevations).

	1,000 m	1,400 m	2,200 m	2,700 m	Novel captures
HYDROMYINI					
Leptomys elegans	oo	o●	oo	oo	1,0
Paramelomys lorentzii	oo	●●	oo	oo	5,1
Paramelomys intermedius	oo	oo	o●	oo	0,4
Paramelomys platyops	●o	o●	oo	oo	0,2
Paramelomys sp. cf. *mollis* AD	oo	oo	●●	●o	6,2
Paramelomys sp. cf. *rubex* A	oo	oo	●●	●●	11,12
Paramelomys sp. cf. *rubex* B	●o	●●	oo	oo	13,4
Uromys caudimaculatus	oo	●o	oo	oo	1,0
RATTINI					
Rattus exulans	oo	●o	oo	oo	5,0
Rattus rattus	oo	oo	o●	oo	0,1
Rattus steini	o●	oo	oo	oo	0,1
Rattus verecundus	●●	oo	oo	oo	9,6
Rattus sp. cf. *niobe* B	oo	oo	●●	●●	42,11
Rattus sp. cf. *niobe* D	o●	●●	oo	oo	38,11
Total Richness each elevation	**5**	**7**	**5**	**3**	

When examining patterns of species capture at different elevations, and at different distances from the ROW, the most obvious patterns are associated with elevation (Table 4.4; compare with Appendix 4.4 that summarises the 2015 survey results). In both survey years, no species of rodent was present in both BAA 1 and BAA 2; i.e. the rodent assemblages above and below 2,000 m in elevation are completely different. While morphologically-based identifications might have suggested that common species such as '*Paramelomys rubex*' and '*Rattus niobe*' are found across the entire elevational range of the study (1,000–2,700 m), the SNP-based genetic identification method showed unambiguously that this was not the case.

In addition, it is clear that the species assemblages differ within each BAA. The species at 2,700 m are a subset of those at 2,200 m. A different situation occurs in BAA 2, where there is slightly higher total Species Richness at 1,400 m (compiled from both years, see Table 4.3); and where some species are found at both 1,000 m and 1,400 m, and others have only been detected in one of the elevational bands.

Finally, an inspection of the pattern of captures by distance category (increasing distance from left to right in each cell of Table 4.4) does not reveal any strong pattern for any species. Abundance aside, no rodent species was associated unambiguously with either the forest edge, or the forest interior.

Table 4.4. Trapping summary from the 2017 survey (symbols in each cell represent the trapping result from each distance category along the transect, beginning at 0 metres from the left; open circle is an absence of captures; closed circle is at least one capture in that distance category; blue shading shows that a species was captured on at least one transect in a particular elevation; species names in parentheses were not captured during the 2017 survey, but were captured during the 2015 survey; see also Appendix 4.4).

Elevation	**1,000 m**	**1,400 m**			
Transect	**M4**	**M1**	**M2**	**M3**	
Species					
HYDROMYINI					
Leptomys elegans	○○○○○○○	○○○○●	○○○○○	○○○○○	
Paramelomys lorentzii	○○○○○○○	○○○○○	○○○○○	●○○○○	
Paramelomys intermedius	○○○○○○○	○○○○○	○○○○○	○○○○○	
Paramelomys platyops	○○○○○○○	○○○○●	○○○○○	○○○○○	
Paramelomys sp. cf. *mollis* AD	○○○○○○○	○○○○○	○○○○○	○○○○○	
Paramelomys sp. cf. *rubex* A	○○○○○○○	○○○○○	○○○○○	○○○○○	
Paramelomys sp. cf. *rubex* B	○○○○○○○	○○●○○	○○○○○	●○●○○	
(*Uromys caudimaculatus*)	○○○○○○○	○○○○○	○○○○○	○○○○○	
RATTINI					
(*Rattus exulans*)	○○○○○○○	○○○○○	○○○○○	○○○○○	
Rattus rattus	○○○○○○○	○○○○○	○○○○○	○○○○○	
Rattus steini	○○○○○○●	○○○○○	○○○○○	○○○○○	
Rattus verecundus	○●●●○●○	○○○○○	○○○○○	○○○○○	
Rattus sp. cf. *niobe* B	○○○○○○○	○○○○○	○○○○○	○○○○○	
Rattus sp. cf. *niobe* D	○○●○○●○	○○●●●	○○○○○	●○○○○	
Elevation	**2,200 m**			**2,700 m**	
Transect	**H1**	**H2**	**H3**	**H5**	**H6**
Species					
HYDROMYINI					
Leptomys elegans	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○
Paramelomys lorentzii	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○
Paramelomys intermedius	○●●●○	○○○○○	○○○○○	○○○○○	○○○○○
Paramelomys platyops	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○
Paramelomys sp. cf. *mollis* AD	○○○○○	○○○○○	●○○○○	○○○○○	○○○○○
Paramelomys sp. cf. *rubex* A	●○○●○	○○○○○	○●●○○	●○○●○	○○○●○
Paramelomys sp. cf. *rubex* B	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○
(*Uromys caudimaculatus*)	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○
RATTINI					
(*Rattus exulans*)	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○
Rattus rattus	○○○○○	●○○○○	○○○○○	○○○○○	○○○○○
Rattus steini	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○
Rattus verecundus	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○
Rattus sp. cf. *niobe* B	○○○○○	●○○○○	○○○○●	●○●●○	●○●●○
Rattus sp. cf. *niobe* D	○○○○○	○○○○○	○○○○○	○○○○○	○○○○○

Statistical analyses

Generalised Linear Mixed Models were created to determine whether there were statistically significant differences in rodent Species Richness and abundance between survey years, and at different distances from the ROW and elevation. There was some expectation that there would be a clear difference between the two surveys, given that the capture rate in 2015 was around two and a half times that in 2017. However, there was much variability amongst treatments levels, and almost no significant differences were observed. The only significant difference was a slightly greater abundance of Rattini in 2017 (Table 4.5). An inspection of the means and standard deviations reveals how similar capture rates were even when results were pooled into distance categories. The patterns are also obvious from boxplots of means, which show some outlier cases with relatively high capture rates, but an overall similar level across treatment levels (Figures 4.10–4.13). The conclusion drawn from these tests is that there has been no detectable change in the overall diversity or population sizes of the rodent assemblage that is clearly attributable to the influence of the ROW. The variability within treatments appears to have some influence on the results.

Table 4.5. Mean ± standard deviation for all distance and elevation categories, and per survey year. Statistical tests had outcomes that were mostly not significant, with the exception of 'year' for the total number of Rattini captures (bold-italics).

	Category	Total Species Richness	Total Captures	Total captures Hydromyini	Total captures Rattini
Distance	0-22	1.53 ± 0.64	3.0 ± 1.77	0.80 ± 1.21	2.20 ± 1.88
from ROW (m)	22-70	1.70 ± 1.25	3.5 ± 2.67	1.10 ± 1.37	2.40 ± 2.01
	70-120	1.40 ± 0.63	2.27 ± 1.44	0.67 ± 0.90	1.60 ± 1.45
	120-170	1.50 ± 0.67	2.25 ± 1.35	0.92 ± 1.08	1.33 ± 0.89
	170-220	2.25 ± 0.71	4.75 ± 2.55	2.0 ± 1.69	2.75 ± 1.28
	220-270	2.0 ± 1.0	2.0 ± 1.0	0.67 ± 1.15	1.33 ± 0.58
	270+	1	1	0	1
Elevation (m)	1,000	1.40 ± 0.70	2.0 ± 1.56	0.2 ± 0.63	1.8 ± 1.55
	1,400	2.05 ± 1.08	4.05 ± 2.12	1.31 ± 1.41	2.73 ± 1.59
	2,200	1.58 ± 0.61	2.68 ± 1.53	1.21 ± 1.03	1.47 ± 1.68
	2,700	1.31 ± 0.48	2.37 ± 2.15	0.75 ± 1.34	1.62 ± 1.09
Year	2,015	1.72 ± 0.89	3.41 ± 2.21	0.97 ± 1.33	***2.43 ± 1.65****
	2,017	1.48 ± 0.65	2.12 ± 1.33	0.96 ± 1.10	1.16 ± 1.03

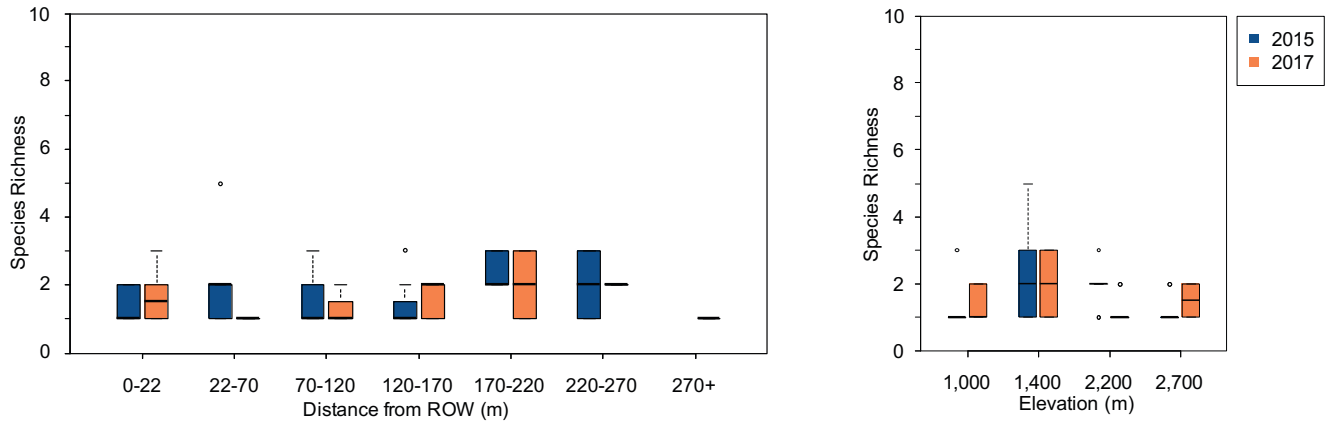

Figure 4.10. Summary of the patterns of Species Richness with increasing distance from the ROW and elevation. All sites have been combined for each of the two factors, but segregated by year. [Boxplot components: central bar—median; boxes—inter-quartile range, with second quartile group below median, third quartile group above median; bars—minimum and maximum values; circles—statistical outliers]

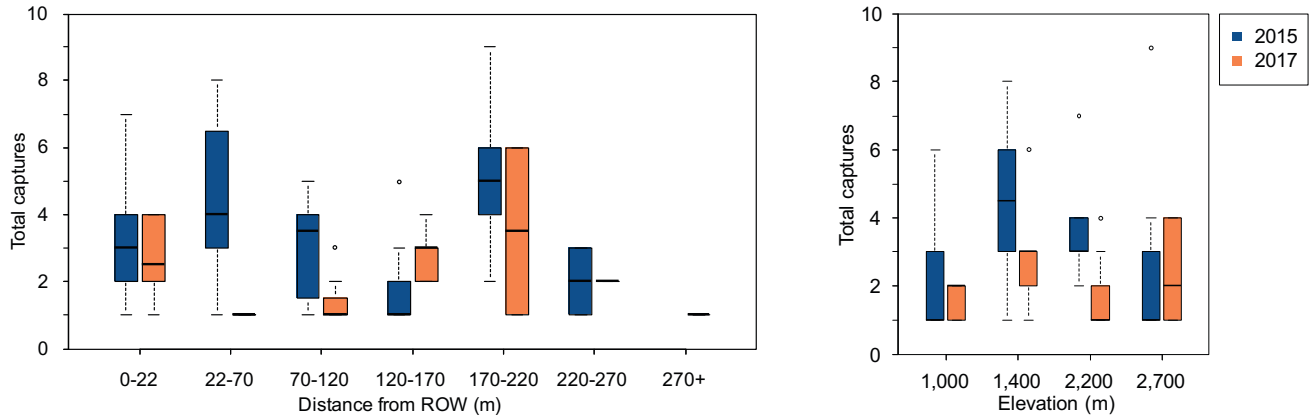

Figure 4.11. Summary plots of the pattern of the total number of captures for all rodent species at increasing distance from the ROW and at increasing elevation.

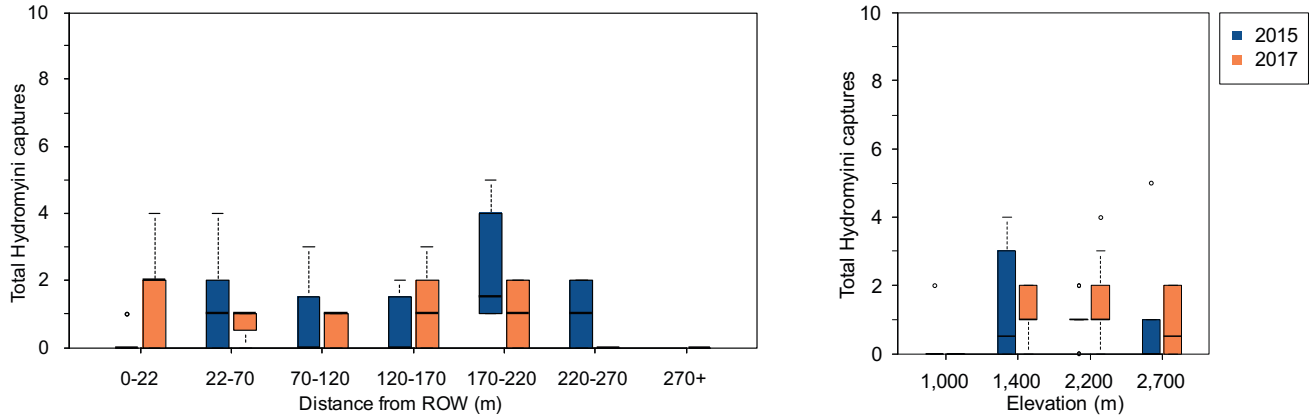

Figure 4.12. Summary plots of the pattern of the total number of captures for Hydromyini rodent species at increasing distance from the ROW and at increasing elevation.

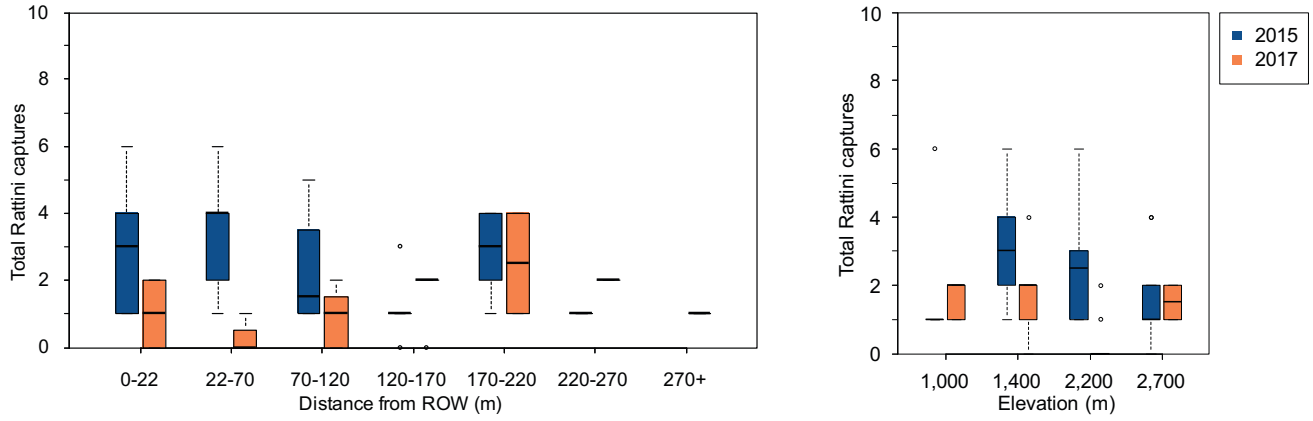

Figure 4.13. Summary plots of the pattern of the total number of captures for Rattini rodent species at increasing distance from the ROW and at increasing elevation.

Discussion

The overall objective of the rodent study component is to detect possible influences of Project linear infrastructure on the diversity and abundance of rodent species. We may expect changes in abundance with rodents because some species are highly fecund, especially compared to bats, and bats may respond more quickly to structural changes in their environment by moving to different foraging areas in a landscape, rather than changing their population size. Two years of monitoring have brought numerous important lessons.

The differences in species composition observed within some elevation bands between the two survey years shows that we are still in the process of documenting the full assemblage of rodents within both BAAs. To best understand how industry-related activities might affect the natural environment, our interpretations need to be based on the best possible information about local native species assemblages, and such knowledge will take sustained effort to acquire. As a bonus, the accumulated knowledge will provide excellent context for similar situations elsewhere, especially in a country where systematic studies of small mammals have been conducted with less frequency than other parts of the world.

The difference in species composition between sampling years also shows that deterministic ecosystems such as closed rainforest in PNG can be variable, and that populations of small mammals sampled two years apart can also show signs of demographic fluctuation. In the present study, we observed that species composition was different because of the addition of four new species (and because two species from 2015 were not detected), and that total captures of the two most common rodents in 2017 were considerably lower.

Biases associated with trapping may have had some influence on the results, but we maintained a high level of diligence with regard to trap maintenance and careful adherence to sampling protocols, so we suspect that unexpected variations such as the much lower numbers of *Rattus* sp. cf. *niobe* B in BAA 1, and *Rattus* sp. cf. *niobe* D in BAA 1 observed during 2017 had less to do with some aspect of trapping and more to do with actual abundance of these species at the time of the survey.

The taxonomy of New Guinea mammals is still profoundly incomplete, which has implications for any biological survey on the island, and the confidence in identifications made by experienced field biologists and taxonomic specialists alike. A high level of experience with PNG rodents can bring an excellent rate of successful morphological-based identification in the field (see Appendix 4.2), but undiscovered morphologically cryptic species that can be diagnosed only with genetic markers will still confound results. The application of genetics-based identification in the present study has demonstrated unambiguously the value of including advanced, but cost-effective and practicable, methods to ensure the consistency of identifications among sites, years and investigators.

Aside from the practical considerations of identifying species, the apparently complete replacement of species at elevations above 2,000 m is of interest in a broader ecological sense. Understanding where these boundaries are will have implications for ecological interpretations in environmental impact assessment. There is also a growing understanding of the role that isolation along vertical environmental gradients has on species evolution in PNG. Both genetics-based identification systems detected two excellent examples ('*Paramelomys rubex*' and '*Rattus niobe*') of populations that have diverged genetically from taxa occurring on other mountain ranges, are likely to be at least part-way through a process of reproductive isolation, given that the gene pools were found to be discrete. This situation may be common, and if so it has implications for estimates of mammal diversity in New Guinea, where advanced genetic methods have not been applied extensively. This should be taken into consideration during future biodiversity studies in New Guinea.

The creation of linear infrastructure corridors through broad expanses of closed forest can bring detectable evidence of additional pressures on native mammals within only a few years. Aplin and Opiang (2017) already documented

increased access by hunting dogs (with and without their owners) on Hides Ridge, and the presence of one introduced species of rodent, *Rattus exulans* at the edges of transects at KP107 (Appendix 4.4). In 2017, we documented the introduced pest species *Rattus rattus* at 2,200 m around 7.5 km from the Hides Gas Conditioning Plant (HGCP) at the edge of transect H2, which is suggestive of this species using the road/ROW to extend its range from areas where it is a commensal. While the origin of this animal or its recent forebears is unknown (i.e. HGCP or local villages), the ROW has likely assisted dispersal of the species. The consequences of increased abundance of this species in natural systems is not well known, but Aplin and Opiang (2017) pointed to the possibility of local declines in native species because of competitive exclusion from the introduced species and the transfer of novel pathogens to naïve native rodent hosts.

The 2017 survey has contributed to each of the six specific objectives of the study:

- The trapping effort expanded our knowledge of local rodent diversity, adding four additional species to the overall total and documenting an apparent lower abundance during 2017 in two of the more common species in particular.

- The genetics-based identification methods used in both 2015 and 2017 have helped identify several likely undescribed species, including one species of *Paramelomys* (sp. cf. *rubex* type 'B') and one species of *Rattus* (sp. cf. *niobe* type 'D') that are apparently only known from the BAA study areas; plus several others that are part of species complexes that have yet to be fully resolved. Understanding the special sensitivities of rodent species requires further study, but it is likely that the higher elevation species may be more sensitive to pressure from commensal predators such as dogs and competitors such as *Rattus rattus* because of fewer available resources.

- *Rattus exulans* was not detected again at KP107 in 2017, but there was evidence of the use of the ROW by the pest species *Rattus rattus*, which was captured a significant distance along the Hides spineline at 2,200 m asl.

- A greater appreciation of apparent population size change in the two most common rodents was gained from the 2017 survey. Temporal fluctuations in local density as part of natural processes will need to be considered as context when making interpretations about the possible effects of linear infrastructure.

- The most relevant threats to native rodents documented during the 2015 and 2017 surveys were the presence of dogs and of exotic rats, *Rattus* spp.. These have the potential to contribute to local declines in native species because of predation, competitive exclusion by the introduced species and the transfer of novel pathogens to naïve native rodent hosts.

- Further long-term study will likely help with assessments of the usefulness of non-volant mammal communities more broadly as potential indicators of change in habitat quality in each of the BAAs.

Conclusions

1. Total captures of small rodents in the groups Hydromyini and Rattini on the 2017 survey were around two and a half times lower than in 2015, however in statistical tests Species Richness and total captures were not significantly different at different distances from linear infrastructure, different elevations, or between survey years.

2. Rather than suggesting a reduced value of this survey component, the lower capture rate recorded in 2017 is a demonstration of the value of long-term studies. The lower capture rate is not thought to be related to an influence of the ROW, but instead is likely to reflect natural patterns of variation that need

to be understood more fully from future work. Capture rates are actually relatively high compared to some other studies where close to zero or nil capture rates have been reported.

3. An appreciation of the diversity of rodents in the BAAs has been helped by the detection of an additional four species of rodent. It is likely that additional species of small rodent are yet to be encountered by the study. Further survey will also assist with an understanding of the potential sensitivities of each native species.

4. Introduced commensal species that have the potential to increase rates of predation, competitive exclusion and the probability of exposure of naïve native rodent species to novel pathogens have now dispersed along ROW in BAA 1; a specimen of the pest species *Rattus rattus* was captured a significant distance along the Hides spineline at 2,200 m asl. during the 2017 survey. However, the source of these introduced agents varies, with evidence that dogs originate from local villages, and non-native *Rattus* come from the transport of plant and equipment to mining operations and their subsequent movement along new linear infrastructure corridors.

5. Genetics-based identification has been the foundation of reliable comparisons between sites, survey years and investigators in this study; and the results (that have included recognition of at least two new species not seen elsewhere) are testament to a likely high, under-estimated level of rodent diversity across New Guinea.

Recommendations

1. It is recommended that the rodent live-trapping component of the study continue, using the same modified methodology (ie camera trap data excluded from this component) adopted in 2017, and that a second trapping line be established at Arakubi Quarry. This will require extra personnel to service all trapping lines.

2. Further attention should be given to ensuring that quarantine and rodent pest control programs are being maintained at the Hides Gas Conditioning Plant in particular. A wider study around the HGCP would provide further information on the abundance of exotic invasive species such as *R. rattus* and *R. exulans*.

3. Future surveys should continue to build upon the genetic work that has been initiated here. Identification of opportunities to expand the genetic work to a national level, partnering with NGOs or industry partners, and to train young Papua New Guinean scientists in advanced survey techniques, would add substantial value to the PMA3 program.

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Plate 1

Figure 4.14. Medium-sized box trap in situ

Figure 4.15. *Leptomys elegans*

Figure 4.16. *Paramelomys* sp. cf. *rubex* B

Figure 4.17. *Rattus rattus*

Figure 4.18. *Rattus* sp. cf. *niobe* B

Figure 4.19. *Rattus* sp. cf. *niobe* D

Appendix 4.1. Summary of whole specimen vouchers taken on the survey, which have been deposited in the South Australian Museum.

Tissue number	Validated species	Transect	Sex
MEL0527–MEL0529	*Leptomys elegans*	M1-30	F
MEL0541–MEL0542	*Lorentzimys nouhuysi*	hand capture	M
MEL0544–MEL0545	*Rattus steini*	M4-48	F
MEL0722	*Rattus* sp. cf. *niobe* B	H5-1.3	F
MEL0724	*Rattus* sp. cf. *niobe* B	H6-20	F
MEL0728	*Paramelomys* sp. cf. *rubex* A	H6-27	F
MEL0731	*Paramelomys* sp. cf. *rubex* A	H1-1.3	F

Appendix 4.2. Correspondence between morphological-based field identification, mitochondrial DNA (mtDNA)-based identification, and genome marker (SNP)-based identification for all samples sequenced successfully.

Year	Trap No	Field ID	mtDNA ID	SNP ID	Field No	ABTC No
2015	H6-1	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	1	ABTC141186
2015	H5-2.3	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	2	ABTC141187
2015	H1-4	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	3	ABTC141188
2015	H1-2.1	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	4	ABTC141189
2015	H1-1	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	5	ABTC141190
2015	H1-34	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	6	ABTC141191
2015	H1-19	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	7	ABTC141192
2015	H1-8	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	8	ABTC141193
2015	H2-4	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	9	ABTC141194
2015	H1-2.6	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	10	ABTC141195
2015	H2-28	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	11	ABTC141196
2015	H2-32	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	12	ABTC141197
2015	H6-28	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	13	ABTC141198
2015	H6-3	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	14	ABTC141199
2015	H6-2	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	15	ABTC141200
2015	H5-27	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	16	ABTC141201
2015	H5-18	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	17	ABTC141202
2015	H5-16	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	18	ABTC141203
2015	H5-6	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	19	ABTC141204
2015	H6-34	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	21	ABTC141206
2015	H6-31	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	22	ABTC141207
2015	H6-28	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	23	ABTC141208
2015	H6-25	*Paramelomys_mollis*	*Paramelomys_cf_mollis_A*	*Paramelomys_ mollis_AD*	24	ABTC141209
2015	H2-31	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	25	ABTC141210
2015	H2-11	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	27	ABTC141211
2015	H2-3	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	28	ABTC141212
2015	H1-19	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	29	ABTC141213
2015	H6-18	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	30	ABTC141214
2015	H6-11	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	31	ABTC141215
2015	H6-6	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	32	ABTC141216
2015	H6-3	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	33	ABTC141217
2015	H1-34	*Paramelomys_cf_ rubex*		*Paramelomys_ rubex_A*	34	
2015	H1-2.5	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	35	ABTC130449
2015	H1-2.6	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	36	ABTC141219

Year	Trap No	Field ID	mtDNA ID	SNP ID	Field No	ABTC No
2015	H6-33	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	38	ABTC141221
2015	H6-28	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	39	ABTC141222
2015	H2-28	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	40	ABTC141223
2015	H2-3	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	41	ABTC141224
2015	H1-2.1	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	42	ABTC141225
2015	H1-2.4	*Paramelomys_cf_ rubex*		*Paramelomys_ rubex_A*	43	
2015	H1-19	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	44	ABTC140467
2015	H1-8	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	45	ABTC141227
2015	H1-4	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	46	ABTC141228
2015	H1-13	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	47	ABTC140468
2015	H6-28	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	48	ABTC141230
2015	H6-29	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	49	ABTC141231
2015	H6-28	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	50	ABTC141232
2015	H6-6	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	51	ABTC141233
2015	H5-40	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	52	ABTC141234
2015	H3-25	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_A*	*Paramelomys_ rubex_A*	53	ABTC141235
2015	H3-21	*Rattus_cf_niobe*	*Rattus_cf_niobe_B*	*Rattus_niobe_B*	54	ABTC141236
2015	H3-19	*Paramelomys_mollis*	*Paramelomys_cf_mollis_A*	*Paramelomys_ mollis_AD*	55	ABTC141237
2015	H3-3	*Paramelomys_mollis*	*Paramelomys_cf_mollis_A*	*Paramelomys_ mollis_AD*	56	ABTC141238
2015	H3-19	*Paramelomys_mollis*	*Paramelomys_cf_mollis_A*	*Paramelomys_ mollis_AD*	57	ABTC141239
2015	H3-26	*Paramelomys_mollis*	*Paramelomys_cf_mollis_C*	*Paramelomys_ mollis_AD*	61	ABTC141246
2015	H3-18	*Rattus_cf_niobe*		*Rattus_niobe_B*	62	ABTC130554
2015	H3-3	*Rattus_cf_niobe*		*Rattus_niobe_B*	63	
2015	H2-4	*Paramelomys_mollis*	*Paramelomys_cf_mollis_A*	*Paramelomys_ mollis_AD*	64	ABTC141248
2015	H2-2	*Rattus_cf_niobe*		*Rattus_niobe_B*	65	ABTC141249
2015	M2-5	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	66	ABTC141250
2015	M2-6	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	67	ABTC141251
2015	M2-7	*Paramelomys_lorentzii*	*Paramelomys_cf_lorentzii*	*Paramelomys_ lorentzii*	68	ABTC141252
2015	M2-22	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	69	ABTC141253
2015	M4-3	*Rattus_sp_spiny*	*Rattus_sp_spiny*	*Rattus_verecundus*	70	ABTC130385
2015	M4-4	*Rattus_sp_spiny*	*Rattus_sp_spiny*	*Rattus_verecundus*	71	
2015	M4-8	*Rattus_sp_spiny*	*Rattus_sp_spiny*	*Rattus_verecundus*	72	ABTC140471
2015	M2-2.1	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	73	ABTC141256
2015	M2-2.2	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	74	ABTC141257

Year	Trap No	Field ID	mtDNA ID	SNP ID	Field No	ABTC No
2015	M2-12	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	75	ABTC141258
2015	M2-13	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	76	ABTC141259
2015	M2-19	*Rattus_cf_niobe*		*Rattus_niobe_D*	77	
2015	M2-32	*Rattus_cf_niobe*	*Rattus_cf_niobe_D (R_ steini_mtDNA)*	*Rattus_niobe_D*	78	ABTC141260
2015	M1-31	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	79	ABTC140472
2015	M1-2.1	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	80	ABTC141262
2015	M3-22	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	82	ABTC141264
2015	M3-17	*Paramelomys_lorentzii*	*Paramelomys_cf_lorentzii*	*Paramelomys_ lorentzii*	83	ABTC141265
2015	M2-32	*Paramelomys_lorentzii*	*Paramelomys_cf_lorentzii*	*Paramelomys_ lorentzii*	84	ABTC141266
2015	M2-17	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	86	ABTC141267
2015	M1-29	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	88	ABTC141268
2015	M1-31	*Paramelomys_lorentzii*	*Paramelomys_cf_lorentzii*	*Paramelomys_ lorentzii*	94	ABTC141274
2015	M1-15	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	95	ABTC141275
2015	M1-16	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	96	ABTC141276
2015	M1-2.3	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	97	ABTC141277
2015	M3-32	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	99	ABTC141278
2015	M3-12	*Rattus_cf_niobe*		*Rattus_niobe_D*	100	ABTC130401
2015	M3-5	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_B*	*Paramelomys_ rubex_B*	101	ABTC141280
2015	M4-43	*Rattus_sp_spiny*	*Rattus_sp_spiny*	*Rattus_verecundus*	102	ABTC140473
2015	M4-21	*Rattus_sp_spiny*	*Rattus_sp_spiny*	*Rattus_verecundus*	103	ABTC140474
2015	M4-14	*Rattus_sp_spiny*	*Rattus_sp_spiny*	*Rattus_verecundus*	104	ABTC140475
2015	M4-4	*Rattus_sp_spiny*	*Rattus_sp_spiny*	*Rattus_verecundus*	108	ABTC140476
2015	M4-11	*Rattus_cf_niobe*	*Rattus_sp_spiny*	*Rattus_verecundus*	109	ABTC141286
2015	M3-22	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_B*	*Paramelomys_ rubex_B*	111	ABTC141287
2015	M3-17	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_B*	*Paramelomys_ rubex_B*	112	ABTC141288
2015	M3-8	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	113	ABTC141289
2015	M3-9	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	114	ABTC141290
2015	M3-6	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	116	ABTC141291
2015	M2-32	*Paramelomys_cf_ rubex*		*Paramelomys_ rubex_B*	117	ABTC141292
2015	M1-18	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	122	ABTC141293
2015	M1-2.3	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	123	ABTC141294
2015	M4-6	*Rattus_sp_spiny*	*Rattus_sp_spiny_*	*Rattus_verecundus*	129	ABTC140477
2015	M4-8	*Rattus_sp_spiny*	*Rattus_sp_spiny_*	*Rattus_verecundus*	130	ABTC130407
2015	M2-10	*Uromys_cf_ caudimaculatus*	*Uromys_cf_caudimaculatus*	*Uromys_ caudimaculatus*	131	ABTC130529
2015	M2-34	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	132	ABTC141299
2015	M2-32	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_B*	*Paramelomys_ rubex_B*	133	ABTC141300

Year	Trap No	Field ID	mtDNA ID	SNP ID	Field No	ABTC No
2015	M2-13	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	134	ABTC141301
2015	M2-9	*Paramelomys_lorentzii*	*Paramelomys_cf_lorentzii*	*Paramelomys_ lorentzii*	135	ABTC141302
2015	M2-8	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	137	ABTC141303
2015	M2-5	*Rattus_exulans*	*Rattus_exulans*	*Rattus_exulans*	138	ABTC141304
2015	M1-31	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	139	ABTC141305
2015	M1-25	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	141	ABTC141306
2015	M1-2.2	*Rattus_exulans*	*Rattus_exulans*	*Rattus_exulans*	142	ABTC141307
2015	M3.33	*Rattus_cf_niobe*	*Rattus_niobe_D*	*Rattus_niobe_D*	143	ABTC141308
2015	M3-32	*Rattus_cf_niobe*	*Rattus_niobe_D*	*Rattus_niobe_D*	144	ABTC141309
2015	M3-21	*Rattus_cf_niobe*	*Rattus_niobe_D*	*Rattus_niobe_D*	145	ABTC141310
2015	M3-6	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_B*	*Paramelomys_ rubex_B*	146	ABTC141311
2015	M3-5	*Rattus_cf_niobe*	*Rattus_niobe_D*	*Rattus_niobe_D*	147	ABTC141312
2015	M4-39	*Paramelomys_cf_ rubex*		*Paramelomys_ rubex_B*	149	
2015	M4-39	*Paramelomys_platyops*	*Paramelomys_platyops*	*Paramelomys_ platyops*	150	ABTC141314
2015	M1-33	*Paramelomys_cf_ rubex*		*Paramelomys_ rubex_B*	154	ABTC141316
2015	M1-31	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	155	ABTC141317
2015	M1-30	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	156	ABTC141318
2015	M1-18	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	157	ABTC141319
2015	M1-2.3	*Rattus_exulans*	*Rattus_exulans*	*Rattus_exulans*	159	ABTC141320
2015	M2-32	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_B*	*Paramelomys_ rubex_B*	161	ABTC141321
2015	M3-23	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	164	ABTC141322
2015	M3-22	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_B*	*Paramelomys_ rubex_B*	165	ABTC141323
2015	M3-12	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	166	ABTC141324
2015	M1-2.3	*Rattus_exulans*	*Rattus_exulans*	*Rattus_exulans*	174	ABTC141325
2015	M2-9	*Paramelomys_cf_ rubex*		*Paramelomys_ rubex_B*	178	ABTC141326
2015	M3-15	*Paramelomys_cf_ rubex*	*Paramelomys_cf_rubex_B*	*Paramelomys_ rubex_B*	179	ABTC141327
2015	M3-4	*Paramelomys_cf_ rubex*		*Paramelomys_ rubex_B*	182	ABTC141328
2015	M3-2.2	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	183	ABTC141329
2015	M3-2.5	*Rattus_cf_niobe*	*Rattus_cf_niobe_D*	*Rattus_niobe_D*	185	ABTC141330
2015	M3-28	*Paramelomys_cf_ rubex*		*Paramelomys_ rubex_B*	189	ABTC141331
2015	M3-2.3	*Rattus_exulans*		*Rattus_exulans*	192	
2017	M3-1.5	*Rattus_cf_niobe*		*Rattus_niobe_D*	MEL0520	
2017	M4-4	*Rattus_verecundus*		*Rattus_verecundus*	MEL0521	
2017	M4-20	*Rattus_verecundus*		*Rattus_verecundus*	MEL0522	

Year	Trap No	Field ID	mtDNA ID	SNP ID	Field No	ABTC No
2017	M3-1	*Paramelomys_rubex*		*Paramelomys_ rubex_B*	MEL0523	
2017	M1-20	*Rattus_cf_niobe*		*Rattus_niobe_D*	MEL0524	
2017	M4-17	*Rattus_verecundus*		*Rattus_verecundus*	MEL0525	
2017	M1-15	*Paramelomys_rubex*		*Paramelomys_ rubex_B*	MEL0526	
2017	M1-30	*Leptomys_elegans*		*Leptomys_elegans*	MEL0527	
2017	M4-17	*Rattus_cf_niobe*		*Rattus_niobe_D*	MEL0530	
2017	M3-1.4	*Paramelomys_platyops*		*Paramelomys_ lorentzii*	MEL0538	
2017	M1-28	*Rattus_niobe*		*Rattus_niobe_D*	MEL0539	
2017	M1-30	*Rattus_niobe*		*Rattus_niobe_D*	MEL0540	
2017	M4-48	*Rattus_sp*		*Rattus_steini*	MEL0544	
2017	M4-20	*Rattus_verecundus*		*Rattus_verecundus*	MEL0546	
2017	M4-39	*Rattus_niobe*		*Rattus_niobe_D*	MEL0547	
2017	M1-20	*Rattus_niobe*		*Rattus_niobe_D*	MEL0549	
2017	M1-30	*Rattus_niobe*		*Rattus_niobe_D*	MEL0550	
2017	M3-12	*Paramelomys_rubex*		*Paramelomys_ rubex_B*	MEL0551	
2017	H3-2	*Paramelomys_rubex*		*Paramelomys_ mollis_AD*	MEL0706	
2017	H1-4	*Paramelomys_rubex*		*Paramelomys_ intermedius*	MEL0710	
2017	H1-22	*Paramelomys_rubex*		*Paramelomys_ intermedius*	MEL0711	
2017	H1-1.5	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0713	
2017	H1-1.3	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0714	
2017	H1-25	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0715	
2017	H5-1.3	*Rattus_niobe*		*Rattus_niobe_B*	MEL0716	
2017	H1-1.1	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0717	
2017	H1-16	*Paramelomys_rubex*		*Paramelomys_ intermedius*	MEL0718	
2017	H1-25	*Paramelomys_rubex*		*Paramelomys_ intermedius*	MEL0719	
2017	H5-24	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0721	
2017	H5-1.3	*Rattus_niobe*		*Rattus_niobe_B*	MEL0722	
2017	H6-20	*Rattus_niobe*		*Rattus_niobe_B*	MEL0724	
2017	H5-24	*Rattus_niobe*		*Rattus_niobe_B*	MEL0725	
2017	H5-1.1	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0726	
2017	H5-25	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0727	

Year	Trap No	Field ID	mtDNA ID	SNP ID	Field No	ABTC No
2017	H6-27	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0728	
2017	H3-2	*Paramelomys_rubex*		*Paramelomys_ mollis_AD*	MEL0730	
2017	H1-1.3	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0731	
2017	H3-14	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0733	
2017	H6-22	*Rattus_niobe*		*Rattus_niobe_B*	MEL0734	
2017	H3-34	*Rattus_niobe*		*Rattus_niobe_B*	MEL0736	
2017	H3-5	*Paramelomys_rubex*		*Paramelomys_ rubex_A*	MEL0737	
2017	H6-12	*Rattus_niobe*		*Rattus_niobe_B*	MEL0738	
2017	H6-2	*Rattus_niobe*		*Rattus_niobe_B*	MEL0739	
2017	H2-2	*Rattus_sp*		*Rattus_rattus*	MEL0743	

Appendix 4.3. Summary of rodent captures in 2015 (Elev: elevation; Tr: transect; TS: trapping success rates; totals in parentheses are number of novel captures, then number of recaptures; compare with Table 4.2). Shaded rows show total numbers for each elevation.

				Leptomys elegans	*Paramelomys lorentzii*	*Paramelomys intermedius*	*Paramelomys platyops*	*Paramelomys* sp. cf. *mollis* AD	*Paramelomys* sp. cf. *rubex* A	*Paramelomys* sp. cf. *rubex* B	*Uromys caudimaculatus*	*Rattus exulans*	*Rattus rattus*	*Rattus steini*	*Rattus verecundus*	*Rattus* sp. cf. *niobe* B	*Rattus* sp. cf. *niobe* D	***Total Species Richness***
Elev	**Tr**	**TS%**	**Total**															
BAA2		7.4	**110**															
1,000	M4	3.6	15 (12, 3)	0	0	0	1	0	0	1	0	0	0	0	13	0	0	***3***
1,000		3.6	**15**	**0**	**0**	**0**	**1**	**0**	**0**	**1**	**0**	**0**	**0**	**0**	**13**	**0**	**0**	***3***
1,400	M1	7.5	24 (17, 7)	0	1	0	0	0	0	1	0	3	0	0	0	0	19	***4***
1,400	M2	8.2	34 (22, 12)	0	5	0	0	0	0	4	1	1	0	0	0	0	23	***5***
1,400	M3	11.5	37 (23, 14)	0	1	0	0	0	0	9	0	1	0	0	0	0	26	***4***
1,400		9.0	**95**	**0**	**7**	**0**	**0**	**0**	**0**	**14**	**1**	**5**	**0**	**0**	**0**	**0**	**68**	***5***
BAA1		3.9	**60**															
2,200	H1	7.4	17 (17, 0)	0	0	0	0	0	3	0	0	0	0	0	0	14	0	***2***
2,200	H2	4.8	11 (10, 1)	0	0	0	0	1	1	0	0	0	0	0	0	9	0	***3***
2,200	H3	8.9	8 (8, 0)	0	0	0	0	4	1	0	0	0	0	0	0	3	0	***3***
2,200		4.0	**36**	**0**	**0**	**0**	**0**	**5**	**5**	**0**	**0**	**0**	**0**	**0**	**0**	**26**	**0**	***3***
2,700	H5	1.9	6 (6, 0)	0	0	0	0	0	0	0	0	0	0	0	0	6	0	***1***
2,700	H6	5.6	18 (18, 0)	0	0	0	0	1	6	0	0	0	0	0	0	11	0	***3***
2,700		3.7	**24**	**0**	**0**	**0**	**0**	**1**	**6**	**0**	**0**	**0**	**0**	**0**	**0**	**17**	**0**	***3***
Overall		6.4	170 (133, 37)	**0**	**7**	**0**	**1**	**6**	**11**	**15**	**1**	**5**	**0**	**0**	**13**	**43**	**68**	***10***

Appendix 4.4. Trapping summary from the 2017 survey (symbols in each cell represent the trapping result from each distance category along the transect, beginning at 0 metres from the left; open circle is an absence of captures; closed circle is at least one capture in that distance category; blue shading shows that a species was captured on at least one transect in a particular elevation; species names in parentheses were not captured during the 2015 survey, but were captured during the 2017 survey; see also Table 4.4).

Elevation	**1000 m**	**1400 m**			
Transect	**M4**	**M1**	**M2**	**M3**	
Species					
HYDROMYINI					
(Leptomys elegans)	ooooooo	ooooo	ooooo	ooooo	
Paramelomys lorentzii	ooooooo	oooo●o	o●oo●o	oo●ooo	
(Paramelomys intermedius)	ooooooo	ooooo	ooooo	ooooo	
Paramelomys platyops	ooooo●o	ooooo	ooooo	ooooo	
Paramelomys sp. cf. *mollis* AD	ooooooo	ooooo	ooooo	ooooo	
Paramelomys sp. cf. *rubex* A	ooooooo	ooooo	ooooo	ooooo	
Paramelomys sp. cf. *rubex* B	ooooo●o	oooo●o	o●oo●o	o●●●●o	
Uromys caudimaculatus	ooooooo	ooooo	o●oooo	ooooo	
RATTINI					
Rattus exulans	ooooooo	●ooooo	o●oooo	●ooooo	
(Rattus rattus)	ooooooo	ooooo	ooooo	ooooo	
(Rattus steini)	ooooooo	ooooo	ooooo	ooooo	
Rattus verecundus	●●●●o●o	ooooo	ooooo	ooooo	
Rattus sp. cf. *niobe* B	ooooooo	ooooo	ooooo	ooooo	
Rattus sp. cf. *niobe* D	ooooooo	●o●●●o	●●●●●o	●●●●●o	
Elevation	**2200 m**			**2700 m**	
Transect	**H1**	**H2**	**H3**	**H5**	**H6**
Species					
HYDROMYINI					
Leptomys elegans	ooooo	ooooo	ooooo	ooooo	ooooo
Paramelomys lorentzii	ooooo	ooooo	ooooo	ooooo	ooooo
Paramelomys intermedius	ooooo	ooooo	ooooo	ooooo	ooooo
Paramelomys platyops	ooooo	ooooo	ooooo	ooooo	ooooo
Paramelomys sp. cf. *mollis* AD	ooooo	o●oooo	●o●●oo	ooooo	ooo●oo
Paramelomys sp. cf. *rubex* A	●o●o●o	oooo●o	ooo●oo	ooooo	o●oo●o
Paramelomys sp. cf. *rubex* B	ooooo	ooooo	ooooo	ooooo	ooooo
Uromys caudimaculatus	ooooo	ooooo	ooooo	ooooo	ooooo
RATTINI					
Rattus exulans	ooooo	ooooo	ooooo	ooooo	ooooo
Rattus rattus	ooooo	ooooo	ooooo	ooooo	ooooo
Rattus steini	ooooo	ooooo	ooooo	ooooo	ooooo
Rattus verecundus	ooooo	ooooo	ooooo	ooooo	ooooo
Rattus sp. cf. *niobe* B	●●●o●o	●●oo●o	●o●●oo	●●●●o●	●●●o●o
Rattus sp. cf. *niobe* D	ooooo	ooooo	ooooo	ooooo	ooooo

Chapter 5 — Bats

Kyle N. Armstrong, Pita Amick and Enock Kale

A possible new species of woolly bat, *Kerivoula* sp., from 2,700 m on Hides Ridge

Summary

Background and aims

The bat component of the PMA3 monitoring study seeks to determine whether there is an ongoing level of habitat change following linear infrastructure construction that is reflected in changes to bat communities. The May 2017 survey used the same ultrasonic recording equipment to detect echolocating bat species, and the same 66 sampling sites as established in 2015 on Hides Ridge (BAA 1) and adjacent Arakubi Quarry and KP107 (BAA 2).

The primary goal of the 2017 survey was to determine if there had been a significant change in the bat communities at increasing distance from the ROW and at different elevations between the two survey years. A variety of analyses was undertaken to better understand the responses of particular ecological guilds of bats, and individual species that may be associated with particular habitats or respond to particular changes in their foraging environment.

Major results

A total of 20 species was detected in the acoustic recordings. Nine echolocating species of bat from the Hipposideridae, Miniopteridae, Rhinolophidae and Vespertilionidae, and two small blossom bats from the Pteropodidae, were captured. Based on both captures and acoustic recordings from the 2015 and 2017 surveys, a total of 26 bat species has now been documented in the PMA3 study. This compares favourably with the previous pre-construction baseline studies of Richards (2005, 2008) who sampled some areas nearby the BAA study areas. The PMA3 study has detected eight species more than Richards detected at Benaria and Hides combined, Most significantly, there has been the capture of two possible species new to science, and a third deemed to be present on the basis of a unique echolocation call.

Statistical tests showed that the bat assemblages were significantly different above and below 2,000 m, with higher diversity at lower elevations. This was due mainly to a greater number of species that forage in Edge habitats (small Emballonuridae) and a greater number of forest interior species (Hipposideridae and Rhinolophidae).

In contrast to the results from the 2015 survey, bat diversity was significantly greater at the open edge of sampling transects compared to the forest interior. This was a trend noticed at 1,000 m in 2015, but the 2017 survey brought greater statistical power to analyses, and the patterns were also obvious from an examination of Indicator Species indices.

Conclusions and recommendations

The combined results from both the 2015 and 2017 surveys suggest that the forest adjacent to the ROW has so far retained its value for bats.

Sites below 2,000 m in elevation have greater bat diversity overall; and the elevations above 2,000 m are dominated by bent-winged bats that would appear to have adaptations for higher elevation conditions.

In contrast to 2015, statistical tests showed a significantly greater bat diversity in the open areas at the start of transects (0 m) compared to the remaining recording sites in the forest interior, which was controlled by the greater numbers of species that forage in Edge and Open flight spaces (mainly the small Emballonuridae, also Miniopteridae).

Taken together, the significant differences above and below 2,000 m in elevation, and the significant differences in bat diversity between the open areas in the ROW and the forest interior, point to a different response of the bat community at high and low elevations. Below 2,000 m, an opening of the forest canopy results in an increase in bat diversity because it supports the influx of species that prefer to forage in the Edge and Open flight spaces next to, and above, stands of vegetation. Above 2,000 m, such an influx is less likely, or would be less dramatic because many of the same the Edge and Open flight space bats are not present.

The combined results from the two previous surveys has provided greater statistical power, resulting in a clearer view of the difference between open habitats at the edge of transects and the closed habitat of the forest interior, and the implication for forest cover change at different elevations.

Continuation of the acoustic bat monitoring component as part of future surveys is strongly recommended; as it has demonstrated utility for detecting bat responses to the open areas and forest edge in the ROW, and encountered up to three species possibly new to science.

To obtain a greater detection rate of *bFM*-emitting interior forest specialist species, the use of an acoustic lure alongside bat detectors to broadcast social calls of these species will be considered. Custom-designed acoustic lures can also record bat passes in infrared / thermal video, which would allow the compilation of total bat activity at each recording site.

Further efforts should be made on future surveys to capture the new species of bat that was detected on the basis of its unique 172 kHz echolocation call close to a small outcrop of limestone on transect M5 near Arakubi Quarry in BAA 2, and nearby at KP87 adjacent to Lake Kutubu. Capture effort need not be confined to the Arakubi Quarry area.

Capture effort for bats should continue on future surveys to target species of *Pipistrellus* that are expected to occur, but have not been detected acoustically because of the similarity of their calls with those of medium- and small-sized *Miniopterus*.

Introduction

Background

In a country like Papua New Guinea that retains around 70% of its natural forest cover (Shearman and Bryan 2015), it may be natural to think that the effects from the construction of a single narrow linear infrastructure corridor through a broad expanse of intact forest would be of profoundly small consequence, and not cause for concern. And for bat species that could fly readily over narrow areas of habitat they regard as unsuitable, the effects from the construction of roads assumed to be undetectable. In reality, the ability to fly gives bats the potential to respond relatively quickly to changes in their habitat. And studies within broad areas of intact habitat have the potential to be informative about the responses of animals to one type of perturbation because the effects are not confounded by decades or centuries of other types of disturbance on the same habitat patches.

It is within this context that the PMA3 monitoring program considers both the short- and long-term effects of linear infrastructure corridors on closed forest ecosystems in PNG, by periodically measuring the diversity and composition of selected major vertebrate groups, including bat communities.

The first survey in 2015 found a clear pattern of increasing bat diversity and changing species composition with decreasing elevation in the BAA project areas (Armstrong 2017). There was no overall significant change in the diversity and composition of bat species assemblages with increasing distance from the open areas of the PNG LNG infrastructure ROW, but some species appeared to benefit from having increased access to open foraging areas and vegetation edges. Sampling two years later provided greater statistical power when comparing bat diversity along transects that extend back through forest edges, and also allowed an examination of potential longer-term changes occurring since the corridor was first constructed in 2011.

Effects of linear infrastructure corridors on bats

The effects of linear infrastructure corridors on the structure, dynamics and components of ecosystems is well documented, mostly in temperate habitats. Roads increase connectivity for people but reduce it dramatically for the populations of animals remaining in dissected landscapes. The remaining natural habitats are then encroached upon

by factors that further reduce habitat quality and biodiversity beyond actual carriageways (Trombulak and Frissel 2000; Spellerberg 2002; Coffin 2007; Fahrig and Rytwinski 2009).

Bats are affected by road construction, sometimes in positive ways, but in many negative ways as well. Road construction creates open habitats, exposing bats to a greater level of real or perceived threat from 'predators' (including vehicles), reduces habitat connectivity, and can introduce high levels of artificial illumination, noise from traffic and wind intrusion into habitats (Kuijper et al. 2008; Schaub et al. 2008; Stone et al. 2009, 2012; Zurcher et al. 2010). Bat species that forage in dense vegetation cover within forest habitats and rely on passive listening for prey capture tend to be affected to a greater extent by roads, but even bats that forage in the open and are attracted by insect accumulations at lights have decreased levels of activity overall closer to roads (Blake et al. 1994; Kerth and Melber 2009; Berthinussen and Altringham 2011).

There are few long-term studies of bat communities occupying forest edge habitats, and most short-term studies derive from Europe where landscapes have been subject to modification for hundreds of years. The PMA3 study represents a unique long-term effort to examine the response of bat communities to linear gaps in broad areas of pristine tropical forest ecosystems.

Bats as indicators of biodiversity value

Bats can be a good indicator group for the long-term monitoring of biodiversity values and habitat quality for a wide variety of environmental disturbance types (Jones et al. 2009). In the context of forest ecosystems, changes in the abundance (or commonness/rarity) of echolocating insectivorous bats may reflect changes in insect prey biomass. The structure of forest habitats also has considerable influence on bat diversity. Extinction risk is greatest for the many specialised bat species that forage within expanses of intact closed forest (Jones et al. 2003), because their flight morphology and echolocation signal type constrains them to this habitat. When forests are reduced in size or transected by roads, these forest interior specialists decline, and generalist species that forage in more open habitats become more common.

When surveying for bats by detecting their signature echolocation calls, not only is the efficiency of survey effort and the probability of species detection maximised (reviewed in Armstrong 2017), but the shape of call signals provides information on the diversity of bat ecological niches. This allows an appreciation of ecosystem complexity beyond the simple view given by a species list. When forest structure and cover changes, the availability of 'flight spaces' for bat species changes, and the relative proportion of species with certain wing shapes and echolocation signal types that allow them to exploit open, edge or closed flight spaces may also change.

Flight spaces are defined by how far the bats fly from vegetation. Because bat species use different echolocation signal types, they vary in their ability to distinguish acoustic echoes of prey items from those derived from background 'clutter' (typically vegetation) that they need to avoid while in flight (Denzinger and Schnitzler 2013). There are three main flight space types, and usage of them can be inferred from the echolocation signal type:

- **Open**: uncluttered space, where clutter echoes are undetectable or clearly distinct from prey echoes. Such flight spaces include open clearings and air space well above the forest canopy or rivers. Used by bat species emitting relatively low frequency, high power, and narrowband calls with a characteristic frequency below 30 kHz.

- **Edge**: background cluttered space, where prey echoes follow closely but do not overlap with clutter echoes. Such flight spaces include the edges of forest, large gaps within forest, open spaces between different vegetation layers (e.g. canopy, subcanopy or understorey), and open space immediately above water and the forest canopy. Used by bat species emitting 'chirp' calls or quasi-constant frequency calls with a characteristic frequency between 30–70 kHz.

- **Clutter** ("narrow" in Denzinger and Schnitzler 2013): highly cluttered space, where prey echoes are intermingled with those from background clutter. Such flight spaces include dense understory or canopy vegetation, and low over the ground. Used by bat species in Australasia emitting low power, short duration, broadband calls and short, medium or long constant frequency calls anywhere between 30 to 170 kHz.

In the present study, the ROW has increased the availability of Open and Edge habitats to bat species having echolocation signals and wing morphologies that are suitable for foraging in these flight spaces.

Aims of the PMA3 bat study

This study addresses the overarching question: "Is there an ongoing level of habitat change following linear infrastructure construction that is reflected in changes to bat communities?".

Specific aims of this second survey in the program were:

1. Document the diversity of bats along the ROW in the PMA3 project area using the same recording sites as in 2015;

2. Determine whether bat communities have responded significantly to the construction of the ROW (here referring also to associate roads) by assessing whether two specific measures of bat diversity, Species Richness and Phylogenetic Diversity, vary with increasing distance from the linear infrastructure corridor;

3. Quantify bat diversity through several additional measures that provide additional perspectives on the potential differences of bat communities at different distances from the ROW, elevations, and since the 2015 survey; and

4. Integrate information from baseline biological surveys conducted prior to construction of the PNG LNG project infrastructure, specifically from a re-analysis of datasets collected by G. Richards (2005, 2008).

Methods

Sampling design

This long-term monitoring study depends on the standardisation of sampling effort, equipment type and site placements. The same number of recordings were taken from the same permanent transects established and used in 2015. Field sampling was undertaken between 11 and 29 May 2017, approximately one month earlier than the previous study in June-July 2015.

Permanent transects are located within two narrow elevational ranges in each BAA: approximately 2,200 m asl and 2,700 m asl in BAA 1 on Hides Ridge; and approximately 1,000 m asl (Arakubi Quarry) and 1,400 m asl (KP107) in BAA 2 on the Agogo Range near Moro.

Bat detectors were deployed at each of the 66 permanent acoustic recording sites along 11 transects in BAA 1 (transects H1–H6; total 36 recording nights over eight sampling nights, 22–30 May 2017) and BAA 2 (M1–M5; total 30 recording nights over six sampling nights, 11–17 May 2017) (Table 5.1). A total of 64 full-night recordings was collected in 2017 (recordings were not available from sites M1_070 and M4_170).

The bat detectors were spaced along each transect at 50 m intervals, and given the high attenuation rate of ultrasonic calls, are assumed to be acoustically independent, so that an individual bat can only be detected by a single recorder at any given moment.

The first detector on each transect was oriented to receive signals from the open area over the ROW (distance '0 m'). The remaining bat detectors (distances of 20–220 m) represented treatments of potentially decreasing edge effect.

Recordings were made in high quality full spectrum format with Pettersson Elektronik D500X bat detectors, which were protected in a plastic box and a waterproof bag. Microphones on a 3 m extension cable were placed in a funnel made from a drink bottle to keep out rain, and set 2.5 m above the ground (Figure 5.11).

The constraints and considerations relevant to the sampling design, acoustic surveys for bats and other aspects of the PMA3 monitoring program are discussed in Armstrong (2017).

Table 5.1. Summary of the experimental design and bat recording site placements. Factors include 'distance from the ROW' (6 treatments, total 66 replicates) and 'elevation' (4 treatments, total 11 replicates). GPS coordinates are listed in Armstrong (2017).

Area	Elevation	Replicate	Distance from ROW (m)						Total
	(m asl)	(m asl)	0	20	70	120	170	220	
BAA 1	'2,700 m'	H4—2,700 m (2,681–2,696 m)	1	1	1	1	1	1	
		H5—2,750 m (2,726–2,756 m)	1	1	1	1	1	1	
		H6—2,730 m (2,725–2,736 m)	1	1	1	1	1	1	
	'2,200 m'	H1—2,150 m (2,148–2,163 m)	1	1	1	1	1	1	
		H2—2,200 m (2,171–2,229 m)	1	1	1	1	1	1	
		H3—2,300 m (2,296–2,327 m)	1	1	1	1	1	1	**36**
BAA 2	'1,400 m'	M1—1,400 m (1,397–1,405 m)	1	1	1	1	1	1	
		M2—1,380 m (1,315–1,397 m)	1	1	1	1	1	1	
		M3—1,380 m (1,369–1,389 m)	1	1	1	1	1	1	
	'1,000 m'	M4—1,030 m (995–1,041 m)	1	1	1	1	1	1	
	(Arakubi)	M5—1,050 m (1,051–1,073 m)	1	1	1	1	1	1	**30**

Captures

Trapping was conducted adjacent to transects in an effort to capture species whose echolocation call type has not yet been documented, to confirm the local presence of species whose call types are difficult to distinguish from another species, and to obtain confirmation and specimens of species that are potentially new to science. A particular target at Arakubi Quarry was the source of the 172 kHz *sCF* call type that is thought to come from an undescribed close relative of the Dusky Leaf-nosed Bat *Hipposideros ater*.

Trapping was undertaken using two triple-bank Austbat harp traps (a 3 m high rectangular frame with a triple-offset arrangement of vertical fishing line strings suspended over a catch bag; Figure 5.12), which were positioned in natural 'flyway' gaps between vegetation. A total of 18 harp trap sites (nine nights with two traps positioned nearby or next to each other) were sampled in BAA 1; and 10 harp trap sites (five nights with two traps positioned nearby or next to each other) were sampled in BAA 2.

Captured bats were identified based on their external features and descriptions in Bonaccorso (1998). A small number of voucher specimens were taken of species that are potentially new to science. Voucher specimens were fixed whole in 10% formalin and then transferred to 70% ethanol for long-term storage. Tissue biopsy samples were preserved in 95% ethanol. Tissue biopsy samples and voucher specimens were deposited in the South Australian Museum. Recordings of reference echolocation calls were made from live animals with a Titley Scientific Walkabout bat detector, either when bats were in flight after being released (mouth-emitting species) or while hanging in a voluminous cloth bag (nasal-emitting species).

Processing of acoustic signals

A customised, multi-step acoustic processing procedure that can filter large bat echolocation recording datasets from Papua New Guinea (Armstrong and Aplin 2014a; Armstrong et al. 2016) was applied to the recordings made on the survey (further details in Armstrong 2017). Processing first involved the recognition of bat echolocation 'call types', followed by a separate step of allocating a species identification to each of these. The 'call types' are defined based on a standardised naming scheme that has been used in many published and unpublished surveys across Papua New Guinea and Wallacea in recent years (Armstrong and Aplin 2011, 2014b,c; Armstrong et al. 2015a,b; K.N. Armstrong and K.P. Aplin unpublished confidential reports; illustrated in Armstrong 2017). This two-step approach, along with the provision of illustrated examples of identified call types, provides a greater level of transparency that allows for future verification of call identifications, retrospective correction of the species name on the basis of updated information, and a comparison of diversity across sites and studies that is independent of taxonomic allocations.

Data analysis

A brief overview of the data analysis is presented here, with further details in Armstrong (2017). Note that the term 'diversity' is used in this chapter in a general sense rather than as a specific measure. The diversity of bats encountered on the survey was summarised and compared among different distances from the ROW, elevations, and between survey years in terms of the number of species ('Species Richness'), the breadth of their evolutionary relationships and ecological roles ('Phylogenetic Diversity', 'Functional Diversity'), how common each species was ('Relative Abundance', 'Indicator Species' indices), and species composition. A brief explanation of each of these six specific measures is provided below.

1. **Species Richness** is the simplest measure of diversity, and is a tally of the number of species at each recording site. A small proportion of echolocation call types recorded could actually have been derived from more than one species (the calls identified as coming from medium- and small-sized *Miniopterus* could have also derived from a species of *Pipistrellus* or *Nyctophilus* in some cases), but Species Richness in this study is assumed to be a reasonably accurate representation of the number of species rather than the number of echolocation call types. Species Richness was compared statistically amongst sites by fitting a Generalised Linear Mixed Model to a site-by-species matrix. Prior to analysis, a check was made to determine which distribution best fit data.

2. **Phylogenetic Diversity** (Faith 1992) is an overall measure of evolutionary diversity among the species present at a recording site, and considers both the number of species, as well as the degree of genetic distance among them. Sites with five species from five different families will have higher Phylogenetic Diversity than sites with five species from the same family, and thus higher value in terms of diversity. The metric is calculated from a genetic distance matrix and phylogenetic tree that was created from mitochondrial DNA barcode sequences (cytochrome-*b*) generated for the 2015 study (Armstrong 2017). The genetic matrix and phylogenetic tree were updated to include three additional species recognised in the study area. Phylogenetic Diversity (PD) was compared statistically amongst sites by fitting a Generalised Linear Mixed Model to a site-by-species matrix of PD values.

3. **Relative Abundance** was calculated to provide a rough indication of how common each species was, given that true abundance cannot be estimated from recordings of echolocation. This is simply the proportion of recording sites with detections of each species (e.g. a value of 0.6 indicates the species was detected at 6 out of 10 recording sites). Proportional representation for defined distances from the ROW and at each elevation was calculated using presence/absence data in the site-by-species matrix.

4. **Functional Diversity** (Petchey and Gaston 2002) is a measure of diversity that incorporates information on the range of 'functional types' (ecological niches) present within bat communities. More complex ecosystems typically show both a greater range of functional types and a greater level of redundancy (more species with similar ecological roles). Functional Diversity is calculated from estimates of Relative Abundance as well as a categorisation of several aspects of the biology of each species (their 'ecological traits', such as wing shape type, echolocation signal shape, foraging habitat, prey capture strategy, flight space, roost type; summarised in Armstrong 2017).

5. **Indicator Species** indices (Dufrene and Legendre 1997) were calculated for each species at different distances from the ROW, and different elevations in each survey year, using presence/absence data in the site-by-species matrix. This index is similar to Relative Abundance, but highlights the association of each species with particular habitats. Species found in many habitat types tend to have low scores. The measure allows comment on which species may be negatively affected by opening the forest canopy when building linear infrastructure, or that may actually take advantage of newly created open flight spaces and forest edges.

6. **Species composition**. is not a discrete metric, but recording sites can be compared in terms of the combination of species detected. Differences among recording sites are most efficiently summarised in a two-dimensional ordination plot. This involves calculating Bray-Curtis Dissimilarity, and then performing Non-metric Multidimensional Scaling. Species composition was also summarised after grouping species according to the similarity of their echolocation call structure ('main body' of the call type; details in Armstrong 2017), which reflects where bats fly when foraging (in the 'Open', at the 'Edge' of vegetation boundaries, or amongst the 'Clutter' of vegetation within stands of forest). Analyses performed on such groupings provide information on whether certain broad ecological groups of bats might be under-represented or dominant.

All analyses were conducted using a custom-written [R] statistical computing language (R Core Team 2016) script, which takes in a standard site-by-species matrix, and contains a record of every manipulation of the matrix and all analytical steps. The script created for analysing the data from the 2015 survey was modified to allow for the incorporation of data from the second sampling year.

Results

Captures

A total of 52 individuals from nine echolocating bat species and two small blossom bat species was captured from the 28 harp trapping nights in both BAAs (Figures 5.13–5.22; Appendix 5.1). Most captures were of the Eastern Blossom Bat *Syconycteris australis*, (38 individuals) with the lowland form encountered at Arakubi Quarry and the undescribed mid-montane form on Hides Ridge. Two putative new species were collected from Hides Ridge: a long-eared bat *Nyctophilus* sp. and a woolly bat *Kerivoula* sp.; as well as two unidentified species of bent-winged bat *Miniopterus* spp. The species producing the *172 sCF* call type was not captured despite targeting areas of limestone outcrop near Arakubi Quarry that may have been used for roosting. All species captured are represented on the acoustic recordings (except the Small-toothed Long-eared Bat *Nyctophilus microdon*).

Acoustic detections

A total of 20 echolocation call types was recognised from the recordings, which probably represents one species in each case (Tables 5.2 and 5.3; Figure 5.1). A brief justification for assigning individual call types to particular bat species is given in Armstrong (2017). A full list of species encountered to date on the two surveys is compiled in Appendix 5.2, which also contains the common names for each species. A raw site-by-species matrix showing results from each recording site is presented in Appendix 5.3.

From a simple inspection of the tabulated presence/absence data at each recording site (Tables 5.2 and 5.3), both the Species Richness and species composition of the two BAA areas are clearly different, with greater bat diversity in BAA2 at lower elevations. In BAA 1, only five species were recorded, with most detections attributable to two species of the Miniopteridae. By contrast, 19 call types were recorded in BAA2.

Two additional species were encountered in 2017: the Greater Northern Free-tailed Bat *Chaerephon jobensis* (call type *20 cFM*) and an unidentified species of free-tailed bat *Otomops* sp. (call type *30 sFM*). These two species represent the sixth family of echolocating bats (Molossidae) recorded by the monitoring program.

In addition, the very similar call types of the horseshoe bat *Rhinolophus mcintyrei* (an updated taxonomic name for *Rhinolophus arcuatus* that was used in Armstrong 2017; call type *70 ICF*) and the eastern Horseshoe Bat *Rhinolophus megaphyllus* (call type *65 ICF*) were able to be distinguished from each other. A re-analysis of the 2015 recordings was undertaken to distinguish these two species and the site-by-species matrix was updated for analyses.

Two species encountered in 2015 were not detected in 2017. These were the unidentified leaf-nosed bat *Hipposideros* sp. cf. *ater* (call type *172 sCF*), and the New Guinea Sheath-tailed Bat *Emballonura furax* (call type *52 i.fFM.d*).

Table 5.2. Summary of species/call type detections at each sampling position in BAA 1 on Hides Ridge. The sequence of circles is increasing distance from the road (0, 20, 70, 120, 170 and 220 m, left to right), with a filled black circle indicating a detection of that species, an open circle an apparent absence, and a hyphen a failed recording. Grey shading indicates flight space association: Open: no shading; Edge: light shading; Clutter: darker shading.

	Elevation	**2,200 m**			**2,700 m**		
	Transect	**H1**	**H2**	**H3**	**H4**	**H5**	**H6**
Scientific name	**Call type**						
EMBALLONURIDAE							
Emballonura dianae	*35 i.fFM.d*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Emballonura furax	*52 i.fFM.d*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Emballonura raffrayana	*45 i.fFM.d*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Mosia nigrescens	*65 i.fFM.d*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Saccolaimus saccolaimus	*25 sFM*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
HIPPOSIDERIDAE							
Aselliscus tricuspidatus	*120 sCF*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Hipposideros cervinus	*140 sCF*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Hipposideros diadema	*58 mCF*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Hipposideros wollastoni	*88 mCF*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Hipposideros sp. cf. *ater*	*172 sCF*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
RHINOLOPHIDAE							
Rhinolophus euryotis	*52 lCF*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Rhinolophus mcintyrei	*70 lCF*	●o●●oo	●ooooo	oooooo	oooooo	oooooo	oooooo
Rhinolophus megaphyllus	*65 lCF*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Rhinolophus sp. cf. *robertsi*	*33 lCF*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
MINIOPTERIDAE							
Miniopterus sp. 1 'large'	*38 st.cFM*	●●●●●●	●●●o●o	●oo●o●	●●oooo	●●ooo●	●ooo●o
Miniopterus sp. 2 'medium'	*45 st.cFM*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Miniopterus sp. 3 'small'	*53 st.cFM*	●o●●o●	o●oooo	●ooo●o	●●●●●●	●●●o●●	●●●●●●
VESPERTILIONIDAE							
Murina sp. cf. *florium*	*80 bFM*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Nyctophilus sp.	*50 bFM*	oo●oo●	oooooo	oooooo	oooooo	o●●ooo	oooooo
Philetor brachypterus	*30 cFM*	oooooo	oooooo	●ooooo	oooooo	oooooo	oooooo
MOLOSSIDAE							
Chaerephon jobensis	*20 cFM*	oooooo	oooooo	oooooo	oooooo	oooooo	oooooo
Otomops sp.	*30 sFM*	oooooo	oooooo	oooooo	oooooo	oooooo	Oooooo
Total Species Richness		**4**	**3**	**3**	**2**	**3**	**2**

Table 5.3. Summary of species/call type detections at each sampling position in BAA 2 on the Agogo Range near Moro. Symbols as for Table 5.2.

	Elevation	**1,000 m**		**1,400 m**		
	Transect	**M4**	**M5**	**M1**	**M2**	**M3**
Scientific name	**Call type**					
EMBALLONURIDAE						
Emballonura dianae	*35 i.fFM.d*	●000-0	●●0000	●0-000	●00000	000000
Emballonura furax	*52 i.fFM.d*	0000-0	000000	00-000	000000	000000
Emballonura raffrayana	*45 i.fFM.d*	●000-0	●●0000	●0-000	●00000	●00000
Mosia nigrescens	*65 i.fFM.d*	●●●0-●	●●●●●●	00-000	●00000	000000
Saccolaimus saccolaimus	*25 sFM*	0000-0	0●0000	00-000	000000	000000
HIPPOSIDERIDAE						
Aselliscus tricuspidatus	*120 sCF*	0●●0-0	●●00●0	00-00●	00●●00	000000
Hipposideros cervinus	*140 sCF*	00●0-0	●●0●00	00-00●	000000	0000●●
Hipposideros diadema	*58 mCF*	0000-0	●00000	00-000	000000	00000●
Hipposideros wollastoni	*88 mCF*	0●●●-●	●●●●●0	00-00●	0●●●●0	●00000
Hipposideros sp. cf. *ater*	*172 sCF*	0000-0	000000	00-000	000000	000000
RHINOLOPHIDAE						
Rhinolophus euryotis	*52 lCF*	0●●0-0	●●●●●0	00-●0●	0●●●●0	000●●0
Rhinolophus mcintyrei	*70 lCF*	●●●0-0	0●●●00	00-000	000000	000000
Rhinolophus megaphyllus	*65 lCF*	0●●0-0	000●00	00-000	000000	000000
Rhinolophus sp. cf. *robertsi*	*33 lCF*	●00●-0	●●●●00	00-000	●●0000	00000●
MINIOPTERIDAE						
Miniopterus sp. 1 'large'	*38 st.cFM*	●000-0	●●0000	●0-00●	●00000	●000●●
Miniopterus sp. 2 'medium'	*45 st.cFM*	0000-0	●00000	●0-000	●00000	●00000
Miniopterus sp. 3 'small'	*53 st.cFM*	●0●0-●	●●0●0●	●0-●0●	●00000	●0●0●●
VESPERTILIONIDAE						
Murina sp. cf. *florium*	*80 bFM*	●000-0	000000	00-000	000000	●00000
Nyctophilus sp.	*50 bFM*	0000-0	000000	00-000	000000	000000
Philetor brachypterus	*30 cFM*	0000-0	●●0000	●0-000	000000	000000
MOLOSSIDAE						
Chaerephon jobensis	*20 cFM*	0000-0	000000	00-000	●00000	000000
Otomops sp.	*30 sFM*	0000-0	000000	00-000	●00000	●00000
Total Species Richness		**13**	**16**	**10**	**12**	**11**

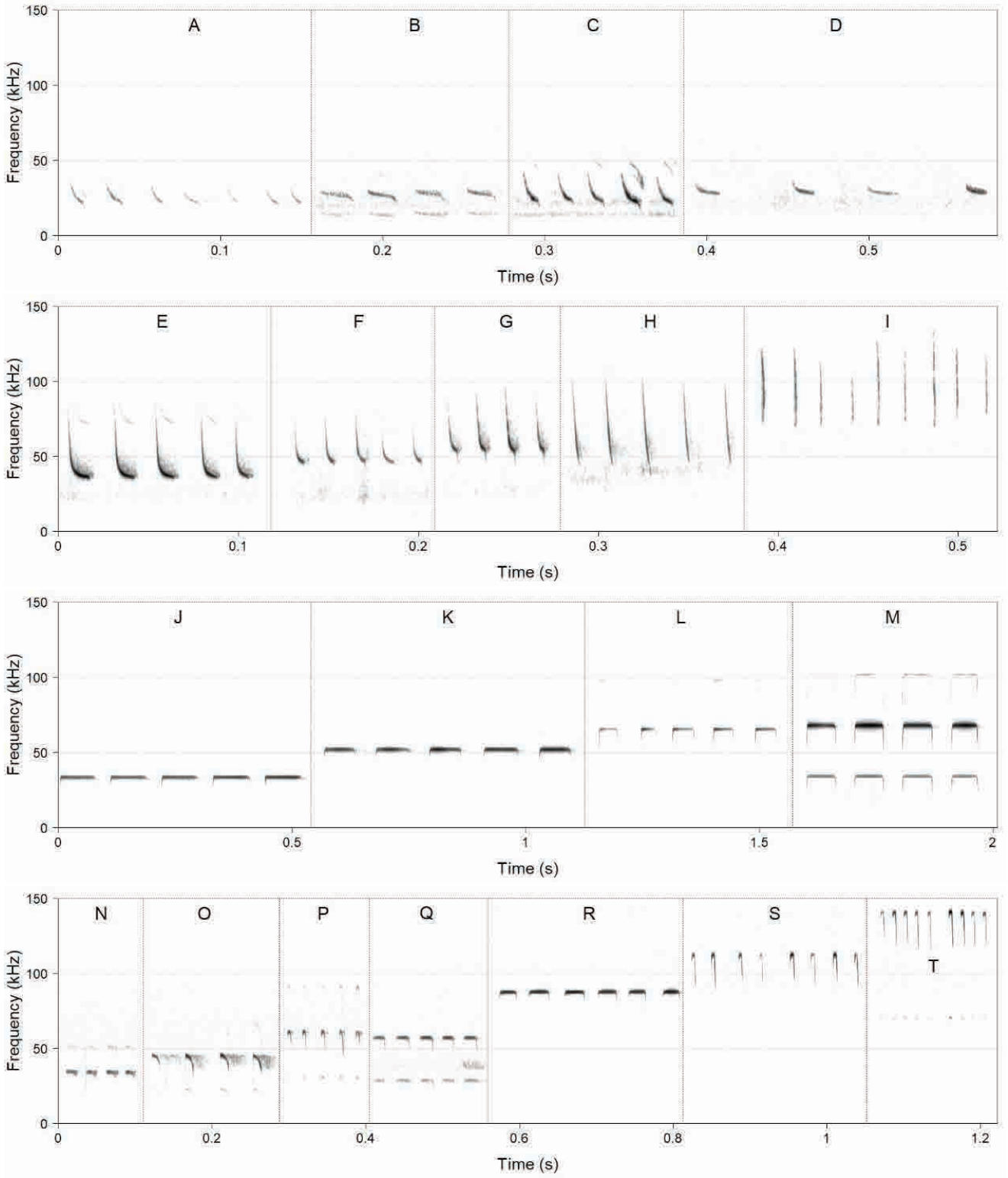

Figure 5.1. Representative sequence portions of the 20 call types recognised from the acoustic recordings in 2017, grouped by main body type of the call (time between pulses is compressed; scale of x and y axes vary).

A: *20 cFM Chaerephon jobensis*; **B**: *25 sFM Saccolaimus saccolaimus;* **C**: *30 sFM Otomops* sp.; **D**: *30 cFM Philetor brachypterus*; **E**: *38 st.cFM Miniopterus* sp. 1 'large'; **F**: *45 st.cFM Miniopterus* sp. 2 'medium'*;* **G**: *53 st.cFM Miniopterus* sp. 3 'small'; **H**: *50 bFM Nyctophilus* sp.; **I**: *80 bFM Murina* sp. cf. *florium*; **J**: *33 lCF Rhinolophus* sp. cf. *robertsi*; **K:** *52 lCF Rhinolophus euryotis*; **L:** *65 lCF Rhinolophus megaphyllus*; **M:** *70 lCF Rhinolophus mcintyrei*; **N**: *35 i.fFM.d Emballonura dianae*; **O**: *45 i.fFM.d Emballonura raffrayana*; **P**: *65 i.fFM.d Mosia nigrescens*; **Q:** *58 mCF Hipposideros diadema*; **R**: *88 mCF Hipposideros wollastoni*; **S**: *120 sCF Aselliscus tricuspidatus*; **T**: *140 sCF Hipposideros cervinus*.

Species Richness

A series of statistical tests was undertaken to compare total Species Richness among different distances from the ROW, different elevations, and between the two survey years. The full statistical model showed no significant interaction terms between the three factors, and the main effects showed a significant difference within all three factors (Table 5.4). Examination of pairwise comparisons revealed that Species Richness was greatest at the beginning of transects (the open areas at the edge of the forest, and the first 20 metres inside), but Species Richness was similar inside the forest canopy. Species Richness was also significantly greater at the lower elevations at Arakubi Quarry (1,000 m) and KP107 (1,400 m). Lastly, there was a significantly greater number of bat detections overall in 2017 compared to 2015 (see mean ± standard deviations for all factors in Table 5.5). The overall patterns in Species Richness in each distance and elevation category are clearly evident in summary plots (Figure 5.2), as are the pairwise comparison results (Figure 5.3).

Given that the start of transects at the edge of the ROW had significantly greater Species Richness, it was relevant to examine whether there was a similar pattern of difference in Species Richness for just those bat species classified as using 'Edge' habitats (flying in open areas but close to vegetation boundaries where the microphones at '0 m' were positioned). This was indeed the case, with a greater number of Edge species detected at a distance of '0 m', and a greater prevalence of these species at lower elevation sites (Table 5.5). The patterns evident from an inspection of the means in Table 5.5 are also clearly evident when the proportion of flight space representatives in each distance and elevation category are plotted (Figure 5.4).

To explore the patterns in Species Richness even further to have a better appreciation of what elements of the bat assemblage were controlling the results, it was also relevant to examine whether one of the main echolocation call types (*cFM*) that is associated with edge habitats varied with the three factors in the same way as total Species Richness. This was indeed the case, with a greater Species Richness of *cFM* bats at distance '0 m' (Table 5.5). A similar test with the other major call type that is used by bats exploiting Edge habitats (*i.fFM.d*) was not possible because assumptions of statistical tests were violated.

Table 5.4. Summary of the tests of the Generalised Linear Mixed Model and post hoc pairwise comparisons to test for the influence on bat diversity (dependent variable 'Species Richness') of the factors 'Distance' from the ROW, 'Elevation', and survey 'Year' (values from the Analysis of Deviance table; Type III Wald chi-square tests; only significant pairwise tests are shown; Significance codes: '*' <0.05, '**' <0.01, '***' <0.001; best model chosen by AICc scores; pairwise values and those in parentheses are from the main effects models; the full model was coded in [R] as: m <- glmer(total_richness ~ dist + elev + year + dist*elev + elev*year + dist*year + dist*elev*year + (1 | transect), data = y, family=gaussian(link="log"), nAGQ = 25)).

Species Richness	**Chi-square**	**df**	**P**	**Pairwise**
Distance	58.69 (203.13)	5	<0.001*** (<0.001***)	0 > 20*** 0 > 70*** 0 > 120*** 0 > 170*** 0 > 220*** 20 > 120*** 20 > 170*** 20 > 220*** 70 > 170*
Elevation	37.66 (85.61)	3	<0.001*** (<0.001***)	1,000 > 2,200*** 1,000 > 2,200*** 1,000 > 2,700*** 1,400 > 2,200* 1,400 > 2,700**
Year	9.15 (12.71)	1	0.002** (<0.001***)	2015 < 2017***
Distance*Elevation	19.92	15	0.17	—
Distance*Year	4.61	5	0.46	—
Elevation*Year	6.92	3	0.074	—
Distance*Elevation*Year	9.21	15	0.86	—
Species Richness—Edge species	**Chi-square**	**df**	**P**	**Pairwise**
Distance	118.58	5	<0.001***	0 > 20*** 0 > 70*** 0 > 120*** 0 > 170*** 0 > 220***
Elevation	30.6	3	<0.001***	1,000 > 2,200*** 1,000 > 2,200*** 1,000 > 2,700***
Year	4.1	1	0.043*	2015 < 2017*
Species Richness—*cFM* species	**Chi-square**	**df**	**P**	**Pairwise**
Distance	86.73	5	<0.001***	0 > 20*** 0 > 70*** 0 > 120*** 0 > 170*** 0 > 220***
Elevation	0.735	3	0.86	—
Year	2.69	1	0.1	—

Table 5.5. Summary of means ± standard deviation for various dependent variables (total Species Richness, Species Richness of all Edge species and Species Richness of all species with a cFM call type (see Tables 5.2 and 5.3; Appendix 5.2) at each distance from the ROW, elevation and survey year, plus the metrics of Phylogenetic Diversity and Functional Diversity. Values in bold are significantly and consistently higher than the others based on pairwise comparisons (see Table 5.3).

Distance (m)	Species Richness	Edge species	*cFM* species	Phylogenetic Diversity	Functional Diversity
0	***4.59 ± 3.42***	***3.41 ± 1.89***	***2.50 ± 1.01***	0.33 ± 0.23	1.37
20	2.50 ± 3.43	1.18 ± 1.40	0.91 ± 1.06	0.23 ± 0.28	1.21
70	2.48 ± 2.06	1.09 ± 0.70	0.76 ± 0.62	0.28 ± 0.17	0.83
120	1.77 ± 1.71	0.59 ± 0.73	0.50 ± 0.60	0.20 ± 0.16	0.65
170	1.67 ± 1.28	0.81 ± 0.68	0.76 ± 0.70	0.18 ± 0.13	0.57
220	2.23 ± 1.90	1.36 ± 0.90	1.13 ± 0.71	0.27 ± 0.20	0.98
Elevation (m)					
1,000	***5.87 ± 3.54***	***2.35 ± 2.21***	1.04 ± 1.33	***0.41 ± 0.25***	1.37
1,400	***2.63 ± 2.36***	1.28 ± 1.77	1.0 ± 1.33	0.24 ± 0.20	1.36
2,200	1.50 ± 1.16	1.14 ± 0.83	1.14 ± 0.83	0.20 ± 0.16	0.76
2,700	1.39 ± 0.69	1.22 ± 0.64	1.19 ± 0.62	0.15 ± 0.11	0.5
Year					
2015	2.33 ± 2.28	1.27 ± 1.27	0.95 ± 0.87	0.23 ± 0.18	—
2017	***2.76 ± 2.89***	***1.56 ± 1.64***	1.25 ± 1.17	0.28 ± 0.23	—

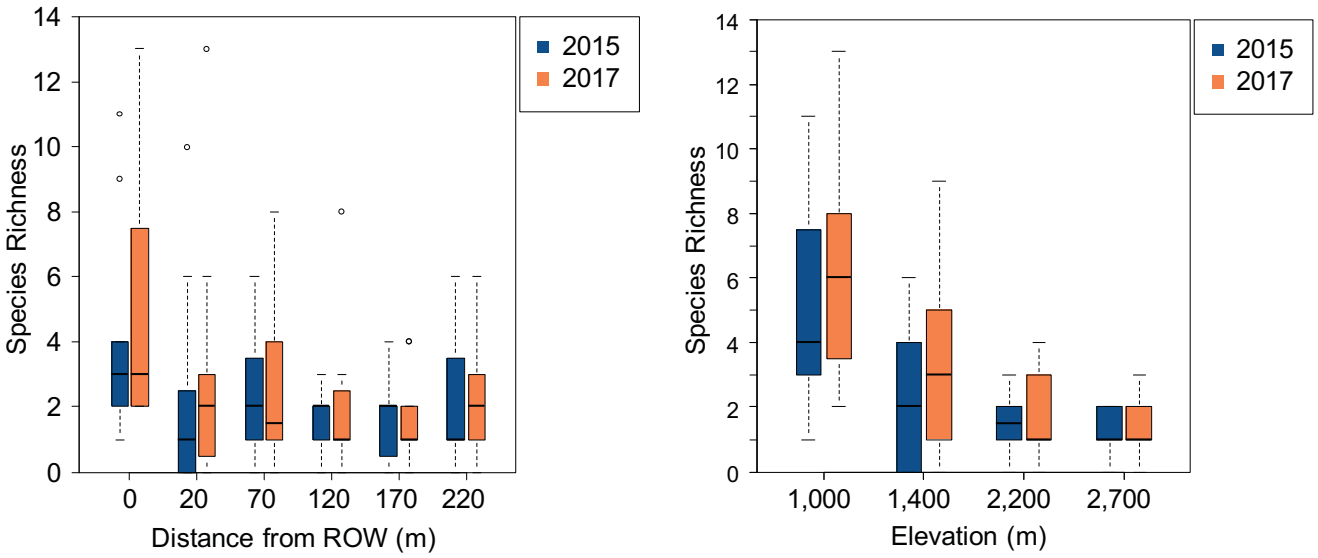

Figure 5.2. Summary of the patterns of Species Richness with increasing distance from the ROW and elevation. All sites have been combined for each of the two factors, but segregated by year. [*Boxplot components*: central bar—median; boxes—inter-quartile range, with second quartile group below median, third quartile group above median; bars—minimum and maximum values; circles—statistical outliers].

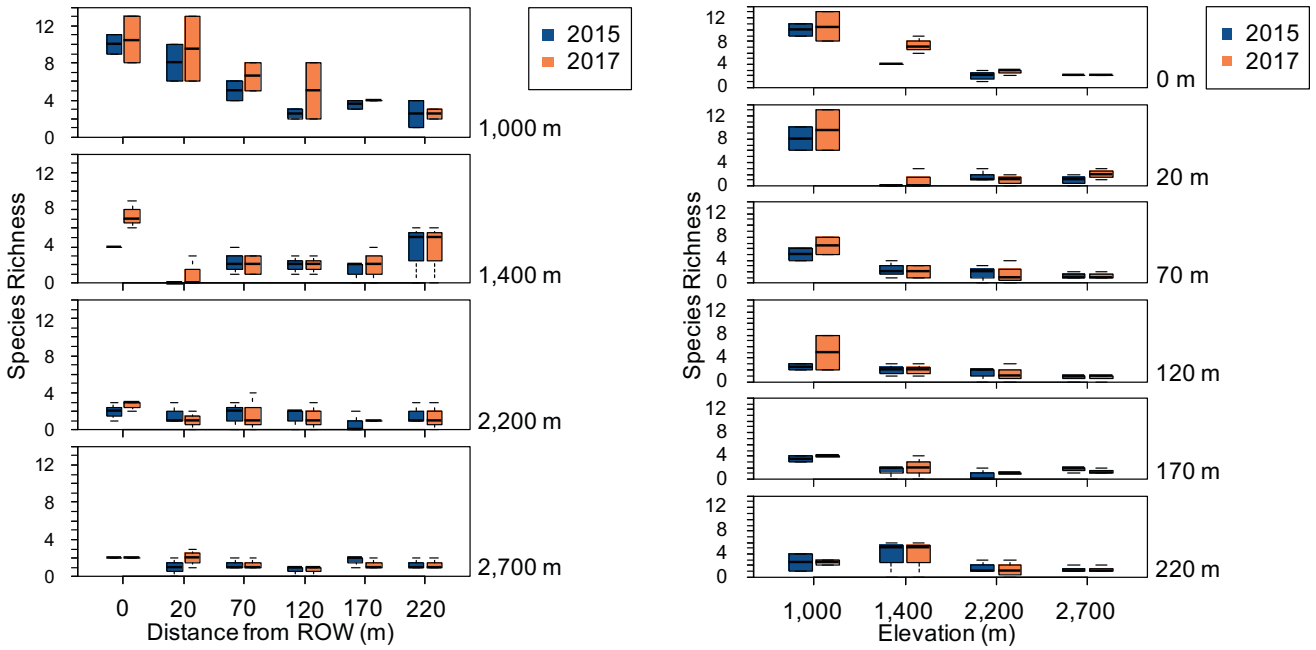

Figure 5.3. Summary of the patterns of Species Richness with increasing distance from the ROW at each elevation, and with different elevation levels for each distance from the ROW.

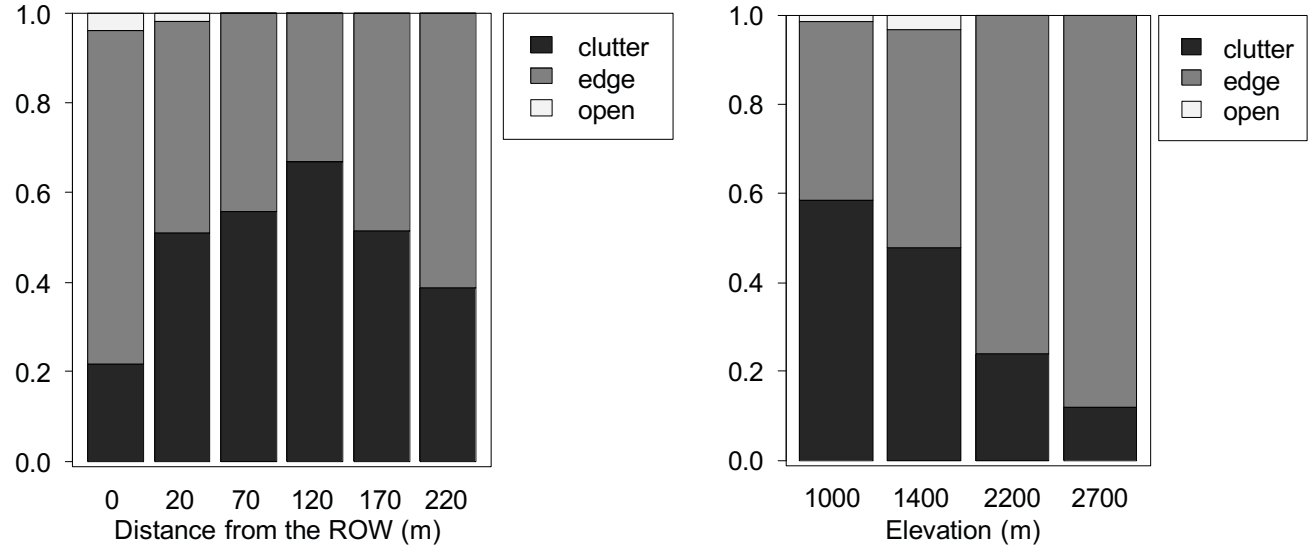

Figure 5.4. Summary plots of the proportion of bats occupying three different flight spaces at increasing distance from the ROW and at increasing elevation.

Phylogenetic Diversity

When plotted against total Species Richness, Faith's (1992) Phylogenetic Diversity increased in an approximate 1:1 relationship (data not shown). Thus, to understand if there were any biases in terms of bat genera or even families that were not evident from numbers of species at each recording site, a statistical test was undertaken to compare Phylogenetic Diversity among different distances from the ROW, different elevations, and between the two survey years. While there was indication that Phylogenetic Diversity might be slightly greater at 1,000 m (Figure 5.5), there was no statistically significant difference in the evolutionary diversity amongst species at each recording site within any factor (Table 5.6). The interpretation is that there is no environmental factor operating at recording sites that favours one particular family of bats. While the Miniopteridae appear to dominate in BAA 1, they are equally as common in BAA 2 (Tables 5.2 and 5.3).

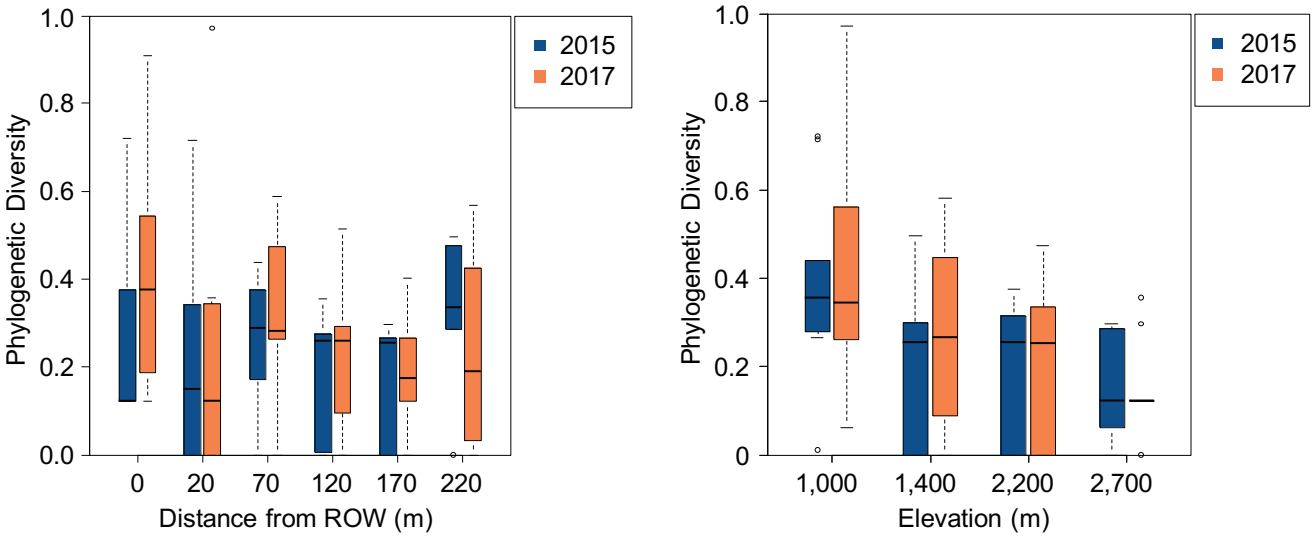

Figure 5.5. Summary plots of the pattern of Phylogenetic Diversity at increasing distance from the ROW and at increasing elevation.

Table 5.6. Summary of the tests of the Generalised Linear Mixed Model and post hoc pairwise comparisons to test for the influence on bat diversity (dependent variable 'Phylogenetic Diversity') of the factors 'Distance' from the ROW, 'Elevation', and survey 'Year'. See Table 5.4 for supplementary information on statistics; the full model was coded in [R] as: m <- glmer(PD.t ~ dist + elev + year + dist*elev + elev*year + dist*year + dist*elev*year + (1 | transect), data = y))

Phylogenetic Diversity	Chi-square	df	P	Pairwise
Distance	7.88 (10.42)	5	0.16 (0.06)	—
Elevation	8.29 (14.78)	3	0.040* (0.002**)	1,000 > 2,700*
Year	0.7 (1.10)	1	0.4 (0.29)	—
Distance*Elevation	16.92	15	0.32	—
Distance*Year	2.09	5	0.84	—
Elevation*Year	3.18	3	0.36	—
Distance*Elevation*Year	6.79	14	0.94	—

Functional Diversity

Values of Petchey and Gaston's (2002) Functional Diversity, or diversity of bat ecological niches, was mostly similar with increasing distance from the ROW, except that it was slightly higher in 2017 at the edges of the transect at the ROW. The source of this is probably the slightly greater number of Open space foraging species of bat detected in 2017 at these recording sites (species of Molossidae, and the detection of the Bare-rumped Sheath-tailed Bat *Saccolaimus saccolaimus* at distances of '0 m' and 20 m' in BAA 2). The greater number of species at the lower elevations at Arakubi Quarry and KP107 contributed to greater values of Functional Diversity (Figure 5.6).

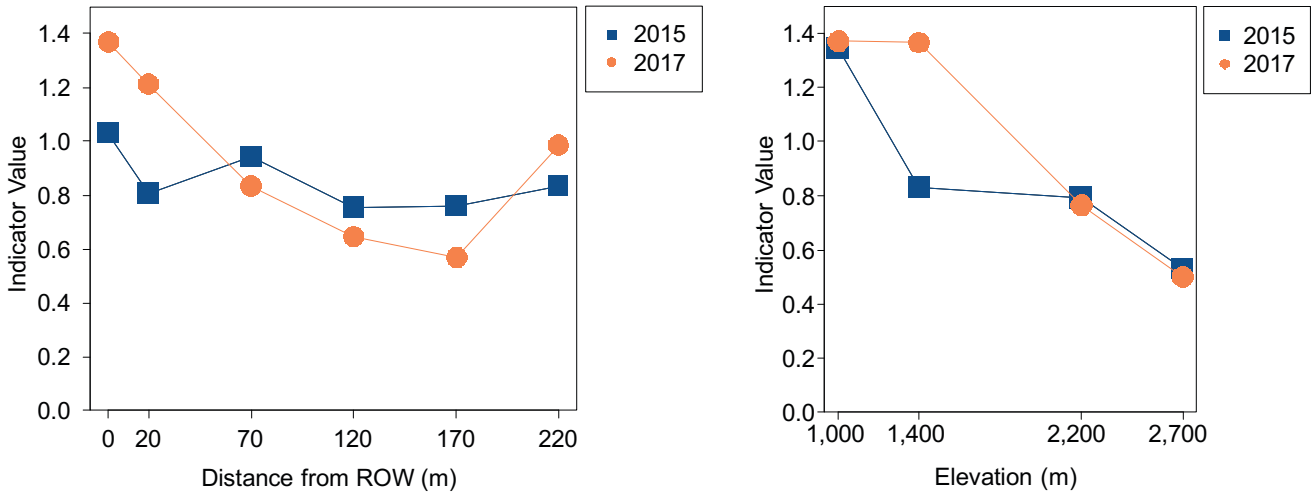

Figure 5.6. Summary plots of Functional Diversity at increasing distance from the ROW and at increasing elevation.

Species composition

Analyses thus far have shown clearly that Species Richness is greatest at the edges of transects and lower elevations, mainly because of species that can exploit forest edges and open habitats. While it is obvious that smaller values of Species Richness will lead to an altered species composition at sites because some species will be missing, it is also relevant to explore whether the species at higher elevations and within the forest interior were different. This is relevant to ask because forest interior species are generally specialists, and thus more dependent on closed habitats that a greater number of bats that will be present in and around a more dissected forest landscape.

Non-metric Multidimensional Scaling (NMDS) ordination plots showed that each elevation differed in the species represented, especially at the two higher elevations in BAA 1 on Hides Ridge (Figure 5.7). There was no strong indication that species composition changed with increasing distance from the ROW, but the sites at '0 m' were clustering more tightly and tending towards lower y-axis values, consistent with statistical results that indicated greater numbers of species ta the edge of the transect.

When the points in same two ordination plots were re-coded to reflect survey year, there was clearly no major difference in species composition between 2015 and 2017 (Figure 5.8).

When the Bray-Curtis Dissimilarity matrix was recalculated for Species Richness grouped by major call type (*ICF, mCF, sCF, cFM, bFM, fFM, sFM*), a similar pattern emerged, showing that the higher elevation sites were dominated by *cFM*-type calls, whereas there was a more even spread of a greater number of call types at the lower elevations (Figure 5.9). Sites at the two Hides elevations differed mainly because of the presence of the horseshoe bat *Rhinolophus mcintyrei* at transects H1 and H2.

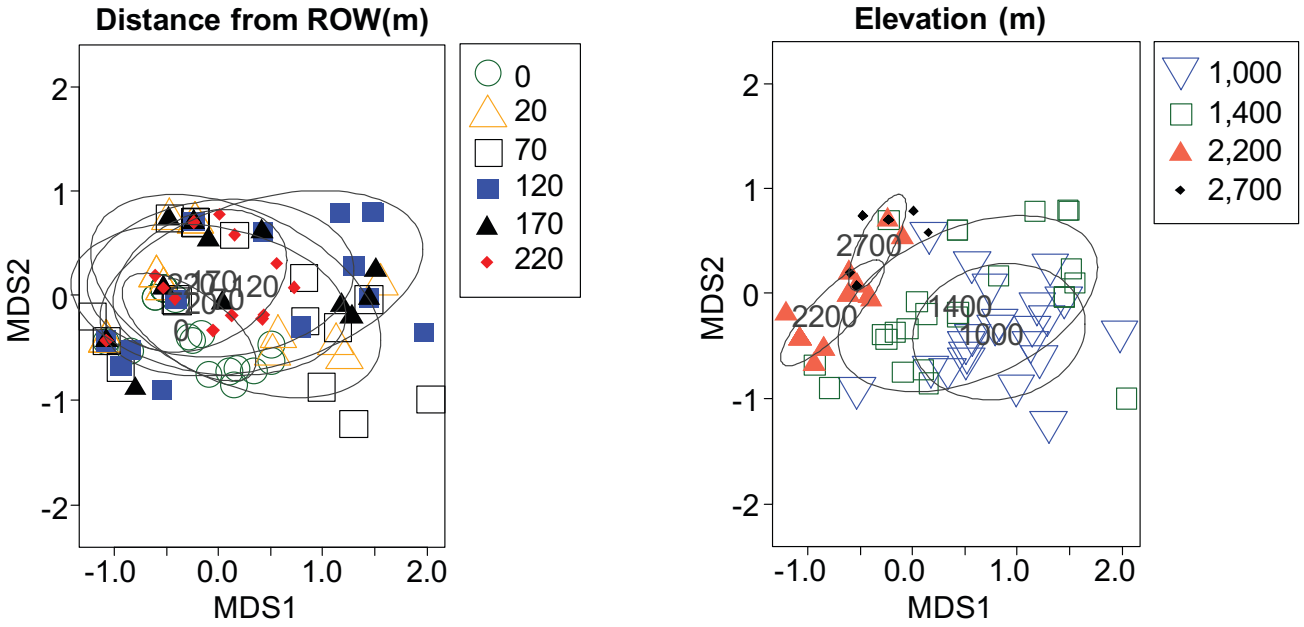

Figure 5.7. Multidimensional Scaling (NMDS) ordinations summarising patterns of species composition (as derived from species lists at each recording site) at increasing distance from the ROW and different elevations, for both survey years combined.

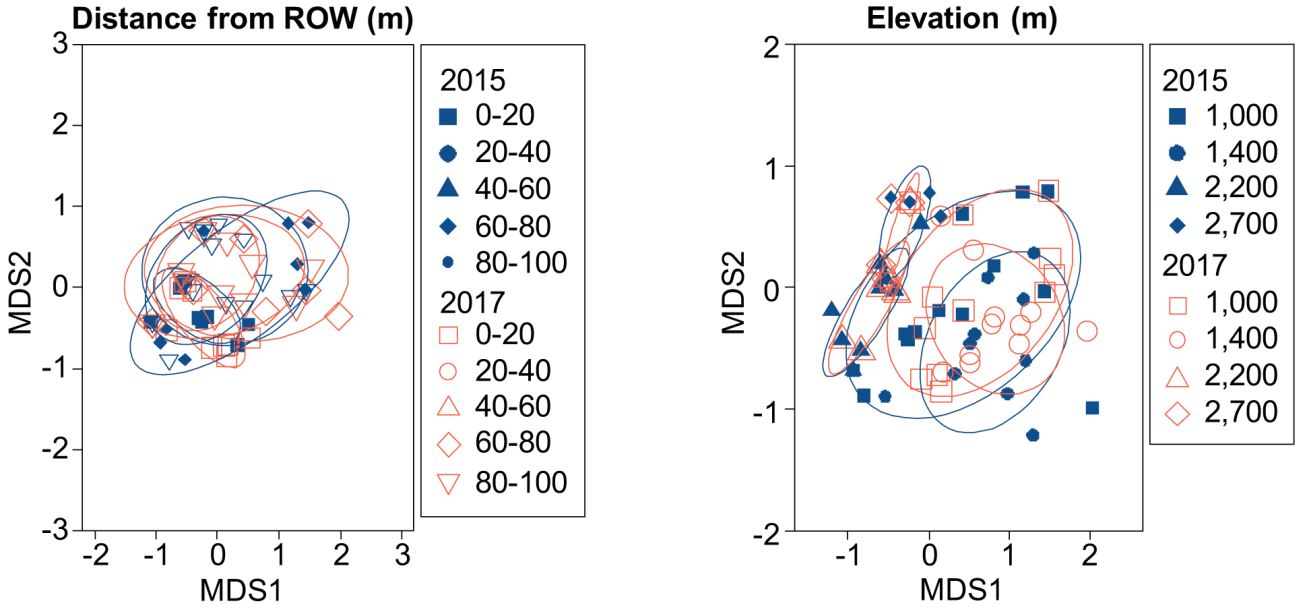

Figure 5.8. Multidimensional Scaling (NMDS) ordinations summarising patterns of species composition (as derived from species lists at each recording site) at increasing distance from the ROW and different elevations, with points recoded to indicate survey year.

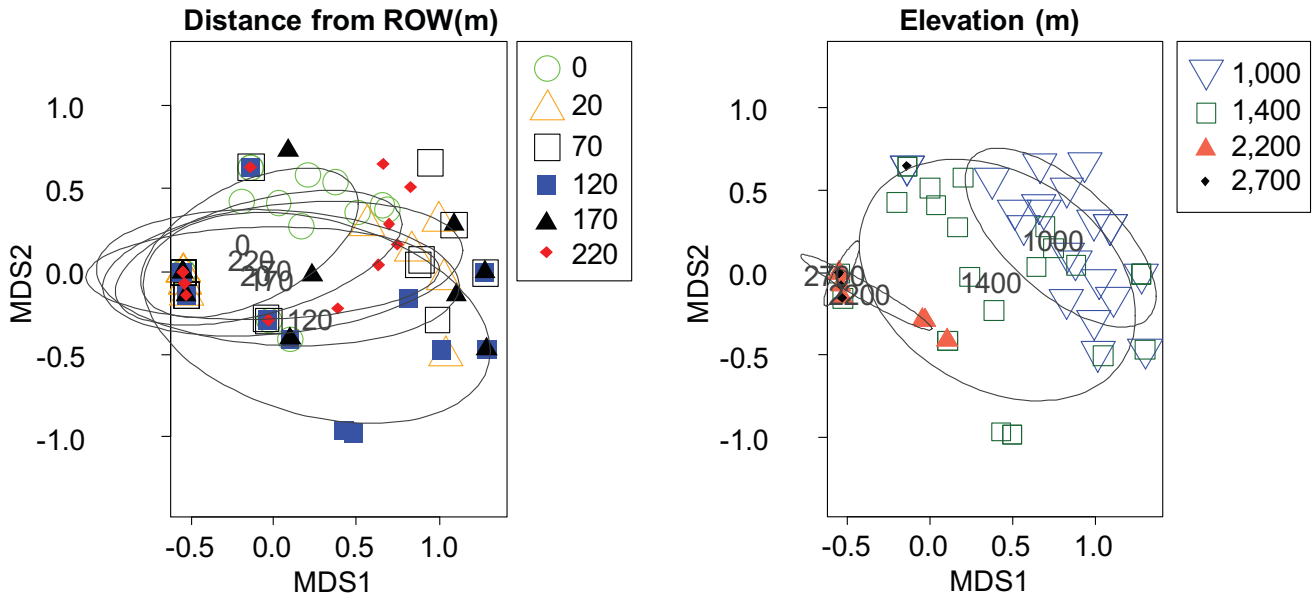

Figure 5.9. Multidimensional Scaling (NMDS) ordinations summarising patterns of species composition (as derived from lists of major echolocation call types at each recording site; echolocation call 'main body types': *lCF, mCF, sCF, cFM, bFM, fFM, sFM*) at increasing distance from the ROW and different elevations, for both survey years combined.

Species-level patterns

Overall patterns change because certain component species are sensitive to changes in their habitat, and respond either positively or negatively to decreased forest cover. It is important to understand which species are the most sensitive, or exploitative; and which are generalists, or the most specialised.

Compiling Relative Abundance shows how commonly each species is recorded amongst the recording sites. This indicates species that are rare or generally common. The only species that appeared to be more common along any point of the sampling transects was the unidentified bent-winged bat *Miniopterus* sp. 3 'small' (call type *53 st.cFM*), which tended to increase with increasing distance from the ROW (Figure 5.10; Appendices 5.4 and 5.5). Both this species and the unidentified bent-winged bat *Miniopterus* sp. 1 'large' (call type *38 st.cFM*) increased in Relative Abundance at higher elevations in BAA 1, relative to other species.

Of perhaps greater utility for impact assessments are metrics that describe biases in the association of species with particular habitats, and, accordingly, Dufrene and Legendre's (1997) Indicator Species index was calculated for each species. Small species of *Emballonura* that emit *i.fFM.d* call types were clearly associated with forest edges and open habitats, as were the large- and medium sized *Miniopterus* species (call types *38 st.cFM* and *45 st.cFM*), the Short-winged Pipistrelle *Philetor brachypterus* (call type *30 cFM*), and the two Molossidae species.

Species associated with particular elevations included *Mosia nigrescens* (*65 i.fFM.d*), three of the Hipposideridae, and all Rhinolophidae at the lowest elevation; and the unidentified bent-winged bat *Miniopterus* sp. 1 'large' at 2,200 m and the unidentified bent-winged bat *Miniopterus* sp. 3 'small' at 2,700 m.

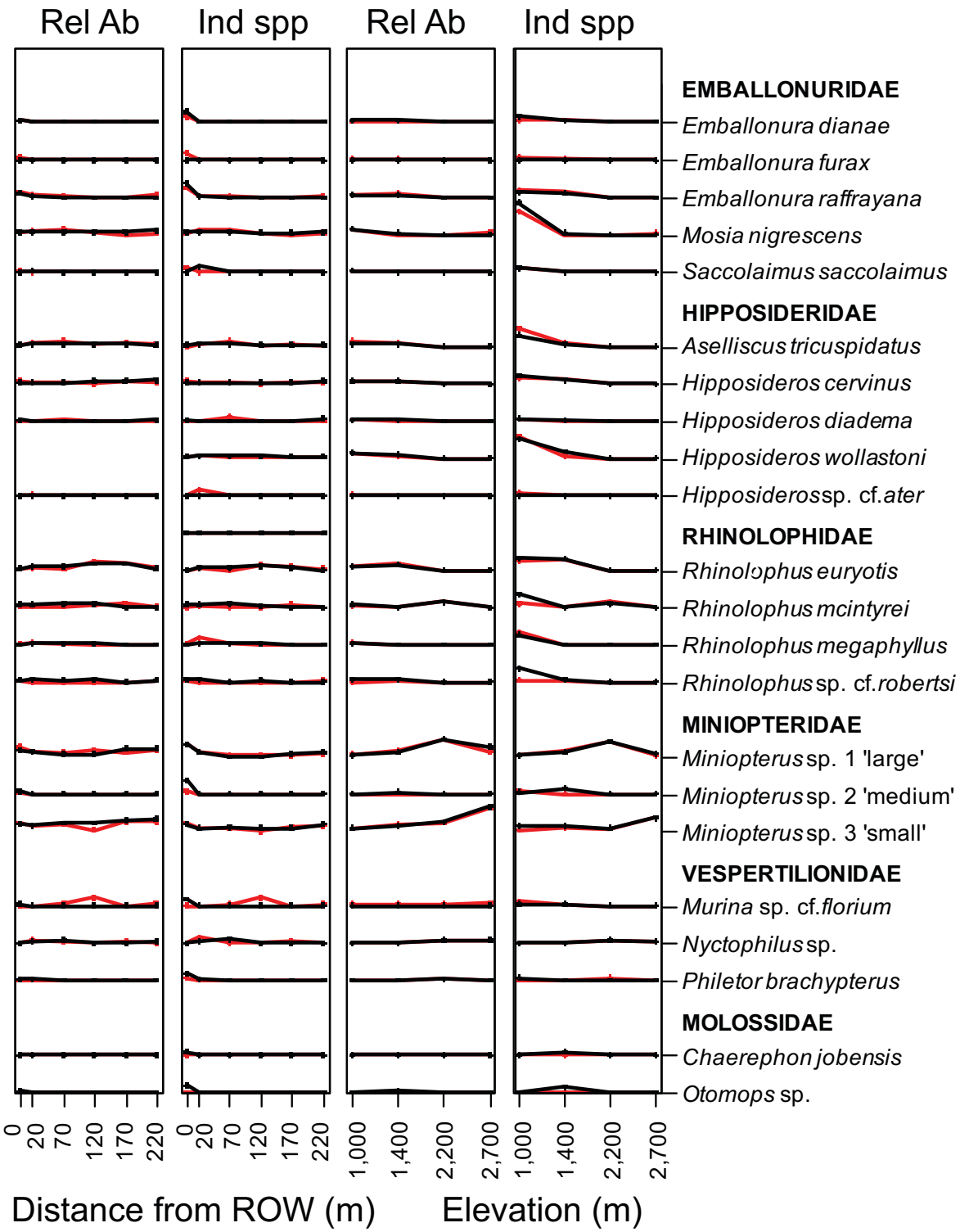

Figure 5.10. Summary of the trends Relative Abundance and Indicator Species indices with increasing distance from the ROW and elevation. Values for the two survey years (2015 in red; 2017 in black) have been separated.

Discussion

Detecting a long-term change

This component of the PMA3 monitoring study seeks to determine whether there is an ongoing level of habitat change following linear infrastructure construction that is reflected in changes to bat communities. This obviously requires that a standardised sampling regime is repeated on multiple occasions at suitable sampling intervals over the long-term. In this second survey, there was a slightly increased level of bat Species Richness detected overall, however it was not

associated with any observation that could be related specifically to a change in the habitat adjacent to the ROW. It is important to note that while this monitoring study does not incorporate a comprehensive set of measurements of the vegetation community along the transects, there had been no obvious changes in forest structure since 2015. The forest edge had not withdrawn, the same trees containing the transect markings were present, and the canopy coverage appeared unchanged. Thus, it is unsurprising that bat diversity remains at similar levels to those two years prior.

Understanding long-term trends in a modified natural landscape also requires a good understanding of natural patterns for context. The second survey in 2017 brought greater statistical power and increased species detection probability through additional sampling effort. In turn, this provided a relatively clear understanding of how bat diversity changes in these mid-montane areas with increasing elevation, and between open and closed foraging spaces. Many of the analyses were designed to detect potential differences in the bat community along a transect that could result from changes in forest structure through the effects of increased wind, heat and light from the open spaces of the ROW. However, in the absence of an obvious and developing environmental gradient along transects, a more accurate view is that analyses were simply examining the difference between bat species using the open habitat at the edge of the ROW, and those using the forest interior at the remaining sites further into the forest. The influx of species that use open areas probably occurs relatively quickly after forest is transected. Species that forage amongst canopy and in the open but close to vegetation on the top of the canopy move down to take advantage of the extra 'forest edge'. Such a response is assumed to be distinct from that derived from a longer-term effect of an environmental gradient relevant to bats that may potentially develop with increasing distance into the forest from linear infrastructure.

An additional consideration for detecting a long-term change in a monitoring study is the comparison with the pre-construction condition. The PMA3 monitoring study began around four years after the construction of the ROW, and the previous report (Armstrong 2017) mentioned the value of comparing the PMA3 study results with those from the pre-construction baseline work of G. Richards (2005, 2008) conducted as part of the original environmental impact assessment for the PNG LNG project. However, direct comparisons with this earlier work are limited because the baseline sampling sites are different from the PMA3 long-term study sites. More importantly, the raw data from Richards (2005, 2008) needed to be re-analysed to take advantage of a better understanding of the attribution of echolocation call types that has come about in the past decade (Armstrong and Aplin 2011, 2014b,c; Leary and Pennay 2011; Robson et al. 2012; Armstrong et al. 2015a,b; Armstrong 2017, and K.N. Armstrong and K.P. Aplin unpublished data).

This re-analysis was indeed undertaken (Specialised Zoological 2017; summary in Appendix 5.6). The most relevant information for the PMA3 study is that there were five species encountered by Richards (2005) that were additional to the 2015 survey. Of those five species, one was detected in the 2017 survey (the free-tailed bat *Otomops* sp.), and a second is not expected because specific habitats are not present (streams with flowing water for the Maluku Myotis *Myotis moluccarum*). A third was detected after re-analysis of the 2015 dataset was undertaken with new information on how to distinguish the horseshoe bat *Rhinolophus mcintyrei* (an updated taxonomic name for *R. arcuatus*) from the Eastern Horseshoe Bat *R. megaphyllus*.

The remaining species (New Guinea Free-tailed Bat *Austronomus kuboriensis*; and any of three species of *Pipistrellus*) were mentioned previously in Armstrong (2017) as being conspicuous absences. These were not detected in 2017, but there is potential for detection on future surveys. Overall, and despite a much smaller sampling area than that of Richards (2005), the recording sites on the 11 sampling transects have a good representation of species expected for the local area. Of particular note, the PMA3 study has detected up to five extra bat species, and discovered another three species that are possibly new to science, with two of those coming from captures on the 2017 survey. There are likely to be further new detections on subsequent monitoring surveys.

Natural patterns of bat diversity

The patterns from both the 2015 and 2017 surveys show clearly that lower elevation sites below 2,000 m have greater bat diversity; and at these elevations an opening of the forest canopy supports the influx of species that prefer to forage in the Edge and Open flight spaces next to, and above, stands of vegetation. But such an influx is less likely, or would be less dramatic at the higher elevations above 2,000 m. Thus, responses of bats are likely to be different at mid and high elevations because of differences in the diversity of source populations. In a general sense for tropical ecosystems in PNG, this suggests higher elevation sites are more likely to show decreased bat diversity and activity with continued dissection of the forest expanse.

One analytical addition to the 2017 survey dataset was Dufrene and Legendre's (1997) Indicator Species index that highlights species associated with particular habitats (Figure 5.10). Indicator Species values were particularly helpful for identifying species that preferred to forage in open spaces against forest edges and were responsible for the significant statistical results, namely species in the Emballonuridae, Miniopteridae and Vespertilionidae with *i.fFM.d* and *cFM* call types. Statistical tests and overall means (across distances from the ROW, at different elevations) undertaken just on these species mirrored the results from using total Species Richness. The simple interpretation is that opening parts of forests invites exploitation by Edge foraging species that are already present nearby in equivalent habitats. Importantly, if large forest patch size is retained, the forest interior species will persist, and overall bat diversity will increase. This is especially the case when rocky outcrop is present that contains underground roosting habitat for the Hipposideridae and Rhinolophidae, which probably explains some of the difference between Arakubi Quarry and KP107.

At higher elevations, species may have a more specialist requirement for closed forest, or a physiology that allows them to live a lower energy activity regime in colder, less productive (because of reduced insect prey biomass) habitats. The Hipposideridae and Rhinolophidae do not appear to be adapted to environments over 2,000 m and the record of the horseshoe bat *Rhinolophus mcintyrei* at 2,200 m on transects H1 and H2 in BAA 1 is surely because of nearby rocky roosting habitat, and possibly represents the upper limit of this species. Thus, disturbances to forest at higher elevations will not be as obvious because the creation of open habitat and forest edges will not be accompanied by an influx of Edge and Open foraging species that are adapted to warmer, more productive lower elevations, especially the small Emballonuridae that appear to be restricted to elevations below 1,600 m (Bonaccorso 1998).

Most of the detections at elevations above 2,000 m were of the Miniopteridae. While they were also present down to 1,000 m, these species are obviously adapted to spending time at the higher elevations. They are capable of a wide nightly foraging range, and it is unknown whether individuals detected above 2,000 m commuted from lower elevations. Most likely, though, there is rocky underground outcrop somewhere within a few kilometres of the recording sites that is suitable for roosting. These species can go into daily torpor and may be well adapted for the relatively low resource environments at higher elevations.

Other forest interior specialist species were present at all elevations, in particular the *80 bFM* call type (see also Armstrong 2017). In 2015, this call type was attributed to the Flute-nosed Bat *Murina* sp. cf. *florium* because it was known to be present above 2,000 m (Bonaccorso 1998; Armstrong et al. 2014c). The discovery of a possible new species of woolly bat *Kerivoula* sp. at 2,700 m suggested that the *80 bFM* call type is attributable to either of these species. Unfortunately, this low amplitude call type is detectable only when bats come within about a metre of the bat detector, so the presence of both species is certainly underestimated. Both species are well adapted to both forest interiors and low resource conditions: they have small home ranges, a wing morphology and call type that allows them to detect and capture prey close to background vegetation clutter, and they have an ability to enter torpor to conserve their energy resources in a habitat that is relatively unproductive. Given that these species will not forage readily outside forest patches in the open, their contribution to the documented patterns is low, and because of the absence of the Hipposideridae and Rhinolophidae at higher elevations, the presence of forest interior specialists at high elevations will be underestimated.

Bat species of conservation significance

No species of conservation significance (in an IUCN threatened category, or as Data Deficient) was detected on the 2017 survey. In 2015, the New Guinea Sheath-tailed Bat *Emballonura furax* was detected, and was listed as Data Deficient at the time. The conservation status of this species has since been reassessed as Least Concern (Armstrong and Aplin 2017).

New call types and possible new bat species

Two species of long-eared bats *Nyctophilus* sp. were captured. The first was the Small-toothed Long-eared Bat *Nyctophilus microdon*. This species is found only in mid-montane areas, between approximately 1,900 to 2,200 according to Bonaccorso (1998). Its capture in 2017 (three individuals at transect H3; Appendix 5.1) was significant because its call frequency had not been documented previously. The call is remarkable in having a much lower minimum frequency than any other Australasian *Nyctophilus*. It is somewhat puzzling that it has not yet been detected at any of the recording sites, and points to a requirement to modify the acoustic processing method.

The second species of long-eared bat captured (2,700 m on transect H6 in BAA 1) is potentially new to science. It resembles the Papuan Long-eared Bat *N. microtis*, which actually has relatively short ears compared to other species of *Nyctophilus*. The Papuan Long-eared Bat is apparently found at elevations up to only 1,450 m (Bonaccorso 1998), and recent captures have suggested the possibility of two distinct forms of this species at low elevations (K.P. Aplin and K.N. Armstrong unpublished data). A high elevation form could also be distinct at the species level. Genetic work is currently ongoing to confirm the novelty of the *Nyctophilus* from H6 on Hides Ridge (K.N. Armstrong unpublished data).

The second of the more exciting captures was of a species of woolly bat *Kerivoula* sp., also from 2,700 m on transect H6 on Hides Ridge. This individual was relatively small and dark in colour compared to lowland forms that have been collected recently at much lower elevation (K.P. Aplin and K.N. Armstrong unpublished data). The published elevational range of the Fly River Woolly Bat *Kerivoula muscina* reaches only to 1,600 m (Bonaccorso 1998). Genetic work is also ongoing to confirm the novelty of this *Kerivoula* (K.N. Armstrong unpublished data).

Despite targeted trapping effort with harp traps around the rocky outcrop in close vicinity to transects at Arakubi Quarry where the *172 sCF* call type was detected in 2015, the species could not be captured. It was however detected not far away prior to the 2017 PMA3 survey closer to Lake Kutubu at KP87 (Kale et al. 2018). As in 2015, a single echolocation sequence was recorded. It is likely that this species is present in the general area around Lake Kutubu and could be encountered with more effort.

Other notable taxa with taxonomic ambiguity

The taxonomy of bent-winged bats (*Miniopterus* spp.) in New Guinea and further afield in Indonesia and other parts of Asia is completely unresolved, as there has been very little application of genetic markers to this group in a modern integrative approach to taxonomy. Applying names based on morphological descriptions (e.g. as from Bonaccorso 1998; Simmons 2005) is fraught with the possibility of misidentification, and some names currently used for PNG populations are probably not applicable in this area. Hence, there is the possibility that one or more *Miniopterus* encountered on the survey are unnamed. The taxonomy of this group in PNG is currently under review, and the tissues, specimens and call recordings from the two size forms captured in 2017 have become part of a postgraduate study (S. Wiantoro, K.N. Armstrong and K.P. Aplin research in progress).

Conclusions

1. The combined results from both the 2015 and 2017 surveys suggest that the forest adjacent to the ROW has so far retained its value for bats.

2. Sites below 2,000 m in elevation have greater bat diversity overall; and the elevations above 2,000 m are dominated by bent-winged bats that would appear to have adaptations to allow them to forage and possibly roost at higher elevations where temperatures are cooler and insect prey biomass is presumably lower.

3. In contrast to 2015, statistical tests showed a significantly greater bat diversity in the open areas at the start of transects (0 m) compared to the remaining recording sites in the forest interior, which was controlled by the greater numbers of species that forage in Edge and Open flight spaces (mainly the small Emballonuridae, also Miniopteridae).

4. Taken together, the significant differences above and below 2,000 m in elevation, and the significant differences in bat diversity between the open areas in the ROW and the forest interior, point to a different response of the bat community at high and low elevations. Below 2,000 m, an opening of the forest canopy results in an increase in bat diversity because it supports the influx of species that prefer to forage in the Edge and Open flight spaces next to, and above, stands of vegetation. Above 2,000 m, such an influx is less likely, or would be less dramatic because many of the same the Edge and Open flight space bats are not present.

5. The combined results from the two previous surveys has provided greater statistical power, resulting in a clearer view of the difference between open habitats at the edge of transects and the closed habitat of the forest interior, and the implication for forest cover change at different elevations. Together with an increasing number of species documented by both acoustic recorders (three species) and trapping (an additional three species), and especially the records of up to three other species new to science, the results from the 2017 survey provide strong grounds for continuation of an acoustic monitoring study for bats into the future.

Recomendations

1. Continuation of the acoustic bat monitoring component as part of future surveys is strongly recommended, as it has demonstrated utility for detecting bat responses to the open areas and forest edge in the ROW.

2. To obtain a greater detection rate of *bFM*-emitting interior forest specialist species, the use of an acoustic lure alongside bat detectors to broadcast social calls of these species might be considered for trial. Acoustic lures bring species with low amplitude calls closer to bat detectors, thus increasing their detectability. They are particularly effective on *bFM* species, and low-cost lures have been developed (K.N. Armstrong unpublished) that can be deployed easily. Lures can be set so that the recording sites are still acoustically independent in terms of broadcast range. Being able to detect *bFM*-emitting forest interior species more reliably will bring further clarity on how these specialists use the study areas.

3. The custom-designed acoustic lures can also record bat passes in infrared / thermal video, which would allow the compilation of total bat activity at each recording site. This may be worth trialling on future surveys, as total activity may also vary considerably amongst treatments.

4. Further efforts should be made on future surveys to capture the new species of bat that was detected on the basis of its unique 172 kHz echolocation call close to a small outcrop of limestone on transect M5 near Arakubi Quarry in BAA 2, and nearby at KP87 adjacent to Lake Kutubu. Capture effort need not be confined to the Arakubi Quarry area.

5. Capture effort for bats should continue on future surveys to target species of *Pipistrellus* that are expected to occur, but have not been detected acoustically because of the similarity of their calls with those of medium- and small-sized *Miniopterus*.

Special Acknowledgement

Appendix 5.6 contains a summary of the re-analysis of datasets collected by Dr Greg Richards as part of the PNG LNG pre-construction baseline biological surveys. This series of surveys saw the first large deployment of bat detectors in Papua New Guinea, and was undertaken when the call types of very few bats in this country were known. To assist in the production of the present report, Greg helpfully provided most of the original recordings for re-analysis in light of a much-improved understanding of bat call types. Greg sadly passed away in 2018 as this report was being written, and he is remembered fondly as a pioneering biologist and a generous, collaborative person with an abundance of character.

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Plate 1

Figure 5.11. Set up of the D500X bat detectors

Figure 5.12. Triple-bank harp trap

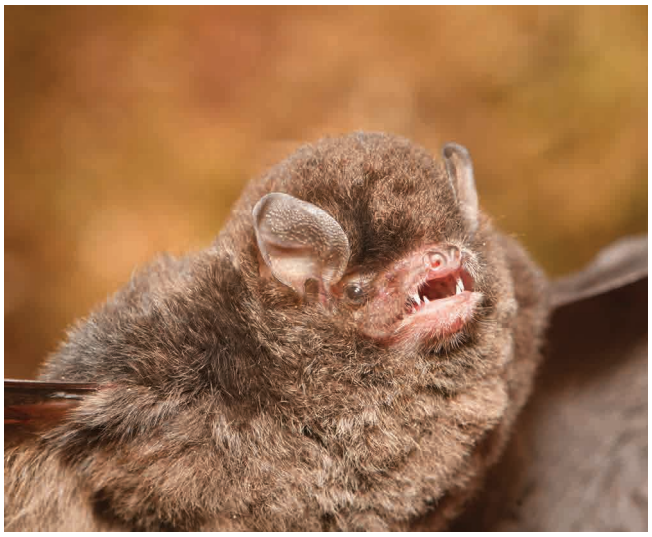

Figure 5.13. Small unidentified species of bent-winged bat *Miniopterus* spp.

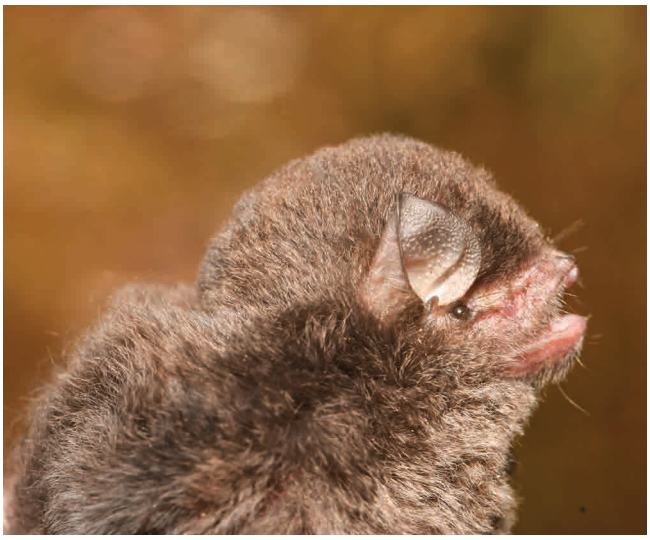

Figure 5.14. Large unidentified species of bent-winged bat *Miniopterus* spp.

Figure 5.15. Small-toothed Long-eared Bat *Nyctophilus microdon*

Figure 5.16. Likely new species of long-eared bat *Nyctophilus* sp. cf. *microtis*

Plate 2

Figure 5.17. Likely new species of woolly bat *Kerivoula* sp. cf. *muscina*

Figure 5.18. Undescribed mid-montane species of blossom bat *Syconycteris* sp. cf. *australis*

Figure 5.19. Temminck's Leaf-nosed Bat *Aselliscus tricuspidatus*

Figure 5.20. Fawn Leaf-nosed Bat *Hipposideros cervinus*

Figure 5.21. New Guinea Horseshoe Bat *Rhinolophus euryotis*

Figure 5.22. The horseshoe bat *Rhinolophus mcintyrei*

Appendix 5.1. Bat captures in 2017 (total 52; Locality codes are: AQ: Arakubi Quarry, HR: Hides Ridge; Tissue types are: L: liver, WP: biopsy from wing punch; Fate codes are: R: released at point of capture, V: whole specimen voucher).

Locality	Night of capture	GPS coordinate	Genus species	Tissue	Sample	Fate
			PTEROPODIDAE—38			
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*	L	MEL0535	V
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*	WP	MEL0536	R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*	WP	MEL0537	R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*	WP		R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-14	6.46251S 143.25465E	*Syconycteris australis*			R
AQ	2017-05-16	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-17	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-18	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-18	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-18	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-18	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-18	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-18	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-18	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-19	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-19	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-19	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-19	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-19	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-19	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-19	6.46621S 143.24825E	*Syconycteris australis*			R
AQ	2017-05-19	6.46621S 143.24825E	*Syconycteris australis*			R

Locality	Night of capture	GPS coordinate	Genus species	Tissue	Sample	Fate
HR	2017-05-23	5.94404S 142.74322E	*Syconycteris* sp. cf. *australis*	WP	MEL0707	R
HR	2017-05-27	5.91380S 142.68995E	*Syconycteris* sp. cf. *australis*	L	MEL0723	V
			HIPPOSIDERIDAE—4			
AQ	2017-05-14	6.46251S 143.25465E	*Aselliscus tricuspidatus*	L	MEL0533	R
AQ	2017-05-14	6.46251S 143.25465E	*Aselliscus tricuspidatus*	WP	MEL0534	R
AQ	2017-05-14	6.46251S 143.25465E	*Hipposideros cervinus*	WP	MEL0532	R
AQ	2017-05-16	6.46621S 143.24825E	*Hipposideros cervinus*	WP	MEL0543	R
			RHINOLOPHIDAE—2			
AQ	2017-05-17	6.46621S 143.24825E	*Rhinolophus mcintyrei*	WP	MEL0548	R
AQ	2017-05-14	6.46251S 143.25465E	*Rhinolophus euryotis*	WP	MEL0531	R
			MINIOPTERIDAE—3			
HR	2017-05-29	5.91380S 142.68995E	*Miniopterus* sp. 1	L	MEL0735 MEL0744	V
HR	2017-05-30	5.91380S 142.68995E	*Miniopterus* sp. 2	WP	MEL0740	R
HR	2017-05-30	5.91380S 142.68995E	*Miniopterus* sp. 2	WP	MEL0741	R
			VESPERTILIONIDAE—5			
HR	2017-05-30	5.91380S 142.68995E	*Kerivoula* sp. cf. *muscina*	L	MEL0742 MEL0745	V
HR	2017-05-22	5.94404S 142.74322E	*Nyctophilus microdon*	L	MEL0705	V
HR	2017-05-23	5.94404S 142.74322E	*Nyctophilus microdon*	WP	MEL0708	R
HR	2017-05-23	5.94404S 142.74322E	*Nyctophilus microdon*	WP	MEL0709	R
HR	2017-05-28	5.91380S 142.68995E	*Nyctophilus* sp. cf. *microtis*	L	MEL0729 MEL0732	V

Appendix 5.2. Summary of bat captures in both survey years, with species common names and totals (C: captured; E: detected from echolocation calls; call type designations are from Armstrong 2017).

Common name	Scientific name	Call type	Main Call type	Flight space	2015	2017
	PTEROPODIDAE—2	—	—	—		
Eastern Blossom Bat	*Syctonycteris australis*	—	—	—	C	C
a blossom bat	*Syctonycteris* sp. cf. *australis*	—	—	—	C	C
	EMBALLONURIDAE—5					
Large-eared Sheath-tailed Bat	*Emballonura dianae*	*35 i.fFM.d*	*fFM*	Edge	E	E
New Guinea Sheath-tailed Bat	*Emballonura furax*	*52 i.fFM.d*	*fFM*	Edge	E	
Raffray's Sheath-tailed Bat	*Emballonura raffrayana*	*45 i.fFM.d*	*fFM*	Edge	E	E
Lesser Sheath-tailed Bat	*Mosia nigrescens*	*65 i.fFM.d*	*fFM*	Edge	E	E
Bare-rumped Sheath-tailed bat	*Saccolaimus saccolaimus*	*25 sFM*	*sFM*	Open	E	E
	HIPPOSIDERIDAE—5					
Temminck's Leaf-nosed Bat	*Aselliscus tricuspidatus*	*120 sCF*	*sCF*	Clutter	CE	CE
Fawn-coloured Leaf-nosed Bat	*Hipposideros cervinus*	*140 sCF*	*sCF*	Clutter	CE	CE
Diadem Leaf-nosed Bat	*Hipposideros diadema*	*58 mCF*	*mCF*	Edge	E	E
Wollaston's Leaf-nosed Bat	*Hipposideros wollastoni*	*88 mCF*	*mCF*	Clutter	E	E
a leaf-nosed bat	*Hipposideros* sp. cf. *ater*	*172 sCF*	*sCF*	Clutter	E	
	RHINOLOPHIDAE—4					
New Guinea Horseshoe Bat	*Rhinolophus euryotis*	*52 lCF*	*lCF*	Clutter	E	CE
a horseshoe bat	*Rhinolophus mcintyrei*	*70 lCF*	*lCF*	Clutter	E	CE
Eastern Horseshoe Bat	*Rhinolophus megaphyllus*	*65 lCF*	*lCF*	Clutter	CE	E
Greater Large-eared Horseshoe Bat	*Rhinolophus* sp. cf. *robertsi*	*33 lCF*	*lCF*	Clutter	E	E
	MINIOPTERIDAE—3					
a bent-winged bat	*Miniopterus* sp. 1 'large'	*38 st.cFM*	*cFM*	Edge	CE	CE
a bent-winged bat	*Miniopterus* sp. 2 'medium'	*45 st.cFM*	*cFM*	Edge	E	E
a bent-winged bat	*Miniopterus* sp. 3 'small'	*53 st.cFM*	*cFM*	Edge	E	CE
	VESPERTILIONIDAE—5					
a woolly bat	*Kerivoula* sp.	*80 bFM*	*bFM*	Clutter	E	CE
Flute-nosed Bat	*Murina* sp. cf. *florium*	*80 bFM*	*bFM*	Clutter	E	E
Small-toothed Long-eared Bat	*Nyctophilus microdon*	*30 bFM*	*bFM*	Clutter		C
a long-eared bat	*Nyctophilus* sp.	*50 bFM*	*bFM*	Clutter	E	E
Short-winged Pipistrelle	*Philetor brachypterus*	*30 cFM*	*bFM*	Edge	E	E
	MOLOSSIDAE—2					
Greater Northern Free-tailed Bat	*Chaerephon jobensis*	*20 cFM*	*cFM*	Open		E
a free-tailed bat	*Otomops* sp.	*30 sFM*	*sFM*	Open		E
Total Species Richness					**23**	**24**

Appendix 5.3. Summary of species detections at each nightly recording site in 2017 (to allow future verification; filled black circle indicate a detection of that species, an open circle an apparent absence, and a hyphen a failed recording).

BAA_transect_elevation	Distance from road (m)	Recording unit serial	Recording night in May 2017	*E. dianae*	*E. furax*	*E. raffrayana*	*M. nigrescens*	*S. saccolaimus*	*A. tricuspidatus*	*H. cervinus*	*H. diadema*	*H. wollastoni*	*H.* sp. cf. *ater*	*R. euryotis*	*R. mcintyrei*	*R. megaphyllus*	*R.* sp. cf. *robertsi*	*Miniopterus* sp. 1 'large'	*Miniopterus* sp. 2 'medium'	*Miniopterus* sp. 3 'small'	*M.* sp. cf. *florium*	*Nyctophilus* sp.	*P. brachypterus*	*C. jobensis*	*Otomops* sp.
				35 i.fFM.d	*52 i.fFM.d*	*45 i.fFM.d*	*65 i.fFM.d*	*25 sFM*	*120 sCF*	*140 sCF*	*58 mCF*	*88 mCF*	*172 sCF*	*52 ICF*	*70 ICF*	*65 ICF*	*33 ICF*	*38 st.cFM*	*45 st.cFM*	*53 st.cFM*	*80 bFM*	*50 bFM*	*30 cFM*	*20 cFM*	*30 sFM*
Hides_H1_2200	0	956	29	o	o	o	o	o	o	o	o	o	o	o	●	o	o	●	o	●	o	o	o	o	o
	20	956	28	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	o	o	o
	70	953	25	o	o	o	o	o	o	o	o	o	o	o	●	o	o	●	o	●	o	●	o	o	o
	120	953	24	o	o	o	o	o	o	o	o	o	o	o	●	o	o	●	o	●	o	o	o	o	o
	170	953	23	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	o	o
	220	953	22	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	●	o	o	o
Hides_H2_2200	0	955	23	o	o	o	o	o	o	o	o	o	o	o	●	o	o	●	o	o	o	o	o	o	o
	20	955	24	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	o	o	o	o	o
	70	953	26	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	o	o	o
	120	953	27	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
	170	953	28	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	o	o	o
	220	953	29	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
Hides_H3_2200	0	957	27	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	o	●	o	o	
	20	957	26	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	
	70	957	25	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	
	120	957	24	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	o	o	
	170	957	23	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o		
	220	957	22	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	o		
Hides_H4_2700	0	956	22	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	o	o	o		
	20	956	23	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	o	o	o		
	70	956	24	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o		
	120	956	25	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o		
	170	956	26	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o		
	220	956	27	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o		
Hides_H5_2700	0	954	22	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	o	o		
	20	954	23	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	●	o		
	70	954	24	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	o	o		
	120	954	25	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o		
	170	954	26	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o		
	220	954	27	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	●	o	o	o		

Appendix 5.3. Species detections at each nightly recording site in 2017—*continued*.

BAA_transect_elevation	Distance from road (m)	Recording unit serial	Recording night in May 2017	*E. dianae*	*E. furax*	*E. raffrayana*	*M. nigrescens*	*S. saccolaimus*	*A. tricuspidatus*	*H. cervinus*	*H. diadema*	*H. wollastoni*	*H.* sp. cf. *ater*	*R. euryotis*	*R. mcintyrei*	*R. megaphyllus*	*R.* sp. cf. *robertsi*	*Miniopterus* sp. 1 'large'	*Miniopterus* sp. 2 'medium'	*Miniopterus* sp. 3 'small'	*M.* sp. cf. *florium*	*Nyctophilus* sp.	*P. brachypterus*	*C. jobensis*	*Otomops* sp.
				35 i.fFM.d	*52 i.fFM.d*	*45 i.fFM.d*	*65 i.fFM.d*	*25 sFM*	*120 sCF*	*140 sCF*	*58 mCF*	*88 mCF*	*172 sCF*	*52 ICF*	*70 ICF*	*65 ICF*	*33 ICF*	*38 st.cFM*	*45 st.cFM*	*53 st.cFM*	*80 bFM*	*50 bFM*	*30 cFM*	*20 cFM*	*30 sFM*
Hides_H6_2700	0	954	28	O	O	O	O	O	O	O	O	O	O	O	O	O	O	●	O	●	O	O	O	O	O
	20	954	29	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	●	O	O	O	O	O
	70	955	28	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	●	O	O	O	O	O
	120	955	27	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	●	O	O	O	O	O
	170	955	26	O	O	O	O	O	O	O	O	O	O	O	O	O	O	●	O	●	O	O	O	O	O
	220	955	25	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	●	O	O	O	O	O

Appendix 5.3. Species detections at each nightly recording site in 2017—continued.

BAA_transect_elevation	Distance from road (m)	Recording unit serial	Recording night in May 2017	*E. dianae*	*E. furax*	*E. raffrayana*	*M. nigrescens*	*S. saccolaimus*	*A. tricuspidatus*	*H. cervinus*	*H. diadema*	*H. wollastoni*	*H.* sp. cf. *ater*	*R. euryotis*	*R. mcintyrei*	*R. megaphyllus*	*R.* sp. cf. *robertsi*	*Miniopterus* sp. 1 'large'	*Miniopterus* sp. 2 'medium'	*Miniopterus* sp. 3 'small'	*M.* sp. cf. *florium*	*Nyctophilus* sp.	*P. brachypterus*	*C. jobensis*	*Otomops* sp.
				35 i.fFM.d	*52 i.fFM.d*	*45 i.fFM.d*	*65 i.fFM.d*	*25 sFM*	*120 sCF*	*140 sCF*	*58 mCF*	*88 mCF*	*172 sCF*	*52 ICF*	*70 ICF*	*65 ICF*	*33 ICF*	*38 st.cFM*	*45 st.cFM*	*53 st.cFM*	*80 bFM*	*50 bFM*	*30 cFM*	*20 cFM*	*30 sFM*
Moro_M1_1400	0	954	14	●	o	●	o	o	o	o	o	o	o	o	o	o	o	●	●	●	o	o	●	o	o
	20	954	15	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
	70	—	—	----------																					
	120	954	12	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	●	o	o	o	o	o
	170	954	11	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
	220	954	13	o	o	o	o	o	●	●	o	●	o	●	o	o	o	●	o	●	o	o	o	o	o
Moro_M2_1400	0	953	16	●	o	●	●	o	o	o	o	o	o	o	o	o	●	●	●	●	o	o	o	●	●
	20	954	16	o	o	o	o	o	o	o	o	●	o	●	o	o	●	o	o	o	o	o	o	o	o
	70	956	12	o	o	o	o	o	●	o	o	●	o	●	o	o	o	o	o	o	o	o	o	o	o
	120	956	13	o	o	o	o	o	●	o	o	●	o	●	o	o	o	o	o	o	o	o	o	o	o
	170	956	14	o	o	o	o	o	o	o	o	●	o	●	o	o	o	o	o	o	o	o	o	o	o
	220	956	15	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
Moro_M3_1400	0	955	14	o	o	●	o	o	o	o	o	●	o	o	o	o	o	●	●	●	●	o	o	o	●
	20	955	13	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o	o
	70	954	10	o	o	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	o	o
	120	955	12	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o	o	o	o	o	o	o
	170	955	11	o	o	o	o	o	o	●	o	o	o	●	o	o	o	●	o	●	o	o	o	o	o
	220	956	11	o	o	o	o	o	o	●	●	o	o	o	o	o	●	●	o	●	o	o	o	o	o
Moro_M4_1000	0	957	11	●	o	●	●	o	o	o	o	o	o	o	●	o	●	●	o	●	●	o	o	o	o
	20	957	16	o	o	o	●	o	●	o	o	●	o	●	●	●	o	o	o	o	o	o	o	o	o
	70	953	11	o	o	o	●	o	●	●	o	●	o	●	●	●	o	o	o	o	●	o	o	o	o
	120	957	12	o	o	o	o	o	o	o	o	●	o	o	o	o	●	o	o	o	o	o	o	o	o
	170	—	—	----------																					
	220	953	15	o	o	o	●	o	o	o	o	●	o	o	o	o	o	o	o	●	o	o	o	o	o
Moro_M5_1000	0	953	13	●	o	●	●	o	●	●	●	●	o	●	o	o	●	●	●	●	o	o	●	o	o
	20	957	13	●	o	●	●	●	●	●	o	●	o	●	●	o	●	●	o	●	o	o	●	o	o
	70	953	14	o	o	o	●	o	o	o	o	●	o	●	●	o	●	o	o	o	o	o	o	o	o
	120	957	14	o	o	o	●	o	o	●	o	●	o	●	●	●	●	o	o	●	o	o	o	o	o
	170	953	12	o	o	o	●	o	●	o	o	●	o	●	o	o	o	o	o	o	o	o	o	o	o
	220	957	15	o	o	o	●	o	o	o	o	o	o	o	o	o	o	o	o	●	o	o	o	o	o

Appendix 5.4. Summary of Relative Abundance and Indicator Species index for each species at increasing distance from the ROW (grey shading indicates the magnitude of the value, with zero as white and 1.0 as black).

	Relative Abundance						Indicator Index					
	0	**20**	**70**	**120**	**170**	**220**	**0**	**20**	**70**	**120**	**170**	**220**
EMBALLONURIDAE												
Emballonura dianae	0.07	0.03	0.00	0.00	0.00	0.00	0.27	0.03	0.00	0.00	0.00	0.00
Emballonura furax	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
E. raffrayana	0.09	0.03	0.00	0.00	0.00	0.00	0.36	0.03	0.00	0.00	0.00	0.00
Mosia nigrescens	0.05	0.06	0.08	0.05	0.06	0.08	0.06	0.05	0.04	0.01	0.01	0.04
Sacc. saccolaimus	0.00	0.03	0.00	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	0.00
HIPPOSIDERIDAE												
Aselliscus tricuspidatus	0.02	0.06	0.08	0.05	0.06	0.04	0.01	0.07	0.06	0.01	0.01	0.01
Hipposideros cervinus	0.02	0.03	0.04	0.05	0.06	0.08	0.01	0.02	0.02	0.02	0.02	0.06
Hipposideros diadema	0.02	0.00	0.00	0.00	0.00	0.04	0.04	0.00	0.00	0.00	0.00	0.06
H. wollastoni	0.04	0.10	0.12	0.14	0.12	0.08	0.02	0.08	0.07	0.07	0.03	0.03
H. sp. cf. *ater*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
RHINOLOPHIDAE												
Rhinolophus euryotis	0.02	0.10	0.12	0.18	0.18	0.04	0.00	0.08	0.07	0.12	0.07	0.01
Rhinolophus mcintyrei	0.05	0.06	0.12	0.09	0.00	0.00	0.07	0.06	0.10	0.05	0.00	0.00
R. megaphyllus	0.00	0.03	0.04	0.05	0.00	0.00	0.00	0.05	0.04	0.04	0.00	0.00
R. sp. cf. *robertsi*	0.05	0.06	0.04	0.09	0.00	0.04	0.08	0.06	0.01	0.05	0.00	0.01
MINIOPTERIDAE												
Miniopterus sp1 'large'	0.20	0.16	0.08	0.09	0.24	0.21	0.33	0.13	0.02	0.02	0.06	0.10
Miniopterus sp2 'med'	0.07	0.00	0.00	0.00	0.00	0.00	0.36	0.00	0.00	0.00	0.00	0.00
Miniopterus sp3 'small'	0.18	0.16	0.23	0.23	0.29	0.33	0.20	0.09	0.11	0.07	0.07	0.19
VESPERTILIONIDAE												
Murina sp. cf. *florium*	0.04	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00
Nyctophilus sp.	0.00	0.03	0.08	0.00	0.00	0.04	0.00	0.03	0.11	0.00	0.00	0.03
Philetor brachypterus	0.05	0.03	0.00	0.00	0.00	0.00	0.19	0.04	0.00	0.00	0.00	0.00
MOLOSSIDAE												
Chaerephon jobensis	0.00	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00
Otomops sp.	0.04	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00

Appendix 5.5. Summary of Relative Abundance and Indicator Species index for each species at each elevation (grey shading indicates the magnitude of the value, with zero as white and 1.0 as black).

	Relative Abundance				Indicator Index			
	1,000	**1,400**	**2,200**	**2,700**	**1,000**	**1,400**	**2,200**	**2,700**
EMBALLONURIDAE								
Emballonura dianae	0.04	0.04	0.00	0.00	0.17	0.06	0.00	0.00
Emballonura furax	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Emballonura raffrayana	0.04	0.06	0.00	0.00	0.15	0.11	0.00	0.00
Mosia nigrescens	0.14	0.02	0.00	0.00	0.84	0.01	0.00	0.00
Saccolaimus saccolaimus	0.01	0.00	0.00	0.00	0.09	0.00	0.00	0.00
HIPPOSIDERIDAE								
Aselliscus tricuspidatus	0.07	0.06	0.00	0.00	0.30	0.08	0.00	0.00
Hipposideros cervinus	0.06	0.06	0.00	0.00	0.22	0.09	0.00	0.00
Hipposideros diadema	0.01	0.02	0.00	0.00	0.05	0.04	0.00	0.00
Hipposideros wollastoni	0.13	0.12	0.00	0.00	0.52	0.17	0.00	0.00
Hipposideros sp. cf. *ater*	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
RHINOLOPHIDAE								
Rhinolophus euryotis	0.10	0.15	0.00	0.00	0.32	0.30	0.00	0.00
Rhinolophus mcintyrei	0.08	0.00	0.15	0.00	0.36	0.00	0.10	0.00
Rhinolophus megaphyllus	0.04	0.00	0.00	0.00	0.27	0.00	0.00	0.00
Rhinolophus sp. cf. *robertsi*	0.08	0.06	0.00	0.00	0.38	0.07	0.00	0.00
MINIOPTERIDAE								
Miniopterus sp. 1 'large'	0.04	0.12	0.48	0.27	0.04	0.10	0.42	0.08
Miniopterus sp. 2 'medium'	0.01	0.06	0.00	0.00	0.03	0.17	0.00	0.00
Miniopterus sp. 3 'small'	0.10	0.15	0.26	0.65	0.15	0.14	0.09	0.36
VESPERTILIONIDAE								
Murina sp. cf. *florium*	0.01	0.02	0.00	0.00	0.05	0.04	0.00	0.00
Nyctophilus sp.	0.00	0.00	0.07	0.08	0.00	0.00	0.08	0.05
Philetor brachypterus	0.03	0.02	0.04	0.00	0.10	0.02	0.02	0.00
MOLOSSIDAE								
Chaerephon jobensis	0.00	0.02	0.00	0.00	0.00	0.08	0.00	0.00
Otomops sp.	0.00	0.04	0.00	0.00	0.00	0.15	0.00	0.00

Appendix 5.6. Summary from a re-analysis of bat echolocation recordings from the PNG LNG Environmental Impact Statement bat study (Specialised Zoological 2017).

1. To allow better interpretation of potential patterns of change in bat community diversity over time during the long-term PMA3 Biodiversity Monitoring Program, it is desirable to have baseline data from the same localities before the construction of the pipeline and associated access road. Potentially useful information was considered to be present in the studies of Richards (2005, 2008), made as part of the preparation of the PNG LNG Environmental Impact Statement (EIS).

2. It was not possible to compare call types directly between the PMA3 and EIS studies (echolocation call examples were not illustrated extensively in the reports of Richards 2005, 2008), plus there was potential for species misidentification in the EIS studies given that very little information about the echolocation calls of Papua New Guinea (PNG) bats was available a decade earlier. Thus, a decision was made to re-analyse the original recordings made as part of the EIS.

3. Most of the recordings from the survey of Richards (2005) were available for re-analysis. These were made at Hides 3 and Benaria.

4. A significant proportion of the identifications were improved upon as part of the re-analysis, which was able to draw upon much more information on PNG bat echolocation calls that has become available since the 2005 study. There is a variety of issues that affected the identification of bat calls in the 2005 study.

5. There was a correspondence of a little less than 50% between the 2005 and 2015 studies at each of the two localities (Hides 3 of Richards (2005) compared with Biodiversity Assessment Area 1 in the PMA3 study (Armstrong 2017); Benaria of Richards (2005) compared with KP107 and Arakubi Quarry of Biodiversity Assessment Area 2 in the PMA3 study). Furthermore, the study of Richards (2005) encountered four species not recorded in the PMA3 study, for a variety of possible reasons that are due mainly to the greater diversity of habitats sampled in the 2005 study.

6. The 2005 baseline data cannot be used directly in PMA3 survey statistical analyses, but it is suitable for other types of analyses that allow comparisons of patterns at different elevations, and for generating expectations around the presence of species not yet detected on the 2015 PMA3 survey. In particular, this includes low frequency emitting species such as *Otomops* sp. and *Austronomus kuboriensis*. These species, plus others such *Emballonura raffrayana*, have the potential to be encountered at higher rates due to their habit of foraging in the open next to or above stands of vegetation, but the analysis process in PMA3 needs to be checked to ensure that it is able to efficiently recognise the two low frequency call types. [Note: this was done; the existing bioacoustics process was assessed as sufficient]