Results of the third PMA3 Biodiversity Monitoring Survey of the PNG LNG Upstream Project Area, 8 August–2 September 2019

Edited by Stephen Richards

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Cover image: A Small Dorcopsis (*Dorcopsulus vanheurni*) camera trapped at Arakubi

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Results of the third PMA3 Biodiversity Monitoring Survey of the PNG LNG Upstream Project Area, 8 August–2 September 2019

Edited by Stephen Richards

A Report to ExxonMobil PNG Limited from the 2019 PMA3 Biodiversity Monitoring Program

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Participants

Kyle Armstrong (Mammals/Frogs)
South Australian Museum; and
School of Biological Sciences,
The University of Adelaide,
South Australia; and
Specialised Zoological
Email: kyle.n.armstrong@gmail.com

George Dahl (Mammals/Frogs)
New Guinea Binatang Research Centre
P. O. Box 604, Madang
Papua New Guinea
Email: dahlgeorge46@gmail.com

Enock Kale (Mammals)
Ecomate Management
P. O. Box 7146, Boroko, NCD,
Papua New Guinea
Email: enockkale@gmail.com

Alfred Mani (Mammals/Camera Trapping)
New Guinea Binatang Research Centre
P. O. Box 604, Madang
Papua New Guinea
Current address:
Forestry Department, PNG University of Technology,
Lae, Papua New Guinea
Email: alfredmani0111@gmail.com

Elizah Nagombe (Frogs)
New Guinea Binatang Research Centre
P. O. Box 604, Madang
Papua New Guinea
Current address:
Wildlife Conservation Society,
Kavieng, New Ireland, Papua New Guinea
Email: elizah_nagombi@hotmail.com

Daniel Okena (Mammals)
New Guinea Binatang Research Centre
P. O. Box 604, Madang
Papua New Guinea
Current address:
Forestry Department, PNG University of Technology,
Lae, Papua New Guinea
Email: dokena25@gmail.com

Stephen Richards (Team leader/Frogs)
Research Associate, Department of Herpetology
South Australian Museum
North Terrace, Adelaide, SA 5000
Australia
Email: richards.steve0@gmail.com

Salape Tulai (Camera Trapping)
New Guinea Binatang Research Centre
P. O. Box 604, Madang
Papua New Guinea
Email: stulai.naturebarter@gmail.com

Iain Woxvold (Camera Trapping)
IWC environmental consultancy,
44 Aroona Rd, Goldie,
VIC 3435 Australia
Email: iainwoxvold@gmail.com

Samson Yama (Camera Trapping)
New Guinea Binatang Research Centre
P. O. Box 604, Madang
Papua New Guinea
Email: samsonnambadoa@gmail.com

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Part of the 2019 PMA3 team on Hides Ridge

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)
PNG	Papua New Guinea
Project	PNG LNG Project
RAI	Relative abundance index
ROW	The pipeline right-of-way
sp.	Abbrev. 'species' (singular)
spp.	Abbrev. 'species' (plural)

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 km^2.
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

Scars of the 2018 earthquake visible from Hides Ridge in 2019

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 phase of the PMA3 biodiversity survey program was conducted during June–July 2015, and the second phase during May 2017. Results of these surveys were presented to EMPNG and subsequently published in two public documents (Richards 2017, 2019). Those reports 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 third phase of PMA3 biodiversity monitoring conducted during August 2019 and compares them with data on species diversity and trends obtained in 2015 and 2017 to identify and interpret any trends in species presence, abundance and diversity in the vicinity of Project infrastructure.

Survey dates

8th August to 2nd September 2019 (Camera traps deployed 10th August to 2nd December 2019).

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.

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. A comprehensive description of the local environments in BAA 1 and BAA 2, including forest structure, classification, and illustrations of forest types, is presented in Richards (2017).

The locations of both BAAs are shown in Figure 1.

BAA 1: 08–20 August 2019.

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: 21 August–02 September 2019.

BAA 2 is located on the Agogo Range near Moro in Southern Highlands Province. Two survey transects were established at elevations of 950–1,080 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).

Survey approach

Surveys for 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 those associated with 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.

Survey modifications for 2019 PMA3 monitoring program

Several modifications were made to the PMA3 survey program in response to results of the 2015 and 2017 surveys:

1. Given the extremely low numbers of butterflies encountered during the 2017 PMA3 monitoring survey, this component of the PMA3 monitoring program was discontinued in 2019.

2. Logistical constraints delayed the 2019 survey until August–September (*vs* May–June for the 2015 & 2017 surveys), introducing the potential influence of seasonality on survey results.

3. A major earthquake in March 2018 caused extensive damage in the Upstream Project Area. During the earthquake tree falls intersected with Transects H4 (Hides Ridge) and M2 (KP107), opening the canopy and disturbing sub-canopy vegetation. The extent of disturbance at H4 is illustrated in Figure 8. Where relevant, the potential impacts of this event on the 2019 PMA3 survey results are discussed.

4. With camera trapping in 2015 restricted to a pilot study, the 2019 data provide the first opportunity to monitor inter-year changes in population estimates. New statistical procedures were introduced to meet this objective.

5. Under the camera trapping program, data collected on nine new environmental covariates have improved statistical model performance and our ability to make reliable inferences about behavioural responses to Project infrastructure.

Major results

A summary of the major results is presented below.

Taxon accounts

Frogs

A total of 37 species of frogs was documented 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 and/or 2017 were not encountered during 2019 but one additional species that was not detected on transects during 2015 or 2017 was found on transects during 2019, and new genetic and acoustic data resolved two outstanding taxonomic issues resulting in the recognition of additional *Oreophryne* species that were present but not recognised during 2015 and 2017.

Four additional undescribed species that were documented during 2015 and 2017 have now been formally described in the scientific literature.

Supporting the results from 2015 and 2017, species diversity was significantly lower at higher elevations in 2019, and both diversity and composition differed between the two BAAs, with ten frog species found in BAA 1, and 27 species in BAA 2. Genetic data suggest that *Oreophryne notata*, the only species previously considered to be shared between transects in BAA 1 and BAA 2 represents two genetically and acoustically distinct taxa – therefore there are currently no frog species known to be shared between transects in BAA 1 and BAA 2.

Analyses of data from both the VAES and the Acoustic Recorders found no consistent evidence for shifts in species diversity or composition with increasing distance from infrastructure clearings across the three survey years. Thus, 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 2019 from a total of 5,692 independent photographic events. Six species are newly reported from the BAAs, and one species represents a new record for the Kikori Basin – Shaw Mayer's Shrew Mouse (*Pseudohydromys ellermani*). Pooling data from all sampling years, more than 94 vertebrate species have now been documented by camera trap within the BAAs, including 59 bird species, 34 mammal taxa and one reptile.

Biennial data are provided for a suite of priority monitoring targets, including seven IUCN listed mammal species – Eastern Long-beaked Echidna (*Zaglossus bartoni*), Woolley's Three-striped Dasyure (*Myoictis leucura*), New Guinea Quoll (*Dasyurus albopunctatus*), Small Dorcopsis (*Dorcopsulus vanheurni*), Pademelon (*Thylogale* sp.), Ifola (*Dendrolagus notatus*) and Goodfellow's Tree Kangaroo (*D. goodfellowi*). The Near Threatened Small Dorcopsis was the most frequently camera trapped of all species with 1,200 photographic events recorded across all sites in 2019.

Compared to 2017 figures, significant declines in statistically modelled population estimates (occupancy or activity rates) were observed for five bird species at individual sites or BAAs. In addition, naïve occupancy rates (the proportion of cameras on which a species is detected) fell sharply for three IUCN listed mammals – the Eastern Long-beaked Echidna and Pademelon at Arakubi, and Woolley's Three-striped Dasyure at KP107. An increase in population estimate was recorded for two IUCN listed mammals at KP107 – the Small Dorcopsis and Ifola. The number of days in which humans and/or dogs were detected increased markedly from 2017 to 2019 at BAA 2 sites, but was similar in both years at BAA 1 sites. It is too early to draw conclusions as to the ongoing status of local populations; continued sampling, standardised for seasonal effects, is required to make reliable inferences about population trends.

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 11 species at one or more sites. Edge avoidance patterns were demonstrated by eight species and were strongest at the BAA 2 sites – for Raffray's Bandicoot (*Peroryctes raffrayana*) and Small Dorcopsis at KP107, and for Collared Brushturkey (*Talegalla jobiensis*) and Pheasant Pigeon (*Otidiphaps nobilis*) at Arakubi and KP107.

Six species displayed reverse-pattern edge effects, with higher rates of activity nearer to the forest edge. Reverse edge effects were the most common trend at BAA 1 and were the only patterns observed at the Hides High site. Reverse-pattern edge effects are counter-intuitive for interior forest species, and causal factors are likely to be environmental rather than anthropogenic.

Non-volant (non-flying) mammals

The total number of captures of small rodents on the 2019 survey (134 individuals) was equivalent to that from 2015 (133 individuals), and over twice that from 2017 (53 individuals). Statistical tests indicated that Species Richness and abundance was not significantly different amongst the categories defining distance from the ROW, elevation and survey year.

The overall patterns in the number of captures are driven by three relatively common species: *Rattus* sp. cf. *niobe* B, *Rattus* sp. cf. *niobe* D, and *Paramelomys* sp. cf. *rubex* A, which together made up 79.3% of captures in 2019.

Two rodent species were detected for the first time on the 2019 survey (*Lorentzimys nouhuysi* and *Pogonomys macrourus*), both of which are scansorial species that are expected to encounter box traps placed on the ground at a much lower rate than ground-dwelling and semi-fossorial rodent species. Their capture does indicate that the inventory of Muridae for the study area is still incomplete. To date, 16 species have been recorded by box trapping on survey transects, and an additional 12 species are also known from the area based on observations of camera trapping, roadkills, remains in owl pellets, and previous baseline environmental impact assessment studies conducted for the project.

Overall, the small rodent survey component has documented a lack of a significant change in Species Richness, abundance and species composition at increasing distances from the ROW, in either BAA, indicating that there has been no detectable impact of edge effects from the ROW on these taxa. The variation in captures over survey years is more likely the result of the slightly different timing in surveys rather than changes in forest habitat quality.

The populations of native rodents sampled have so far shown good resilience to the removal of adjacent forest for the pipeline and access road, using forest habitat right to the edge. However, the forest edge is still relatively intact, and we may yet see changes that reflect a change in habitat structure and the increased presence of invasive rodents.

Genetics-based identification has been the foundation of reliable comparisons between sites, survey years and investigators in this study, and the remarkable results (that have included the discovery of at least two new species not seen elsewhere) are indicative of an under-estimated level of rodent diversity across New Guinea.

Bats

A total of 20 bat species was detected in the ultrasonic acoustic recordings, equivalent to previous surveys (2015: 21 spp.; 2017: 20 spp.). No trapping was conducted in 2019. Based on both captures and acoustic recordings from the 2015 and 2017 surveys, and on acoustic recordings from the 2019 surveys, a total of 27 described bat species has now been documented in the PMA3 study area.

In addition, recent genetic studies have given strong support to the species-level distinctness of two bats captured in 2017 at 2,700 m asl on Hides Ridge. They are high elevation taxa that are closely related to the Fly River Woolly Bat *Kerivoula muscina* and the Small-toothed Long-eared Bat *Nyctophilus microdon*.

No bat species of conservation significance (classified in a threatened category or as Data Deficient by the IUCN) have been detected on any of the PMA3 surveys conducted to date.

The number of bat species present was significantly greater in BAA 2 than in BAA 1. Over three surveys, a total of 22 species has been detected in BAA 2, compared with eight species in BAA 1. The greater diversity in BAA 2 was due mainly to the presence at lower elevations of numerous species of small Emballonuridae that forage in the forest Edge flight space, and species of Hipposideridae and Rhinolophidae that forage in the Clutter flight space in the forest interior. Six of the eight bat species detected in the high elevation forests in BAA 1 were shared with BAA 2; the other two species appear to be high elevation specialists (*Austronomus kuboriensis, Nyctophilus microdon*).

No gradual change was detected in the bat community with increasing distance from the forest edge during any of the three surveys. However, there was a significantly higher number of species at the forest edge (0–20 m) than on the remainder of the transect (20–220 m). This was driven by a greater proportion of species that forage in the forest Edge flight space (transect distance of 0 m), and higher proportions of species that forage in the Clutter flight space within the forest (20–220 m), particularly in BAA 2. This pattern is more suggestive of a response to the creation of open habitat, rather than a consequence of an edge effect and diminishing forest habitat quality adjacent to the Project linear infrastructure.

The bat communities within each of the BAAs have not changed during the monitoring period. No spatial or temporal shifts in bat diversity or composition have been detected in either BAA since 2015. The combined results from the 2015, 2017 and 2019 surveys suggest that the forest adjacent to the ROW has so far retained its value for a diverse community of bats.

Table 1. Number of species documented during the 2019 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.

	Frogs	Camera traps (birds and mammals)	Non-volant Mammals	Bats	TOTALS
Total Species	37	80+	11	20	**148**
Undescribed Species	15	1	7	0	**23**
IUCN Species	0	7	0	0	**7**

Threats

Two potential 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. These and other potential threats are summarised below.

Edge effects

The frog, rodent and bat studies found no consistent evidence for deleterious impacts of edge effects. However, the camera trap study revealed patterns of edge avoidance in eight species. Evidence for edge avoidance was strongest at the BAA 2 sites, particularly for Raffray's Bandicoot (*Peroryctes raffrayana*) and Small Dorcopsis at KP107, and for Collared

Brushturkey (*Talegalla jobiensis*) and Pheasant Pigeon (*Otidiphaps nobilis*) at Arakubi and KP107. These species may avoid near-edge environments at these sites due to the presence of degraded forest near infrastructure (particularly at Arakubi) and/or an aversion to frequent human activity along roads and the pipeline ROW. By contrast, camera trapping has revealed no compelling evidence that any terrestrial mammal or bird species avoid forest edge at BAA 1.

Hunting, gardening, resource harvesting, 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 almost certainly led to an increase in both direct hunting pressure by local people and predation by dogs. Camera trapping recorded the highest number of forest incursions by humans and/or dogs at Arakubi in 2019. This represents an eightfold increase in activity at Arakubi since 2017, and corresponds with a sharp decline in records at that site for two IUCN Vulnerable species – the Long-beaked Echidna and Pademelon – both of which are susceptible to hunting. A link cannot be proved, but further sampling is warranted to understand the local status of these high value species.

Although the number of incursions recorded at BAA 1 was similar in both years, the observation of hunting parties and timber harvesting during PMA3 surveys, together with indirect evidence obtained through informal conversations with Project personnel and local residents, suggest that Project operations may have resulted in an increase in resource harvesting along Hides Ridge compared with pre-construction rates.

Dieback

Observations during the three survey monitoring years have revealed that, in some areas of BAA 1, canopy trees along the edge of linear clearings are becoming increasingly stressed and, in many cases, dying. This is particularly evident for *Nothofagus* trees along the eastern (lower) half of Hides Ridge.

Removal of trees along linear infrastructure

In contrast to the 2017 survey, removal of trees from on or immediately adjacent to transects was not observed during the 2019 survey. However, the establishment and expansion of gardens in both BAAs, involving the removal of numerous trees adjacent to Project linear infrastructure, had increased substantially since 2017 and is likely to be impacting biodiversity in various ways.

Exotic rodents

The only invasive *Rattus* species encountered in 2019 was *R. exulans*. Four individuals of this species were trapped on transects in BAA 2 and, like previous captures of this species during the 2015 survey, all were from trap locations close to the forest boundary or disturbed sections of the transect (as in the first c. 150 m of M4 at Arakubi Quarry). *No Rattus rattus* were captured during the 2019 survey.

Major conclusions

1. Results of the 2019 PMA3 survey indicate that both BAAs retain high biodiversity values for all surveyed taxa, with both areas continuing to support rare, conservation listed, restricted range and hunting-sensitive species.

2. However, improved accessibility along the ROW and Project roads is likely to have facilitated hunting by local people and predation by dogs; camera traps detected an eightfold increase in incursions by humans and/or dogs at Arakubi, corresponding with a sharp decline in records at that site for two IUCN Vulnerable species that are susceptible to hunting – the Long-beaked Echidna and Pademelon. Although this pattern was not detected on Hides Ridge, our field observations suggest that hunting activity and the harvesting of other resources has increased there since 2017.

3. There have been no consistent temporal shifts in frog, rodent or bat 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. Bat diversity was significantly greater in open areas at the forest edge compared to the forest interior, which reflects an influx of species that forage in edge and open flight spaces, particularly in BAA 2, since the creation of the linear infrastructure. These species, mostly small Emballonuridae, have benefitted from creation of additional forest-edge habitats.

5. Overall, increases in hunting pressure and feral dog predation and the potential spread of exotic rodent species, both almost certainly associated with installation of the pipeline ROW and associated roads, remain the two major factors most likely to threaten biodiversity values in the BAAs.

General recommendations

1. **Survey dates**
   We recommend that future PMA3 surveys be undertaken biennially during May – June to remove seasonality as a variable that may influence survey results.

2. **Continue both VAES and Acoustic Recorder sampling for frogs**
   Following the 2017 PMA3 survey, Richards et al. (2019) recommended that the use of VAES be reassessed after the 2019 survey due to the logistical difficulties associated with conducting field work at night. However, VAES surveys continue to generate valuable genetic and acoustic data that are not collected by Acoustic Recorders alone, and have proven vital for elucidating species boundaries in order to permit accurate species identifications and better assess diversity and community structure. We therefore recommend that the VAES component of the PMA3 frog monitoring program be continued while logistical constraints permit.

3. **Continued use of improved genetic assessment methods**
   Genetics-based identification has continued to provide a foundation for reliable comparisons between sites, survey years and investigators for multiple taxa during the PMA3 surveys by providing a robust method for species identifications in groups that contain morphologically cryptic fauna. The genomics-based technique should be continued. For frogs, additions to the comparative framework will continue to help resolve the identity and taxonomic classification of several undescribed species. For small rodents, morphologically diagnostic characters for most species in the study area are inadequate for consistently accurate identifications whereas the genetic markers provide unambiguous identifications. For bats, it will help to identify future captures of several taxa that are difficult to identify because of unresolved taxonomic issues or a lack of useful diagnostic morphological features.

4. **Assessment of pest invasive rats in human habitation surrounding Project infrastructure.**
   We recommend that consideration be given to a rapid assessment of the presence of *Rattus rattus* and *R. exulans* in inhabited areas around the HGCP to provide context on how common these species are, and how significant a source they might be for invasions along the access road and pipeline on Hides Ridge.

5. **Modification of camera trapping design.**
   We recommend that the camera trapping program continue in 2021 and in subsequent survey years. As far as practical, the biennial schedule should be maintained as fewer data points will extend the time required to make reasonable inferences about population trends. Each monitoring survey should take place at the same

time of year to control for seasonal effects; we recommend reverting to the 2017 timing to test for reversal in the potentially seasonal changes observed for some species

The current camera trap sampling design – based on the clustering of 20 cameras within sites of c. 70–180 ha – is suitable for modelling edge effects but limits our ability to monitor wildlife population trends because: (1) it is not possible to draw conclusions as to the status of populations beyond the site scale, and; (2) the close spacing of many cameras constrains our ability to use the preferred occupancy modelling approach. Future datasets are likely to yield diminishing returns in terms of revealing novel edge response patterns, particularly on Hides Ridge (BAA 1). We therefore recommend that the sampling design be expanded (using the same number of cameras) within BAAs beyond the site scale, as far as practical, to broaden sampling of important local populations and to improve the scope for occupancy modelling.

6. **Collection of data on hunting and harvesting activities.**
   We recommend that ExxonMobil PNG, in consultation with independent experts, develop a structured survey to gather information from local people living in or accessing the area regarding their hunting activities and harvesting of other resources at BAA 1. Survey interviewees should be allowed to remain anonymous in order to maximise the potential for free flow of information. The survey should be completed at least twice in the first 12 months to capture any seasonal differences, and annually thereafter for three years to establish trends, prior to a review.

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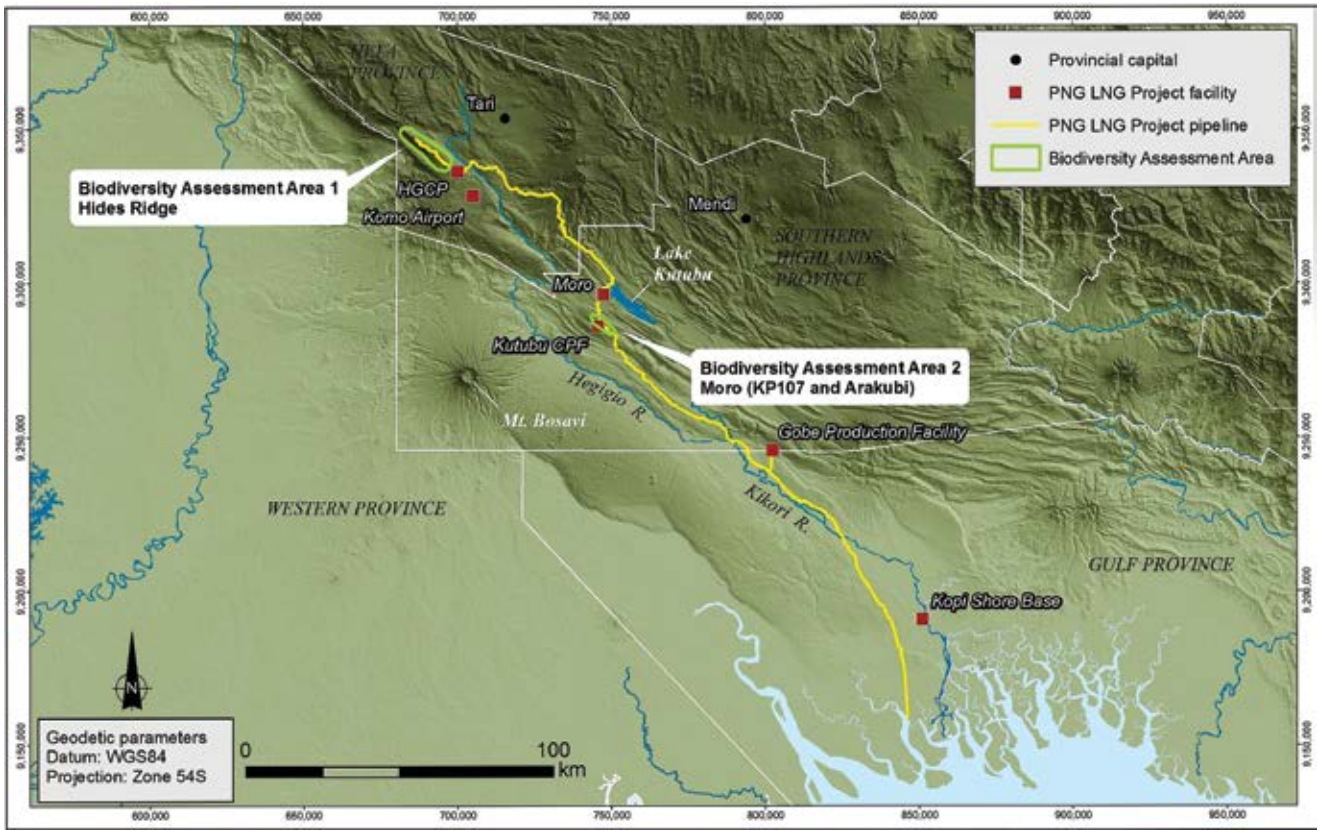

Figure 1. Regional map showing location of the two BAAs surveyed during the PMA3 surveys.

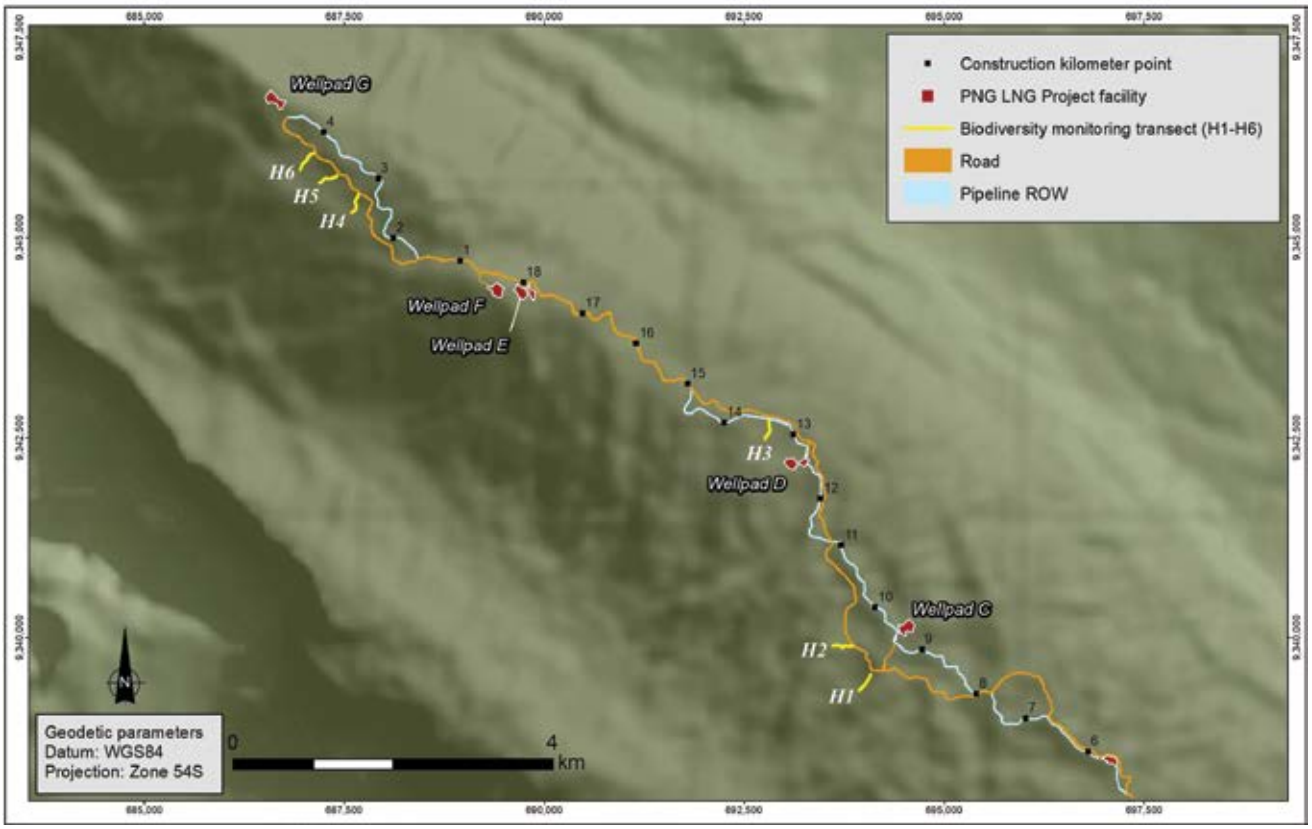

Figure 2. Map showing loctaions of the six major transcets in BAA1.

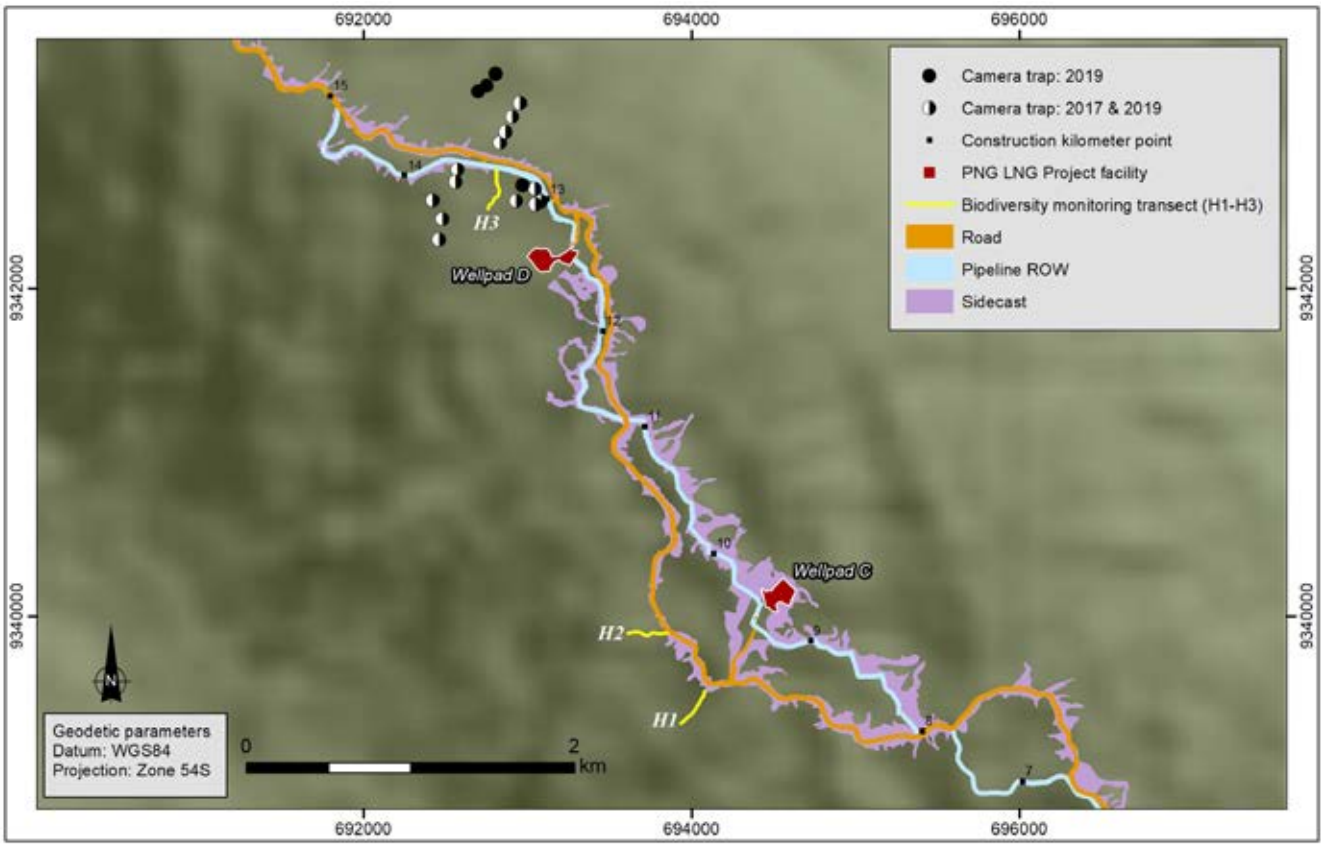

Figure 3. Map of lower elevations in BAA1 showing details of Transects 1–3, and camera trap arrays.

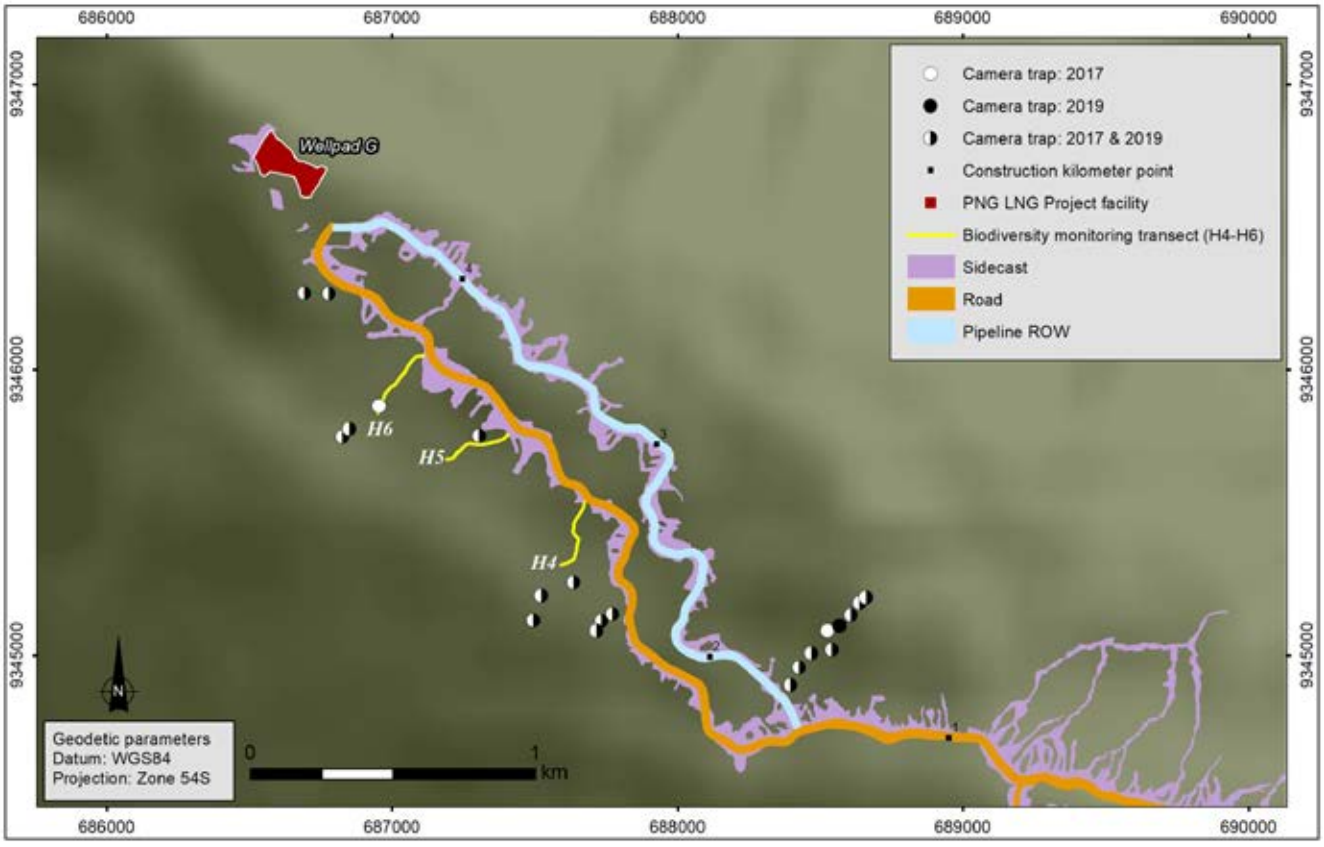

Figure 4. Map of upper elevations in BAA1 showing details of Transects 4–6 and camera trap arrays.

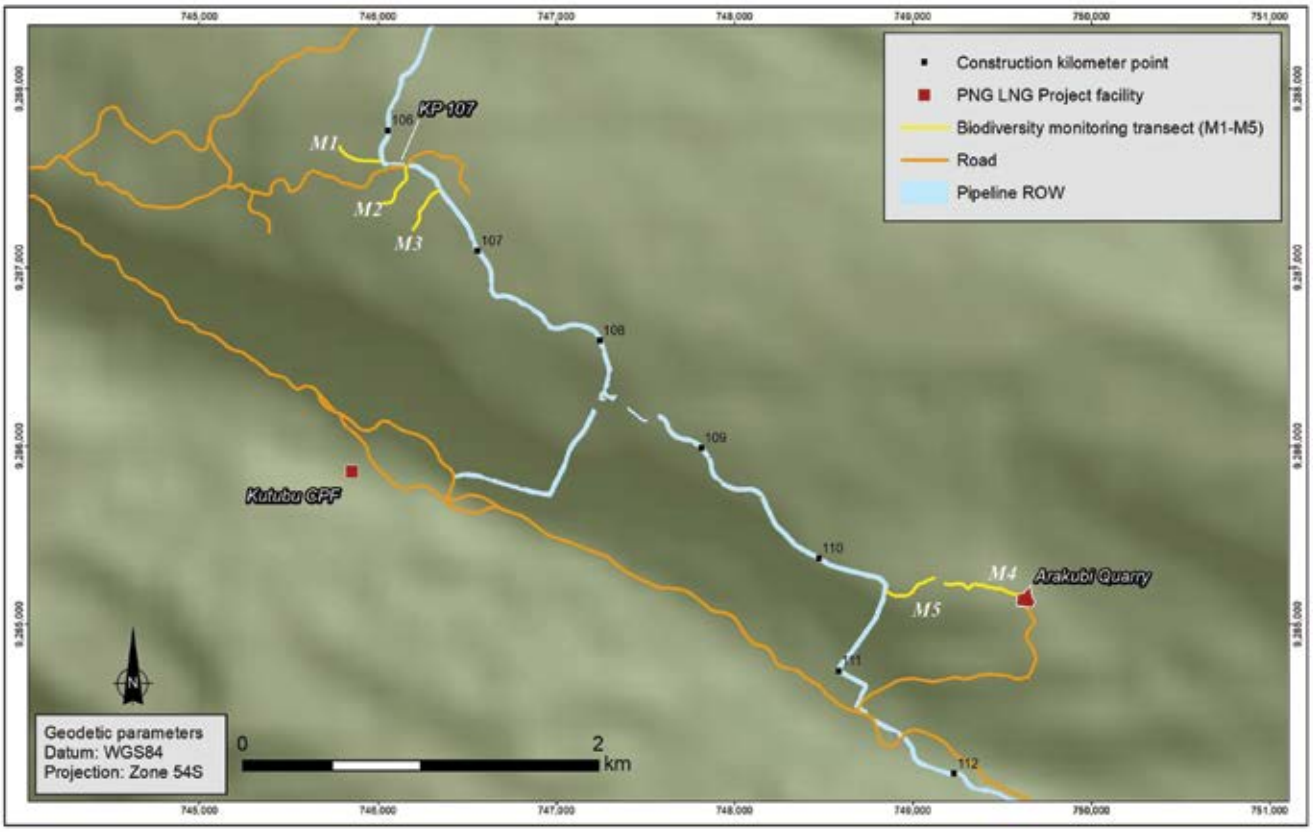

Figure 5. Map showing locations of the five major transects in BAA2.

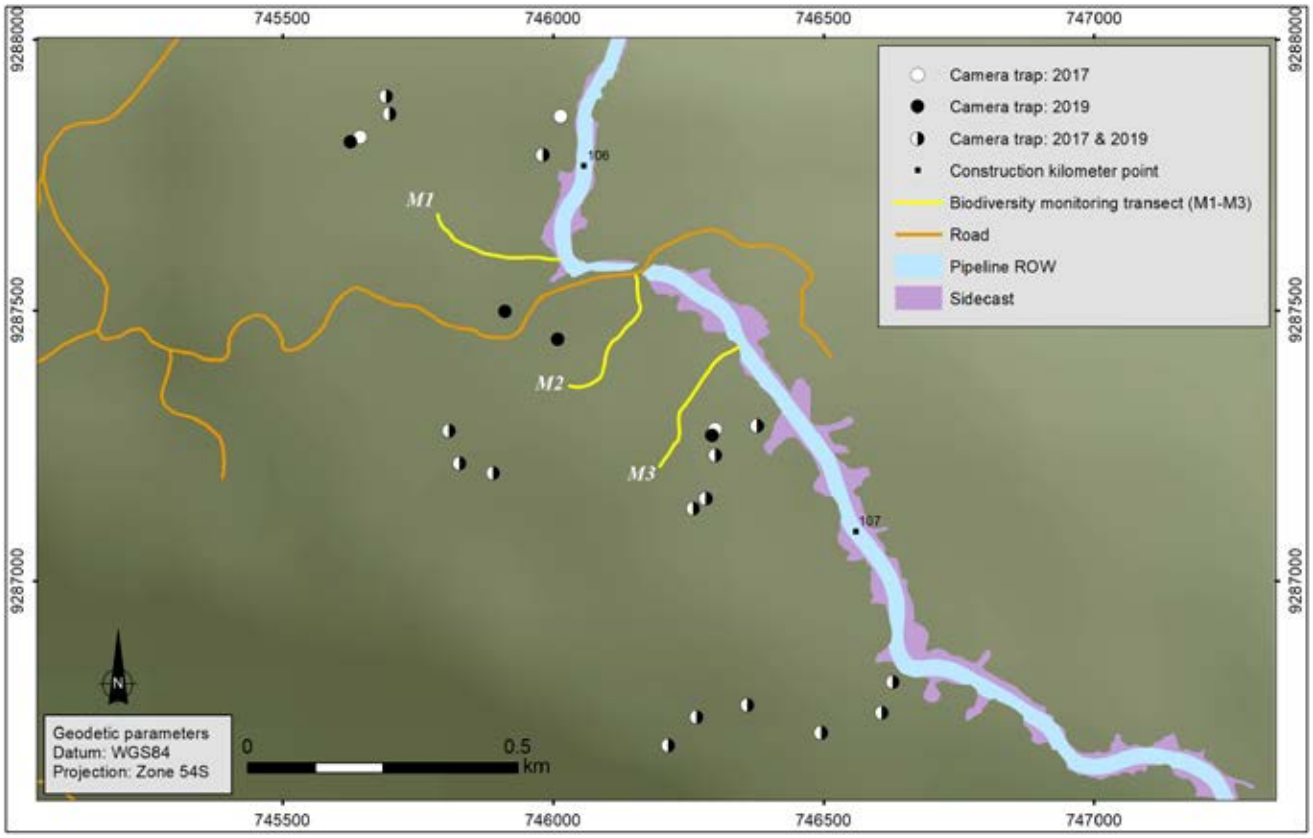

Figure 6. Map showing locations of the three major transects and camera trap arrays at KP107 in BAA2.

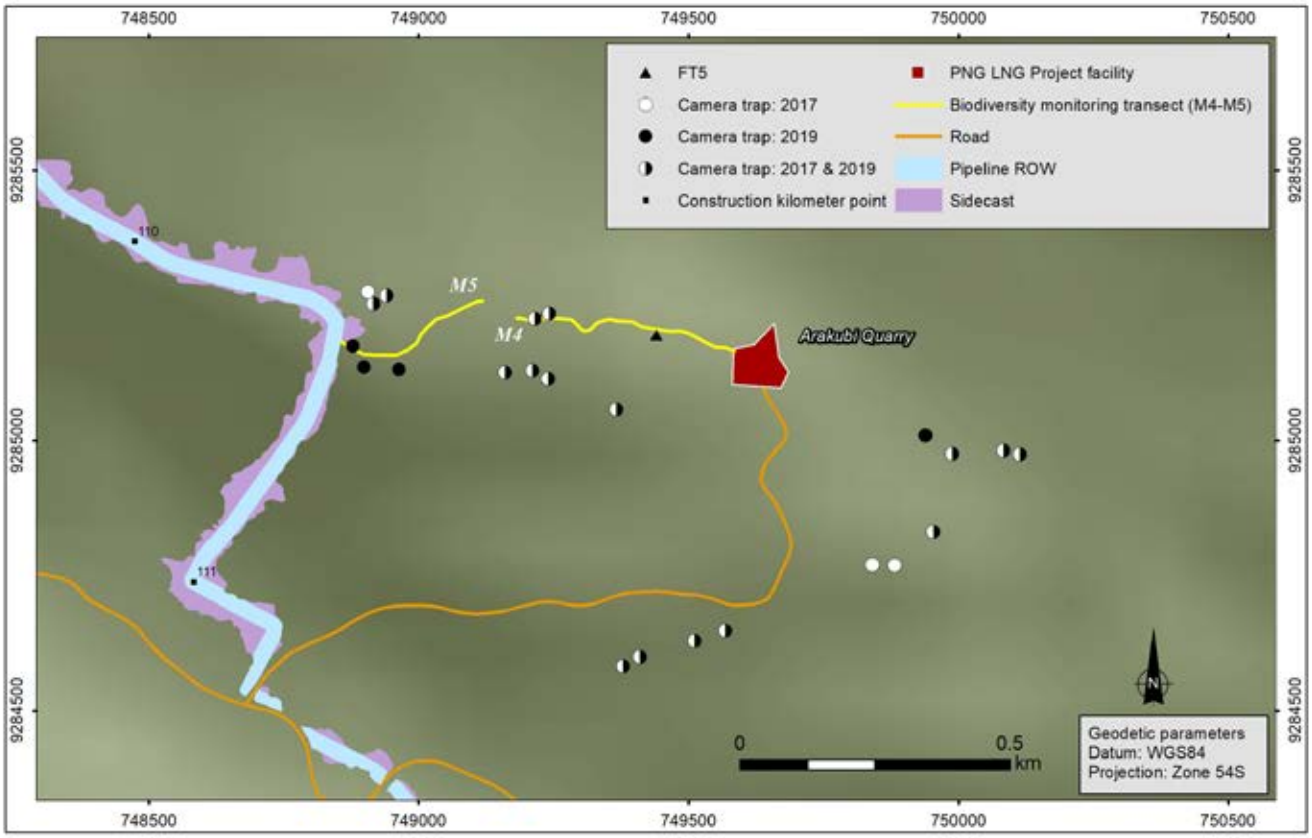

Figure 7. Map showing locations of the two major transects and camera trap arrays at Arakubi Quarry in BAA2.

Figure 8. Treefall caused by the 2018 earthquake at Transect H4 on Hides Ridge in BAA 1.

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
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 – Frogs

Stephen J. Richards, Kyle N. Armstrong, Elizah Nagombi and George Dahl

A probable undescribed treefrog, *Litoria* sp. cf. *becki*, encountered on Hides Ridge during the 2019 PMA3 survey

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). Established in 2015, the biennial monitoring program uses 1) Visual and Audio Encounter Surveys (VAES) and 2) automated sound recording of frog calls (Acoustic Recorders) along permanent transects established adjacent to linear infrastructure. This report presents the results of the 2019 monitoring survey and compares them with the 2015 and 2017 results to assess whether Project infrastructure is having an impact on frog populations in either BAA.

Major results

A total of 37 frog species was documented in both BAAs in 2019. Three species that were detected in 2015 and/or 2017 were not encountered in 2019, but one additional species that was not detected during 2015 or 2017 was found on transects during 2019. New genetic and acoustic data resolved two outstanding identification issues resulting in the recognition of three additional *Oreophryne* species that were present but not recognised during previous sampling years.

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 across the three survey years.

Of 108 species by transect detection events recorded in 2019, 65 (60%) were detected by both survey methods, 29 (27%) were detected only by Acoustic Recorders and 14 (13%) were detected only by VAES. Overall, 27 of the 37 recorded species (73%) were detected at least once by both survey methods with just four species (11%) detected only by VAES and six species (16%) detected only on automated sound recordings.

As for 2015 and 2017, in 2019 species diversity was significantly lower at higher elevations, and both diversity and composition differed between the two BAAs, with ten frog species found in BAA 1, and 27 species in BAA 2. Genetic and acoustic data suggest that *Oreophryne notata*, the only species previously considered to be shared between transects in BAA 1 and BAA 2, represents two genetically and acoustically distinct taxa – therefore there are currently no frog species known to be shared between transects in BAA 1 and BAA 2.

During 2019 the DNA identification framework developed for the PMA3 program proved to be a powerful tool for providing consistent identifications across surveys and matching genetic types with call types, specimens and names. It resulted in greatly enhanced interpretation of total species diversity in BAA 2, particularly in the frog genus *Oreophryne* which currently contains several acoustically similar but genetically distinct species.

Conclusions and recommendations

Results of the 2019 PMA3 survey indicate that there have been no detectable temporal shifts in frog 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. The biodiversity values of frogs in these areas remain intact.

Richards et al. (2019) recommended that the ongoing value of the VAES method should be reassessed after the 2019 survey due to the logistical difficulties associated with doing night work. However, the results of the 2019 survey demonstrated that VAES surveys are the best method for detecting two poorly-known, undescribed species that are currently known only from the Upstream Project Area. Furthermore, VAES surveys generated valuable genetic and

acoustic data that helped to resolve two difficult identification issues, permitting a more reliable assessment of species diversity and community structure, particularly in BAA 2.

We therefore recommend that the use of surveys on VAES transects as well as Acoustic Recorders be continued in 2021 because they facilitate collection of data to improve species identification capacity and enhance the accuracy of call-based monitoring.

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. Accordingly, the PMA3 frog monitoring program was designed predominantly 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), and results of the 2017 survey are presented in Richards et al. (2019). Here we present the results of the third frog monitoring survey, conducted during August 2019.

Methods

Frog surveys in 2019 were conducted along the same permanent transects that were established during 2015: on Hides Ridge (BAA 1) between 09 and 20 August, and on the Agogo Range in the Moro area (BAA 2) between 21 and 31 August (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 (hereafter 'Hides Low').
    - Transects H4–6: between Wellpad E and Wellpad G, at 2,660–2,780 m asl (hereafter 'Hides High').
- Moro area (BAA 2):
    - Transects M1–3: on the Agogo Range in the vicinity of KP107, at 1,340–1,410 m asl (hereafter 'KP107').
    - Transects M4 and M5 (audio recorders)/M4 and FT5 (VAES): west of Arakubi Quarry and east of the pipeline ROW, at 1,000–1,070 m asl (hereafter 'Arakubi').

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) so only a brief summary of each is provided below. The first 30 m of Transect H4 was shifted by approximately 5 m to avoid debris from a major treefall (Figure 8 in Report Summary), but this is unlikely to have affected survey results at this site.

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 approximately 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, the VAES transect starts at a transition point (see Figure 7 in Report Summary), from regrowth forest (previously cleared for the quarry) to original forest. This transition point was less obviously sharp in 2019 than it was in 2015.

Coordinates for the beginning and end of each VAES transect are presented in Appendix 1.1. 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. Two transects were surveyed each night, the first survey beginning between approximately 19:30–21:00, and the second survey 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, noted as seen and/or heard, and its location on the transect (which 20 m segment, i.e. distance from the forest edge) was recorded. 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. The VAES transects generally overlap with two of the three Acoustic Recorders positioned on each transect (those at 5 m and 70 m from the forest edge; see below). This is not the case for Transect H6 in BAA 1 and Transect M5 in BAA 2 for which VAES data were not obtained in any sampling year.

Audio monitoring with acoustic recorders

In each sampling year, automated unattended 'Acoustic Recorders' collected high quality sound data on calling frogs using a standardised recording effort at permanently marked positions on each transect. Wildlife Acoustics Song Meter SM3 recorders were used in all sampling years. In 2019 we placed a Frontier Labs Bioacoustic Audio Recorder (BAR) adjacent to each SM3 recorder as part of a phased replacement of SM3s with the smaller and lighter BAR recording units. All other protocols remained unchanged.

Acoustic Recorders were placed at three recording positions at increasing distances from the forest edge (5 m, 70 m and 170 m) on transects H1–6 in BAA 1 and transects M1–4 and FT5 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 or pipeline ROW. Units recorded continuously in WAV format at a sampling rate of 48 kHz for two consecutive nights at each recording position 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.

A summary of the design is presented in Table 1.1 and coordinates for each recording position are presented in Appendix 1.2.

Table 1.1. Summary of the experimental design and frog acoustic recording site placements.

BAA	Site	Transect	Distance from forest edge			Total
			5 m	70 m	170 m	nights
BAA 1	Hides High	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	
	Hides Low	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	KP 107	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	
	Arakubi Quarry	M4—1,030 m (995–1,041 m)	2	2	2	
		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 remains the only known locality for *Litoria vivissimia*, a spike-nosed treefrog discovered during the EIS surveys. We conducted one VAES night survey for 30 minutes around the edge of the pond on 12 August 2019 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 BAR Acoustic Recorder was also deployed at the pond for two consecutive nights, 17 and 18 August 2019, with the microphone angled across the centre of the pond. The resulting data were screened 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. up to a maximum of 100 m 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. Frog presence in 2019 was scored using the modified method developed in 2017, as follows: for each 24-hour recording period at each recording position we 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). 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. We also randomly selected five equivalent sound blocks from SM3 and BAR recorders to assess any differences in species detection between the units. None was detected so analyses were conducted primarily on sound

files from BAR recorders. Exceptions included five recording positions in BAA 1 where a BAR recording was not obtained; data from the paired SM3 recorder were analysed at these sites so there were no data gaps in subsequent analyses, and the issue with the recorder has been resolved.

Indicator Species

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, we calculated Dufrêne and Legendre's (1997) Indicator Species index, a metric that is sensitive to the association of individual species with particular locations and environmental conditions. Low index scores are associated with species found in many habitat types, and higher scores result for species associated with a narrow range of sites or conditions.

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 (1) 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 (2) because we wished to explore further the relative contributions of the two datasets to assess whether it might 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 Linear Mixed Effects 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 of 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 and 2017 surveys.

DNA barcoding

Not all frog species in the PMA3 study areas have taxonomically stable names, and a significant proportion of taxa encountered in the 2015 and 2017 studies were undescribed at that time. The use of genetic markers in the PMA3 frog study has proven to be a powerful tool for confirming species identities, providing greater clarity on species boundaries in closely related taxa by assessing phylogenetic relationships, and providing a genetics-based voucher for call types. To provide a robust genetic basis for consistent identifications of frogs in future, particularly of individuals that cannot be identified by their calls (e.g. females, froglets), we developed a 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. 2012; 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

Technology Pty Ltd, Canberra). Individuals and loci that had insufficient coverage were removed, and a Neighbour-Joining distance phylogram 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.

Results and Discussion

A species list showing the frog species recorded on each transect within the two BAAs in 2019 is presented in Table 1.2, which also illustrates the detection method (VAES survey and Audio Recorder) for each species on each transect. A summary of species detections at increasing distances from the disturbance edge are also presented for VAES transects in Appendix 1.3 and for Acoustic Recorders in Appendix 1.4.

Table 1.2 Summary of species encountered on each transect in both BAAs, indicating the detection method for each encounter (V = VAES; A = Acoustic Recorder).

Species	BAA 2					BAA 1					
	Arakubi		KP107			Hides Low			Hides High		
	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5	H6
PELODRYADIDAE											
Litoria iris						A					
Litoria sp. 1 'yellow legs'	V	AV	A	V							
Litoria sp. cf. *becki*									V	V	
LIMNODYNASTIDAE											
Lechriodus aganoposis						A					
MICROHYLIDAE											
Asterophrys slateri	AV	AV									
Austrochaperina fulva	A	AV									
Austrochaperina laurae			AV	AV	AV						
Callulops omnistriatus	AV	A	A	AV	A						
Callulops wilhelmanus									AV	AV	A
Choerophryne alainduboisi	AV	AV	AV	AV	AV						
Choerophryne brevicrus						A	A	AV	AV	AV	A
Choerophryne burtoni			AV	V	V						
Choerophryne crucifer		A									
Choerophryne multisyllaba			AV	AV	V						
Choerophryne murrita			AV	A							
Choerophryne sp. 1 'arboreal'						AV	AV	AV			
Choerophryne sp. 2 'tiny'						A	AV	AV			
Cophixalus cateae			A	V	A						
Cophixalus wempi		V	AV	AV	AV						
Cophixalus sp. 1 'musical call'			A	AV	A						
Cophixalus sp. 2 'tiny A'			V	V	V						
Cophixalus sp. 3 'tiny B'			A	A	A						
Cophixalus sp. 5 'loud grunter'						AV	AV	AV			
Copiula bisyllaba	A	A									

Species	BAA 2					BAA 1					
	Arakubi		KP107			Hides Low			Hides High		
	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5	H6
Hylophorbus richardsi						A		A			
Hylophorbus sp. 1 'slow call'											
Hylophorbus sp. 2 'fast call'	AV	AV	AV	A	A						
Liophryne schlaginhaufeni		AV									
Oreophryne anamiatoi											
Oreophryne flavomaculata	AV	AV	AV	AV	AV						
Oreophryne nicolasi		AV									
Oreophryne notata						AV	AV	AV	AV	AV	A
Oreophryne sp. cf. *notata*	AV	AV	AV	AV	AV						
Oreophryne oviprotector	AV	AV									
Oreophryne pseudunicolor	AV	AV	AV	A							
Oreophryne sp. 2 'ratchet call'			AV	AV	AV						
Sphenophryne cornuta	AV	AV									
Xenorhina sp. 1 'slow call'	V										
Xenorhina sp. 2 'fast call'											
Gen. nov. sp. nov.		V									
Species Richness Acoustic	11	15	16	13	11	8	5	6	3	3	3
Species Richness VAES	11	14	12	13	9	3	4	5	4	4	—
Total Species Richness	13	17	17	17	14	8	5	6	4	4	3

Overview of the frog fauna

A total of 37 species of frogs was documented on the permanent transects in 2019, including ten species in BAA 1 and 27 species in BAA 2 (Table 1.2). This is the same number of species that was encountered during 2015 but slightly higher than the total encountered during 2017 (34 species). Three species that were encountered during at least one of the previous surveys were not encountered during 2019, but one species in BAA 1 was encountered on transects for the first time, and one species in BAA 2 was recognised as a distinct taxon for the first time in 2019 (see '*Significant species and taxonomic uncertainties*' below). Examples of species encountered in 2019 are illustrated in Figures 1.7–1.18.

Thirty-three of the 37 species (89%) 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 slightly lower than the percentage in 2015 (92%) and 2017 (97%) because all of the non-microhylid species recorded during 2015 and 2017 (when several non-microhylids were not detected; Richards et al. 2019), plus one additional pelodryadid treefrog, were detected on transects in 2019.

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 the same ways as presented in 2015 and 2017 (Richards and Armstrong 2017; Richards et al. 2019) 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, 2017 and 2019 at increasing distances from the forest edge on each of the VAES transects, and by acoustic recordings, are shown in Figure 1.1. The slight (non-significant) trend for increasing species diversity with increasing distance from infrastructure at KP107 in both the VAES and Acoustic Recorder data sets for 2017 is again apparent in 2019 (Figure 1.1, lower). However, the statistical analysis using GLMM (Table 1.4) found no significant influence of distance from infrastructure on species diversity, whether measured by the VAES transect method or acoustic recordings, at any site. The slight reverse trend, with a possible small drop in diversity with increasing distance from infrastructure that was detected by Acoustic Recorders (only) at Hides Low in BAA 1 during 2015 and in the acoustic survey data (only) in 2017, is no longer apparent.

Statistical analysis of Acoustic Recorder data found no significant differences in pairwise comparisons of species diversity at different distance segments from the ROW. However, for the VAES data, and consistent with the 2017 results, the pairwise comparisons of distance segments across all transects at both BAA's returned a significant difference with species richness at 0–20 m from the ROW being less than at 80–100 from the ROW (Table 1.4). With the 2019 data incorporated the analysis also documented a significant difference between diversity at the two adjacent distance categories (60–80 vs 80–100 m) furthest from the ROW (Table 1.4). Given that there is no clear general pattern of difference in species diversity across the transects, it suggests that the variation is derived from factors other than edge effects. If there was a strong influence of edge effects, we may expect to see larger differences between the categories further apart rather than those adjacent to each other. Examination of boxplots in Figure 1.1 reinforces the notion that there is no strong or consistent shift in Species Richness at increasing distances from the ROW across the two BAAs. Overall, these results support the hypothesis that edge effects are not having an impact on frog diversity.

Although there were several statistically significant interaction terms (Table 1.4), these are generally difficult to interpret because no obvious patterns are evident from plots such as Figure 1.1. For example, there is no evidence for a higher level of species richness at one distance category at a particular elevation in all years, or only one year. The statistically significant interaction results are most likely the result of the level of sampling and general variation in habitats, weather patterns and frog population size over the years, and they do not contribute any further understanding to the effect of linear infrastructure.

The lack of a temporal shift in species diversity at different distances along the ROW since 2015 strongly suggests that the Project infrastructure in BAA 1 and BAA 2 is currently having no detectable impact on the ongoing viability of local frog communities.

The relative roles (if any) of seasonality and improved field experience of investigators in generating the increase in documented species across both BAAs between years is difficult to determine without further data. However, it is likely that to a large extent the increase in diversity is simply a natural trend reflecting increased search effort over time; this will become apparent over coming surveys when, with increasing data points, construction of species accumulation curves will become viable.

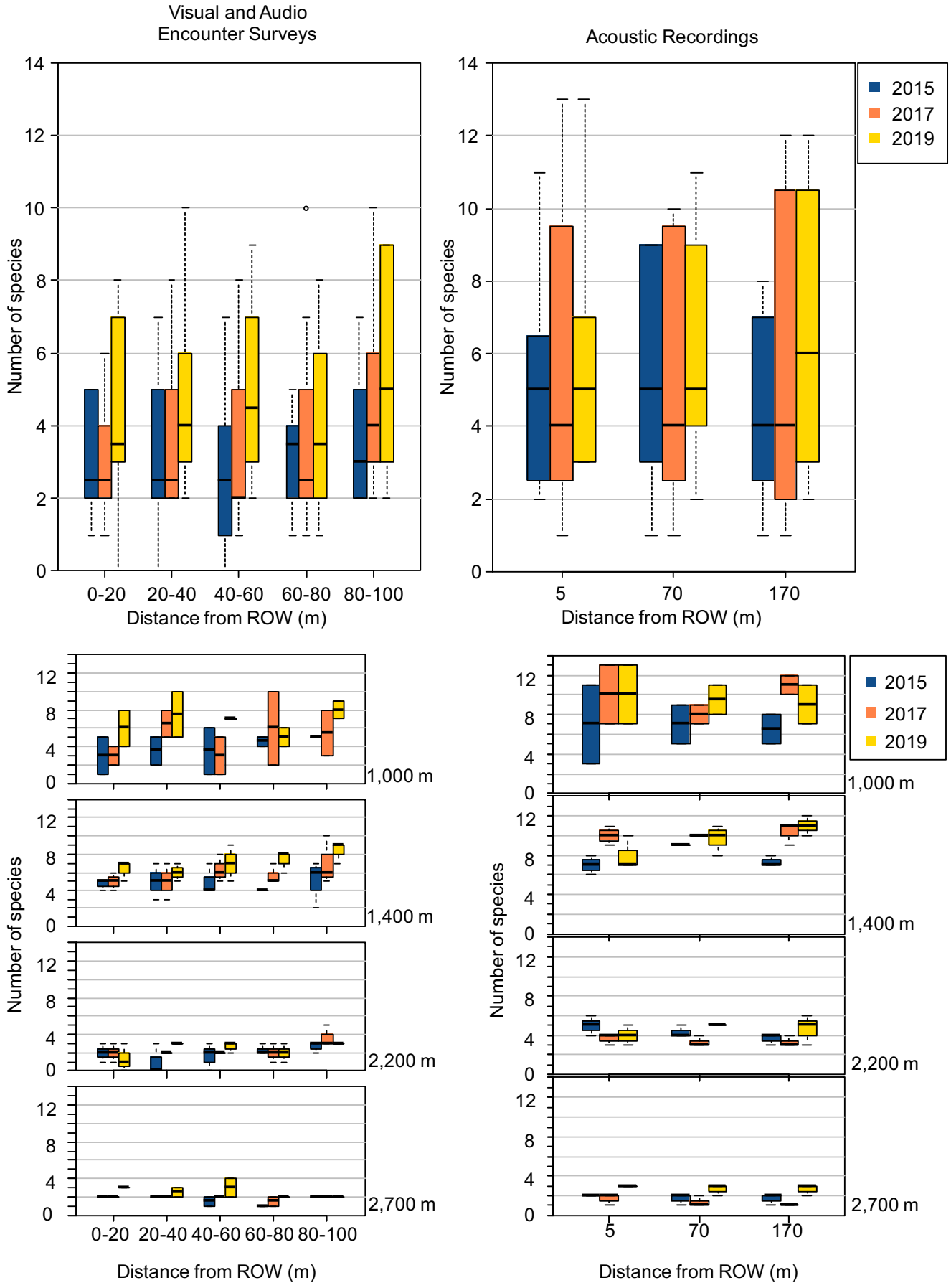

Figure 1.1. Summary of frog diversity (as number of species) at different distances from the forest edge based on data from VAES transects (left column) and the acoustic survey (right column) in 2015, 2017 and 2019. For each of the two series, the uppermost graphs are pooled across all elevations, while those below are for each of the elevational zones. 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.

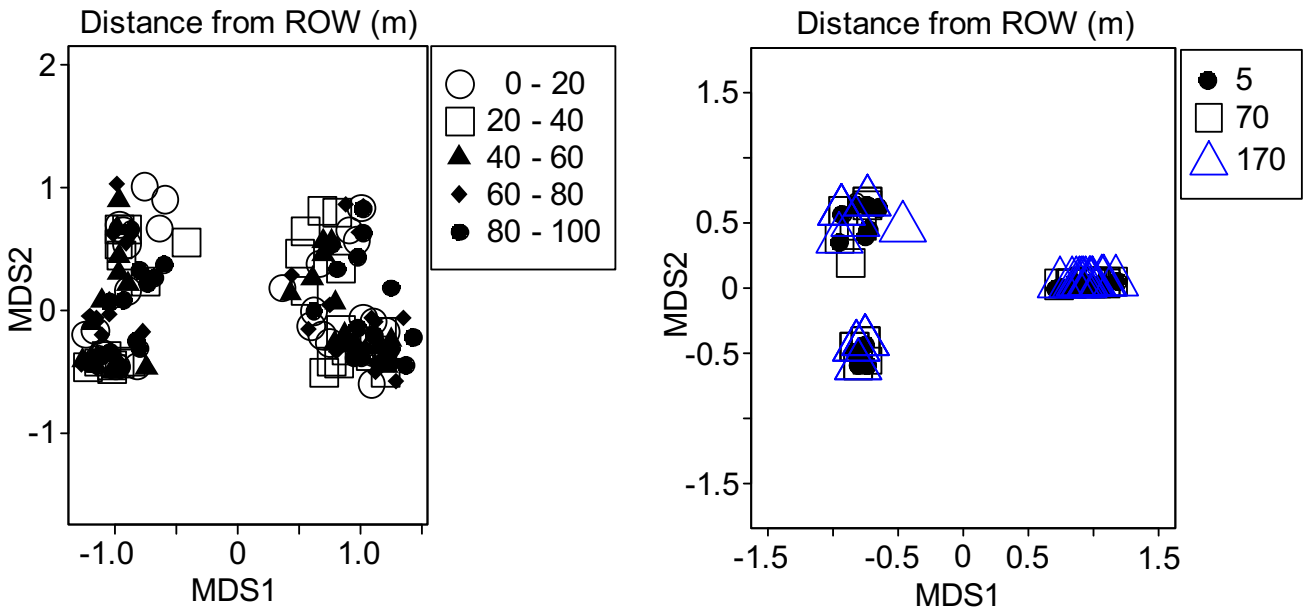

Figure 1.2. Non-metric Multi-dimensional Scaling (NMDS) ordinations summarising patterns of species composition at different distances from the road or ROW based on each of the VAES transect (left) and acoustic recording (right) datasets in 2015, 2017 and 2019.

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 2015, 2017 or 2019 (Figure 1.2).

The analyses presented above 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 without causing their actual 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 1.3 shows trends in the Indicator Species indices derived from each of the VAES transect and acoustic recording datasets in 2015, 2017 and 2019.

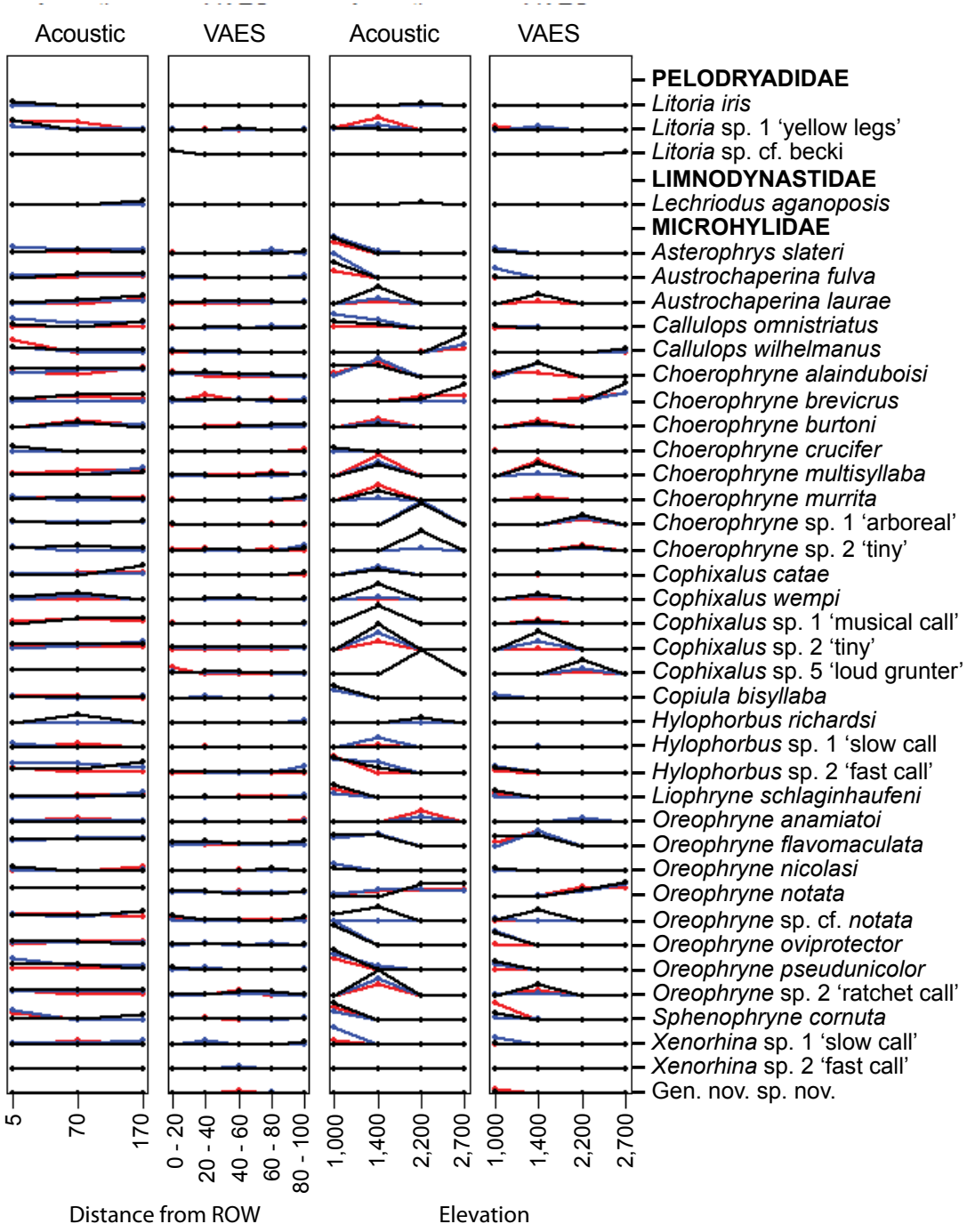

Figure 1.3. Summary of trends in Indicator Species indices (y-axis) for increasing distances (m) from linear infrastructure based on data from VAES transects and acoustic recordings in 2015 (red), 2017 (blue) and 2019 (black).

Results of the 2019 Indicator Species analysis closely mirror those obtained in 2015 and 2017 (Figure 1.3). The Indicator Species indices for each species at different elevations illustrate the difference in frog diversity between low and high elevations, and trends are similar for both the acoustic recording and VAES survey methods (Figure 1.3). The indices particularly highlight the restriction of each species to one, or at most two, elevational bands; conspicuous examples are *Choerophryne* sp. 1 'arboreal' and *Cophixalus* sp. 5 'loud grunter' at 2,200 m asl, and *Austrochaperina laurae*, *Cophixalus* sp. 2 'tiny' and *Oreophryne* sp. 2 'ratchet call' at 1,400 m asl. There were only minor differences between years for each species, and these are probably an artefact of sampling effects or natural variation in population demographics.

In contrast to the patterns of frog diversity at different elevations, the Indicator Species indices examining increasing distance from Project infrastructure do not show any obvious trends in all three years (Figure 1.3). The 2019 data

confirmed that two species identified as possible Indicator Species based on 2015 data, *Choerophryne burtoni* and *Liophryne sclaginhaufeni*, are unlikely to be useful indicators due to low encounter rates. The only other species showing a consistent pattern (for VAES only) is the high-elevation microhylid frog *Callulops wilhelmanus*. This species occurs at extremely high densities on the rocky verges of the ROW in the highest elevation band on Hides Ridge. *Callulops wilhelmanus* appears to be continuing to benefit from structurally similar habitat created during construction of the road and pipeline ROW. It is therefore a suitable candidate as an Indicator Species for habitat changes that cause an increase in abundance at the highest elevation transects.

Elevational trends in frog diversity and community composition

As reported in previous sampling years, there was a pronounced reduction in frog diversity with increasing elevation – the frog fauna in BAA 2 is substantially more diverse than that encountered on Hides Ridge, with nearly three times as many species (27 vs 10) detected there in 2019. Figure 1.4 illustrates the rapidly dropping species richness with increasing elevation that was documented in all years. In all three years elevation was the major factor influencing differences in the number of species recorded in each BAA (Table 1.3; Figure 1.4) and statistical analysis of the 2019 data demonstrated that these differences are significant, with BAA 2 sites having significantly higher diversity than BAA 1 sites (Table 1.4). This pattern is widely repeated in the mountains of New Guinea (e.g. Richards and Dahl 2011; Tallowin et al. 2017).

Table 1.3. Summary of means ± standard deviation of frog diversity in 2019 at each distance from the road or ROW, elevation (site) and year, for the two different frog survey methods.

Distance (m)	**Acoustic recordings**	**Distance (m)**	**VAES transects**
5	5.7 ± 3.4	0–20	3.4 ± 2.0
70	5.7 ± 3.3	20–40	3.8 ± 2.4
170	5.7 ± 3.7	40–60	3.8 ± 2.4
—		60–80	3.7 ± 2.4
—		80–100	4.6 ± 2.6
Site elevation (m asl)	**Acoustic recordings**	**Site elevation (m asl)**	**VAES transects**
Arakubi (995–1,073 m asl)	8.7 ± 2.8	Arakubi (995–1,073 m asl)	5.1 ± 2.6
KP107 (1,315–1,405 m asl)	9.1 ± 1.6	KP107 (1,315–1,405 m asl)	5.8 ± 1.8
Hides Low (2,148–2,367 m asl)	4.1 ± 0.9	Hides Low (2,148–2,367 m asl)	2.2 ± 1.0
Hides High (2,681–2756 m asl)	2.0 ± 0.7	Hides High (2,681–2756 m asl)	2.0 ± 0.6
Year	**Acoustic recordings**	**Year**	**VAES transects**
2015	5.0 ± 2.8	2015	3.1 ± 1.8
2017	5.8 ± 4.0	2017	3.8 ± 2.4
2019	6.3 ± 3.4	2019	4.7 ± 2.6

Within BAA 1 the lower diversity at the high elevation site compared to the low elevation site (4 vs. 8 species; Table 1.2) confirms the pattern documented in 2015 and repeated in 2017. Two species (*Litoria iris* and *Lechriodus aganoposis*) that were encountered on transects at the low elevation sites in BAA 1 in 2015 were not detected there in 2017 but were encountered again in 2019. *Lechriodus aganoposis* appears to occur at naturally low densities on Hides Ridge, and so encounter rates are expected to be low and highly variable. By contrast, *Litoria iris* is abundant on Hides Ridge, but it occupies small ponds that are absent from transects so it is unlikely to be encountered in large or consistent numbers.

Documentation for the first time of the treefrog *Litoria* sp. cf. *becki* on Transects H4 and H5 in the BAA 1 high-elevation site, and the failure to detect it as well as *Callulops wilhelmanus* in the BAA 1 low elevation site in 2019, suggests that the frog fauna at higher elevations on Hides Ridge is not simply a subset of the fauna in the lower elevation site, as suggested previously (Richards et al. 2019). *Callulops wilhelmanus* is abundant at higher elevations on Hides Ridge but has not been detected on a transect at lower elevations in BAA 1 during any of the surveys completed to date. This species has a reported lower elevational limit of 2,500 m asl (Menzies 2006) so its rarity at lower elevations in BAA 1, where it was heard calling occasionally near the transects in 2015, is not surprising.

Turnover of species is also high between the two elevation bands in BAA 2. Just eight of the 27 species (30%) found in BAA 2 were detected at both KP107 and Arakubi despite these sites being in close proximity and having similar numbers of species (17 and 18, respectively).

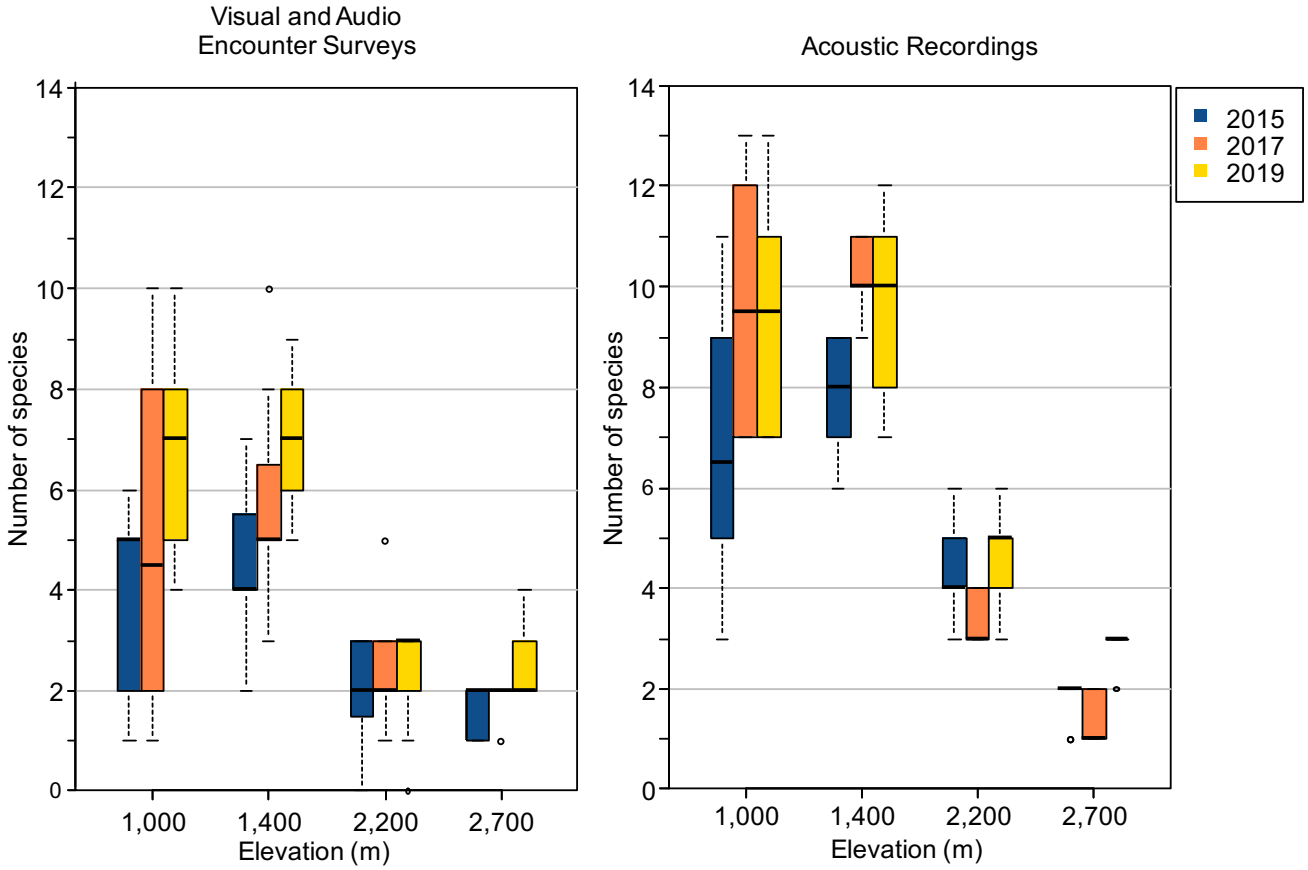

Figure 1.4. Summary of frog diversity (as number of species, or richness) at different elevations based on data from VAES transects (left) and acoustic recordings (right) in 2015, 2017 and 2019. For each of the two plots, data are pooled across all distances from linear infrastructure. See Figure 1.1 for explantation of boxplots.

It is also clear that the frog communities in BAA 1 are not simply a sub-set of the frogs found in BAA 2. The 2015 and 2017 surveys reported just one species, *Oreophryne notata*, from transects in both BAA 1 and BAA 2 but noted uncertainty about the taxonomic status of the BAA 2 population. Genetic data collected during 2019 has helped to resolve this uncertainty, demonstrating that the two populations are not conspecific (see '*Significant species and taxonomic uncertainties*' below). There is therefore currently no overlap between species encountered on transects in BAA 1 and BAA 2. The only species now known to occur in both BAAs is *Lechriodus aganoposis*, but this species has not been encountered on a transect in BAA 2. The 2019 PMA3 survey results reinforce the importance of Hides Ridge as a habitat for a small suite of high-elevation frogs, several of which are undescribed and known from few or no other localities.

Table 1.4. Analysis of Deviance Table (Type II Wald F tests with Kenward-Roger df) summarising the tests from a Linear mixed model fit by REML ['lmerMod'], and post hoc pairwise comparisons to test for differences in frog species richness at different elevations and distances from the road or ROW, and year (2015, 2017 and 2019) for each of the acoustic recording and the VAES data sets. Only significant pairs for the main effects are shown; values are elevations in metres; significance codes: *** <0.001, ** <0.01, * <0.05); formula: total_richness ~ dist + elev + year + dist * elev + elev * year + dist * year + dist * elev * year + (1 | transect) + (1 | transect.dist) + (1 | transect.year).

Acoustic recordings	**Chi-square**	**Df, Df.res**	**Pr(>F)**	**Pairwise**
Distance	0.06	2, 14	0.94 NS	All NS
Elevation 1,000 m = Arakubi sites 1,400 m = KP107 sites 2,200 m = Hides Low sites 2,700 m = Hides High sites	25.84	3, 7	0.0003***	1,000 > 2,200* 1,000 > 2,700** 1,400 > 2,200** 1,400 > 2,700***
Year	14.48	2, 14	0.0003***	2015 < 2017** 2015 < 2019***
Distance*Elevation	1.35	6, 14	0.29 NS	—
Distance*Year	4.12	4, 28	0.009**	—
Elevation*Year	7.59	6, 14	0.0009***	—
Distance*Elevation*Year	2.68	12, 28	0.015*	—
VAES transects	**Chi-square**	**Df, Df.res**	**Pr(>F)**	**Pairwise**
Distance	4.7	4, 24	0.006**	0–20 < 80–100** 60–80 < 80–100*
Elevation 1,000 m = Arakubi sites 1,400 m = KP107 sites 2,200 m = Hides Low sites 2,700 m = Hides High sites	8.25	3, 6	0.015*	1,400 > 2,200* 1,400 > 2,700*
Year	20.07	2, 12	0.0001***	2015 < 2019*** 2017 < 2019**
Distance*Elevation	12.6	12, 24	0.25 NS	—
Distance*Year	25.57	8, 48	0.83 NS	—
Elevation*Year	14.59	6, 12	0.059 NS	—
Distance*Elevation*Year	41.23	24, 48	0.42 NS	—

The differences in composition of frog communities at different elevations are confirmed by NMDS ordinations of species presence based on the VAES transect and acoustic recording datasets in 2015, 2017 and 2019 (Figure 1.5). NMDS ordinations emphasize the strong differentiation not only between the BAA 1 and BAA 2 frog communities but also between frog communities in each of the two elevational zones within each BAA. The ordinations differ somewhat from the 2017 results in that both the VAES and acoustic recordings show a consistent difference between species composition of the high and low Hides Ridge sites with all years combined (Figure 1.5), whereas this was not detected by the VAES data (only) for the 2015 and 2017 data alone.

Overall, the frog communities documented on transects in the BAAs are strongly influenced by elevation, with diversity in each altitudinal band decreasing with increasing elevation (albeit the totals being similar at the two lowest elevations), and with high species turnover among elevation bands.

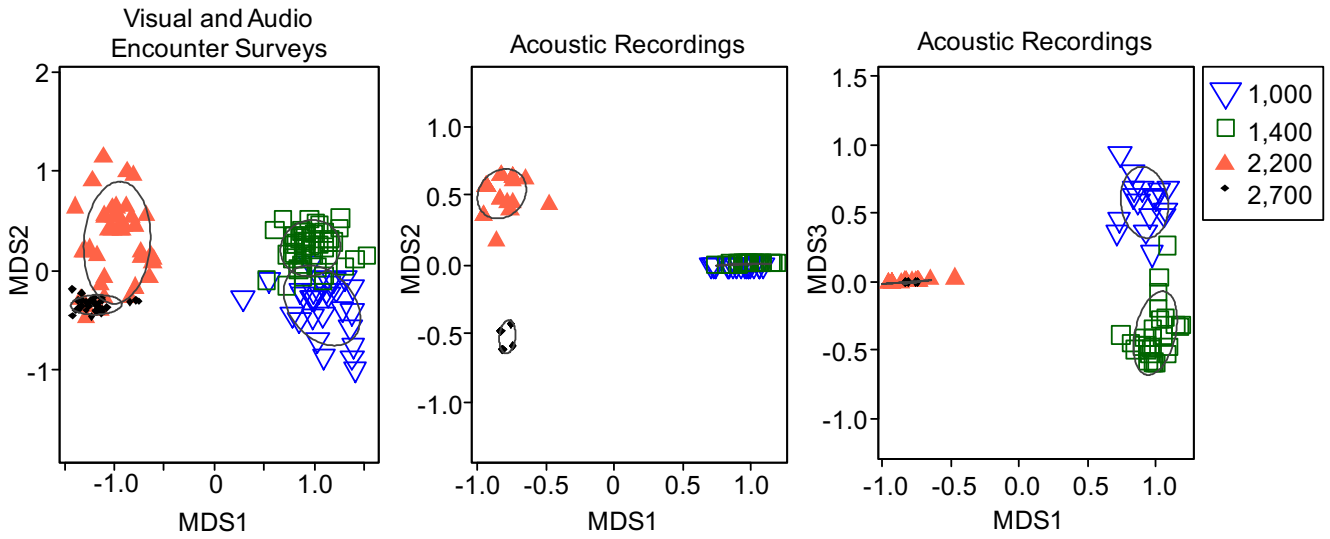

Figure 1.5. Non-metric Multi-dimensional Scaling (NMDS) ordinations summarising patterns of species composition at different elevations within the BAAs in 2015, 2017 and 2019 (data ellipses are one standard deviation).

Significant species and taxonomic uncertainties

Taxonomic studies since the 2017 survey have resulted in the formal descriptions of an additional four frog species occurring in BAA 2 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 1.5.

Other taxonomic considerations include:

1. A single specimen of an unidentified torrent-dwelling treefrog (*Litoria*; sp. cf. *becki*, see chapter cover) was encountered near Transect H5 during the 2017 survey. Given the lack of suitable breeding habitat at high elevations on Hides Ridge, Richards et al. (2019) suggested that this species is probably not resident there. However, several individuals of this species were encountered on Transects H4 and 5 during the 2019 survey suggesting that it should be considered a resident of the forests on Hides Ridge. This species appears to be undescribed, and genetic and other taxonomic studies are currently underway. If its status as a new species is confirmed, it will represent a second species of treefrog (the other being *Litoria vivissimia*) that is known to date only from Hides Ridge.

2. The taxonomic status of frogs referred to *Oreophryne notata* from KP107 and Arakubi appears to have been resolved. A small *Oreophryne* species (Figure 1.16) resembling *O. notata* was captured for the first time at Arakubi during the 2019 survey. It is genetically distinct from *O. notata* and, although we have yet to associate a call with a voucher specimen, we now consider that the peeping call at KP107 and Arakubi that was previously attributed to *O. notata* belongs to this species. As a result of this new information there are now no frog species shared between transects in BAA 1 versus BAA 2, although *Lechriodus aganoposis* is known to occur within both BAAs.

3. Throughout the PMA3 monitoring program, the identity of several small arboreal frogs of the genus *Oreophryne* with 'rattling' calls in BAA 2 has been uncertain. These are tree-dwelling frogs that are rarely seen calling and are difficult to capture for DNA sampling. Although DNA barcoding indicates that at least two species occur at KP107 (*Oreophryne flavomaculata* and 1–2 unidentified species labelled in Figure 1.6 as *Oreophryne* ' rattler long first note' [see also Figure 1.17] and *O.* 'long call'), analyses of calls extracted from acoustic recorders flag the presence of at least four acoustically and ecologically similar *Oreophryne* species at KP107, only two of which

(*O. flavomaculata* and *O.* 'ratchet call') have been recognised consistently (Table 1.2). Additional DNA samples, preferably associated with vouchered calls, are needed to resolve this issue. For the purposes of integrating our 2019 captures with the previous (2015, 2017) genetic data, we again combined all unidentified rattling calls at KP107 and Arakubi with *O. flavomaculata*. However, it is likely that with the availability of additional DNA samples in future it will be demonstrated that *O. flavomaculata* does not occur at Arakubi, and it will be possible to re-analyse data from the four putative 'rattling *Oreophryne* species' at KP107 separately.

4. For the purposes of data analysis and interpretation in this report we also continue to combine two species, *Cophixalus* sp 2 'tiny A' and *Cophixalus* sp 3 'tiny B', that are genetically distinct (Figure 1.6), into a single 'species'. Both of these species occur at KP107 where they are impossible to distinguish morphologically in the field, and uncertainty remains about the call types produced by each species. Data from the 2019 survey suggest that at least one of these species may make both single- or multi-note calls. Given the species' morphological and apparently ecological similarity, they are not only combined for analyses in this report, but the detection method indicated for these two species in Table 1.2 should be considered tentative. Obtaining additional call recordings associated with genetic samples for these two species will be a high priority for the 2021 survey.

Species of conservation significance (IUCN-Listed)

Three species of frog known from the two BAAs (*Choerophryne burtoni, Hylophorbus richardsi*, and *Oreophryne notata*) were classified previously as Data Deficient by the IUCN. However, the conservation status of all of these species was downgraded to Least Concern during the 2019 IUCN Red List workshop for Melanesian amphibians. Two of these species remain common in the study area, while the third (*H. richardsi*) appears to be naturally rare wherever it occurs (S. Richards, unpublished observations). There appear to be no threats to local populations of these species.

No other species of frogs in either BAA has an IUCN Red List conservation status higher than Least Concern.

Frogs at Wellpad D on Hides Ridge

Smaller numbers of Rainbow Treefrogs (*Litoria iris*) were present around the small pond at Wellpad D during the 2019 survey than were documented during 2015 and 2017 (Richards et al. 2019). The pond was also much shallower during 2019 than during previous surveys (S. Richards, personal observation). Despite this, numbers of both adult *L. iris* and their egg masses exceeded the highest abundance class (>10) during the 30-minute VAES survey around the pond, and calls of this species were present on 100% of the ten 1-hour time blocks of BAR recordings over the two days that the BAR units were recording calls at Wellpad D. The Hides Ridge population of this species appears to be secure.

No calls that could be attributed to *Litoria vivissimia*, a species known only from a single adult collected at this pond in 2005 (Oliver et al. 2019) were detected on the BAR recordings or during the VAES survey around the pond in 2019.

DNA barcoding

The 2019 survey generated additional important tissue vouchers for several taxonomically difficult frog groups, and these were incorporated into an expanded genomic-scale genetics-based identification program that also included a larger number of comparative 'context species' from across Papua New Guinea (Figure 1.6). This increasingly speciose and robust data set is providing a much better understanding of the relationships of species from the Upstream Project Area with other described and undescribed species.

The genome-scale DNA sequencing continues to significantly improve 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, during the 2019 survey in BAA 2 we obtained the first available DNA sample of the species previously referred to as *Oreophryne notata* at KP107 and Arakubi. Our latest barcoding study demonstrates that the BAA 2

population of *O. notata* is genetically distinct from that in BAA 1 (MEL1284 in Figure 1.6), being more closely related to a species from Tualapa in the upper Strickland River basin. This result further emphasises the lack of overlap between the faunas of the two BAAs, and has confirmed the presence of an additional, poorly-known undescribed species of frog from BAA 2.

The barcoding results also support the recognition of multiple genetic types within morphologically and ecologically similar *Oreophryne* species at KP107 (Figure 1.6), but additional DNA material is required to further understand the relationships among these species so that a final species tally can be determined.

In summary, the genome-scale DNA identification framework developed here continues to provide 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.

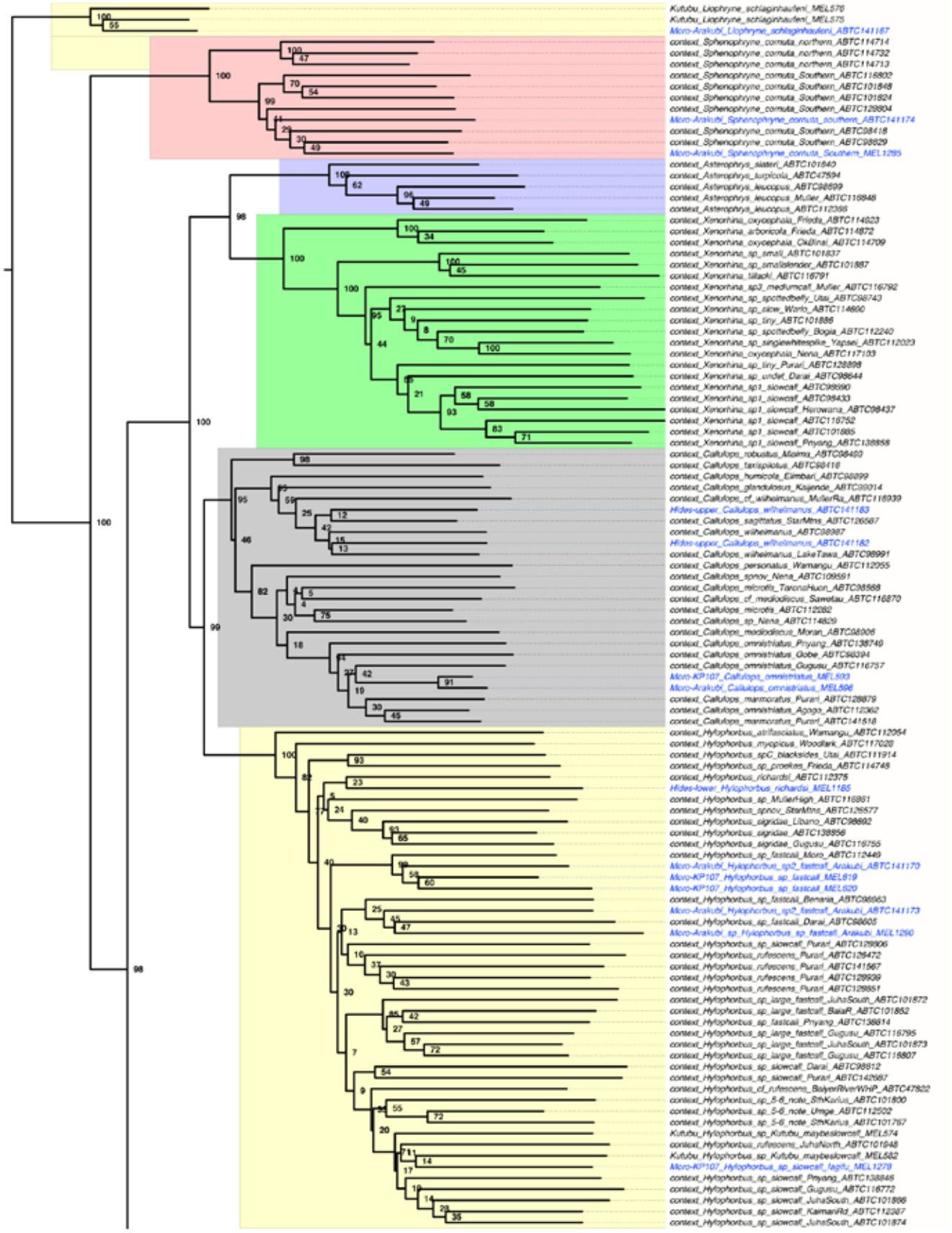

Figure 1.6. Neighbour Joining distance phylogram showing the relationship of ArTseq genotyped captures on the 2015, 2017 and 2019 PMA3 surveys, plus samples of various selected taxa from the Australian Biological Tissue Collection.

Figure 1.6. (cont.)

Figure 1.6. (cont.)

Comments on efficacy of the two survey methods

The activity levels and calling behaviour of each frog species are influenced differently by changes in temperature, humidity and rainfall, so 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 continued to use two quantitative field methods, VAES and Acoustic Recorders for the 2019 PMA3 frog monitoring program.

The same number of species by transect detection events were recorded from both survey methods in 2019 as in 2017 (108). Of these, 65 (60.2%) were detected by both survey methods, 29 (26.8%) were detected only by Acoustic Recorders and 14 (13%) were detected only by VAES. Overall, 27 of the 37 species (73%) were detected at least once by both survey methods. Just four species (11%) were detected only by VAES and six species (16%) were detected only on automated sound recordings.

It is clear from both the statistical results and the patterns observed in the summary boxplots and NMDS plots (Figures 1.1–1.5) that the two survey 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.

Richards et al. (2019) recommended that a detailed assessment of the future use of VAES transects should be made after the 2019 survey because VAES methodology may become logistically less feasible during future surveys. However, the VAES surveys during 2019 generated valuable genetic samples and other data (acoustic and voucher) that have contributed to a much better understanding of the frog fauna within the BAAs than would have been possible using Acoustic Recorders only. We therefore recommend that VAES surveys be continued, alongside Acoustic Recorders, while logistical constraints permit it.

Observations on damage to vegetation adjacent to Project infrastructure

Richards et al. (2019) reported that during the two years between 2015 and 2017 several trees were removed by members of the local communities from the vicinity of monitoring transects, for use as construction materials and other purposes. Removal of 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. Our observations during 2019 suggest that since 2017 forest vegetation is not regenerating at the beginning of these transects, where the new clearings remain open and are being invaded by grass and other weeds. It is likely that the new location of the forest edge will be permanent for both of these transects. In contrast, the gap created by a treefall within the forest on Transect M4 (Richards et al. 2019) shows signs of rapid forest regeneration.

No evidence of additional anthropogenic damage to vegetation at transects in either BAA was detected during 2019 (although clearing of vegetation for gardens adjacent to the access road on Hides Ridge has accelerated and may encroach upon lower elevation transects in future). However, the major earthquake of March 2018 resulted in numerous treefalls within both BAAs, including one on Transect H4 that substantially damaged the forest along the first ~30 m of the transect (Figure 8 in Report Summary); and another on Transect M2 which similarly severely altered the forest structure along the first ~30 m of the transect. The extent of regeneration of these treefall areas will be noted on future surveys.

Our latest results indicate that these major treefall events did not significantly impact the frog faunas where they intersected the VAES transects, probably because sufficient canopy cover remained to maintain the cool, moist conditions required by the local microhylid frog species that dominate the local fauna.

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

2. Four species of undescribed frogs that had been recorded from the two BAAs during previous surveys have been formally described since 2017.

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

4. However, statistical analysis of frog communities at different distances from linear infrastructure across three surveys (2015–2019) found no evidence for shifts in species diversity with increasing distance from the forest edge.

5. Overall, the results from the third 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 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. Although 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 continued after the 2019 survey as long as logistical difficulties associated with conducting field work at night permit because VAES transects are generating valuable data on poorly-known species that cannot be obtained using only Acoustic Recorders.

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 1.7. Limnodynastidae. *Lechriodus aganoposis*

F**igure 1.8.** Microhylidae. *Asterophrys slateri*

Figure 1.9. Microhylidae. *Austrochaperina fulva*

Figure 1.10. Microhylidae. *Callulops wilhelmanus*, adult

Figure 1.11. Microhylidae. *Callulops wilhelmanus*, juvenile

Figure 1.12. Microhylidae. *Choerophryne alainduboisi*

Plate 2

Figure 1.13. Microhylidae. *Cophixalus* sp. 1 'musical call'

Figure 1.14. Microhylidae. *Hylophorbus richardsi*

Figure 1.15. Microhylidae. *Oreophryne nicolasi*

Figure 1.16. Microhylidae. *Oreophryne* cf. *notata*

Figure 1.17. Microhylidae. *Oreophryne* 'rattler long first note'

Figure 1.18. Pelodryadidae. *Litoria* sp. cf. *becki*

Appendix 1.1. 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 1.2. 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	Recording location	Latitude	Longitude	Elevation (m asl)
Arakubi		M4_005	S6.462013°	E143.256616°	1,017
	M4	M4_070	S6.461926°	E143.256018°	1,030
		M4_170	S6.461667°	E143.255006°	1,041
		M5_005	S6.461944°	E143.250132°	1,052
	M5	M5_070	S6.462124°	E143.250560°	1,057
		M5_170	S6.461528°	E143.251531°	1,056
KP107		M1_005	S6.440230°	E143.224085°	1,403
	M1	M1_070	S6.440240°	E143.223590°	1,398
		M1_170	S6.440079°	E143.222562°	1,408
		M2_005	S6.440718°	E143.225566°	1,395
	M2	M2_070	S6.441409°	E143.225425°	1,378
		M2_170	S6.442099°	E143.224895°	1,391
		M3_005	S6.441778°	E143.227103°	1,379
	M3	M3_070	S6.442142°	E143.226678°	1,375
		M3_170	S6.443061°	E143.226314°	1,392
Hides Low		H1_005	S5.972520°	E142.753279°	2,163
	H1	H1_070	S5.972856°	E142.752890°	2,155
		H1_170	S5.973729°	E142.752471°	2,151
		H2_005	S5.969087°	E142.751274°	2,167
	H2	H2_070	S5.969068°	E142.750669°	2,187
		H2_170	S5.969126°	E142.749804°	2,217
		H3_005	S5.943807°	E142.741784°	2,289
	H3	H3_070	S5.944572°	E142.741865°	2,284
		H3_170	S5.945233°	E142.741622°	2,322
Hides High		H4_005	S5.918423°	E142.695320°	2,695
	H4	H4_070	S5.919144°	E142.694951°	2,702
		H4_170	S5.919827°	E142.694924°	2,692
		H5_005	S5.916343°	E142.692853°	2,751
	H5	H5_070	S5.916471°	E142.692311°	2,749
		H5_170	S5.916749°	E142.691230°	2,731
		H6_005	S5.913796°	E142.690169°	2,733
	H6	H6_070	S5.914176°	E142.689647°	2,737
		H6_170	S5.914911°	E142.688983°	2,729

Appendix 1.3. 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				
	995-1,073 m asl		1,315-1,405 m asl			2,148-2,327 m asl			2,681-2,756 m asl	
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	oooo●	ooooo	o●●oo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Litoria sp. cf. *becki*	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	●oooo	oo●oo
LIMNODYNASTIDAE										
Lechriodus aganoposis	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
MICROHYLIDAE										
Asterophrys slateri	oooo●	ooo●o	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Austrochaperina fulva	ooooo	●●ooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Austrochaperina laurae	ooooo	ooooo	oo●●o	●●●●●	o●o●●	ooooo	ooooo	ooooo	ooooo	ooooo
Callulops omnistriatus	o●●oo	ooooo	ooooo	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Callulops wilhelmanus	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	o●ooo	●o●oo
Choerophryne alainduboisi	●●●oo	o●●o●	●●o●●	●●●●●	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne brevicrus	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooo●o	●●●●●	●●●●●
Choerophryne burtoni	ooooo	ooooo	ooo●o	oo●o●	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne crucifer	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne multisyllaba	ooooo	ooooo	o●●●●	●oo●●	●●ooo	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne murrita	ooooo	ooooo	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Choerophryne sp. 1 'arboreal'	ooooo	ooooo	ooooo	ooooo	ooooo	●●●o●	o●o●●	●o●●o	ooooo	ooooo
Choerophryne sp. 2 'tiny'	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	oooo●	o●●o●	ooooo	ooooo
Cophixalus cateae	ooooo	ooooo	ooooo	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Cophixalus wempi	ooooo	o●●oo	●o●o●	o●o●o	oo●o●	ooooo	ooooo	ooooo	ooooo	ooooo
Cophixalus sp. 1 'musical call'	ooooo	ooooo	ooooo	oo●●●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Cophixalus sp. 2 'tiny A' / sp. 3 'tiny B'	ooooo	ooooo	●o●●●	●●●●●	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo
Cophixalus sp. 5 'loud grunter'	ooooo	ooooo	ooooo	ooooo	ooooo	●●●o●	o●●●o	o●●●●	ooooo	ooooo
Copiula bisyllaba	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Hylophorbus richardsi	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Hylophorbus sp. 1 'slow call'	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Hylophorbus sp. 2 'fast call'	ooo●o	●●●o●	oo●o●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Liophryne schlaginhaufeni	ooooo	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne anamiatoi	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne flavomaculata	●●●●●	●●●●●	●●●●●	●●●●●	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne nicolasi	ooooo	o●o●o	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne notata	ooooo	ooooo	ooooo	ooooo	ooooo	●●●●●	o●●o●	o●oo●	●●●●●	●●●●●
Oreophryne sp. cf. *notata*	oooo●	●ooo●	●●o●●	●o●oo	●●●●●	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne oviprotector	●●●●●	●●●o●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne pseudunicolor	●●●●●	●●o●●	●oooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Oreophryne sp. 2 'ratchet call'	ooooo	ooooo	●●●●●	●●●●o	ooo●o	ooooo	ooooo	ooooo	ooooo	ooooo
Sphenophryne cornuta	oo●o●	●●o●o	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Xenorhina sp. 1 'slow call'	oooo●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Xenorhina sp. 2 'fast call'	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo
Gen. nov. sp. nov.	ooooo	oo●o●	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo	ooooo

Appendix 1.4. Summary of species detections for all calls detected in 2019 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					
	995-1,073 m asl		1,315-1,405 m asl			2,148-2,327 m asl			2,681-2,756 m		
Transect	**M4**	**M5**	**M1**	**M2**	**M3**	**H1**	**H2**	**H3**	**H4**	**H5**	**H6**
PELODRYADIDAE											
Litoria iris	ooo	ooo	ooo	ooo	ooo	o●o	ooo	ooo	ooo	ooo	ooo
Litoria sp. 1 'yellow legs'	ooo	o●o	o●o	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Litoria sp. cf. *becki*	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
LIMNODYNASTIDAE											
Lechriodus aganoposis	ooo	ooo	ooo	ooo	ooo	●oo	ooo	ooo	ooo	ooo	ooo
MICROHYLIDAE											
Asterophrys slateri	oo●	●●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Austrochaperina fulva	●o●	●o●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Austrochaperina laurae	ooo	ooo	●oo	●o●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Callulops omnistriatus	o●●	o●o	●oo	●oo	●oo	ooo	ooo	ooo	ooo	ooo	ooo
Callulops wilhelmanus	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	●●o	●●●	o●●
Choerophryne alainduboisi	●●●	●●●	●●●	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne brevicrus	ooo	ooo	ooo	ooo	ooo	●oo	oo●	●o●	●●●	●●●	●●●
Choerophryne burtoni	ooo	ooo	oo●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne crucifer	ooo	o●o	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne multisyllaba	ooo	ooo	●o●	●●o	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne murrita	ooo	ooo	●●●	oo●	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Choerophryne sp. 1 'arboreal'	ooo	ooo	ooo	ooo	ooo	●●●	●●●	●●o	ooo	ooo	ooo
Choerophryne sp. 2 'tiny'	ooo	ooo	ooo	ooo	ooo	●●●	oo●	●●●	ooo	ooo	ooo
Cophixalus cateae	ooo	ooo	●oo	ooo	●oo	ooo	ooo	ooo	ooo	ooo	ooo
Cophixalus wempi	ooo	ooo	oo●	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 A'	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Cophixalus sp. 3 'tiny B'	ooo	ooo	●●●	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Cophixalus sp. 5 'loud grunter'	ooo	ooo	ooo	ooo	ooo	●●●	●●●	●●●	ooo	ooo	ooo
Copiula bisyllaba	o●o	●o●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Hylophorbus richardsi	ooo	ooo	ooo	ooo	ooo	oo●	ooo	oo●	ooo	ooo	ooo
Hylophorbus sp. 1 'slow call'	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Hylophorbus sp. 2 'fast call'	●●●	●●●	●oo	●●●	●oo	ooo	ooo	ooo	ooo	ooo	ooo
Liophryne schlaginhaufeni	ooo	●●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne anamiatoi	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne flavomaculata	●●●	●●●	●●●	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne nicolasi	ooo	o●o	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne notata	ooo	ooo	ooo	ooo	ooo	●●●	●●●	●●●	●●●	●●●	●●●
Oreophryne sp. cf. *notata*	●oo	●●●	●●●	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne oviprotector	o●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo

Elevation	BAA 2					BAA 1					
	995-1,073 m asl		1,315-1,405 m asl			2,148-2,327 m asl			2,681-2,756 m		
Transect	**M4**	**M5**	**M1**	**M2**	**M3**	**H1**	**H2**	**H3**	**H4**	**H5**	**H6**
Oreophryne pseudunicolor	●●●	●●●	oo●	o●o	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Oreophryne sp. 2 'ratchet call'	ooo	ooo	●●●	●●●	●●●	ooo	ooo	ooo	ooo	ooo	ooo
Sphenophryne cornuta	●oo	●●●	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo	ooo
Xenorhina sp. 1 'slow call'	ooo	ooo	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 1.5. Summary of taxonomic changes to frog names since 2015 that are incorporated into this report.

2015	2017	2019
HYLIDAE	**PELODRYADIDAE**	**PELODRYADIDAE**
Litoria iris	*Litoria iris*	*Litoria iris*
Litoria sp. 1 'yellow-legs'	*Litoria* sp. 1 'yellow legs'	*Litoria* sp. 1 *'yellowlegs'*
not detected on transects in 2015	not detected on transects in 2017	*Litoria* sp. cf. *becki*
LIMNODYNASTIDAE	**LIMNODYNASTIDAE**	**LIMNODYNASTIDAE**
Lechriodus aganoposis	*Lechriodus aganoposis*	*Lechriodus aganoposis*
MICROHYLIDAE	**MICROHYLIDAE**	**MICROHYLIDAE**
Metamagnusia slateri	*Asterophrys slateri*	*Asterophrys slateri*
Austrochaperina sp. 2 'long call'	*Austrochaperina* sp. 2 'long call'	*Austrochaperina fulva*
Austrochaperina sp. 1 'short call'	*Austrochaperina laurae*	*Austrochaperina laurae*
Callulops sp.	*Callulops omnistriatus*	*Callulops omnistriatus*
Callulops wilhelmanus	*Callulops wilhelmanus*	*Callulops wilhelmanus*
Choerophryne sp. 3 'buzz call'	*Choerophryne alainduboisi*	*Choerophryne alainduboisi*
Choerophryne brevicrus	*Choerophryne brevicrus*	*Choerophryne brevicrus*
Choerophryne burtoni	*Choerophryne burtoni*	*Choerophryne burtoni*
Choerophryne sp. 5 'lowland clicker'	*Choerophryne crucifer*	*Choerophryne crucifer*
Choerophryne sp. 4 'montane clicker'	*Choerophryne multisyllaba*	*Choerophryne multisyllaba*
Choerophryne murrita	*Choerophryne murrita*	*Choerophryne murrita*
Choerophryne sp. 1 'arboreal'	*Choerophryne* sp. 1 'arboreal'	*Choerophryne* sp. 1 'arboreal'
Choerophryne sp.2 'tiny'	*Choerophryne* sp. 2 'tiny'	*Choerophryne* sp. 2 'tiny'
Cophixalus sp. 5'peeping call'	*Cophixalus* sp. 5 'peeping call'	*Cophixalus cateae*
Cophixalus wempi	*Cophixalus wempi*	*Cophixalus wempi*
Cophixalus sp. 1 'musical call'	*Cophixalus* sp. 1 'musical call'	*Cophixalus* sp. 1 'musical call'
Cophixalus sp. 2 'tiny A'	*Cophixalus* sp. 2 'tiny'	*Cophixalus* sp. 2 'tiny A'
Cophixalus sp. 3 'tiny B'	*Cophixalus* sp. 3 'tiny B'	*Cophixalus* sp. 3 'tiny B'
Oreophryne? sp. 5 'loud grunter'	*Cophixalus* sp. 6 'loud grunter'	*Cophixalus* sp. 5 'loud grunter'
*Copiula*sp. 1 '2-note call'	*Copiula* sp. '2-note call'	*Copiula bisyllaba*
not detected in 2015	*Hylophorbus richardsi*	*Hylophorbus richardsi*
Hylophorbus sp. 1 'small'	*Hylophorbus* sp. 1 'slow call'	*Hylophorbus* sp. 1 'slow call'
*Hylophorbus*sp. 2 'large'	*Hylophorbus* sp. 2 'fast call'	*Hylophorbus* sp. 2 'fast call'
Liophryne schlaginhaufeni	*Liophryne schlaginhaufeni*	*Liophryne schlaginhaufeni*
Oreophryne anamiatoi	*Oreophryne anamiatoi*	*Oreophryne anamiatoi*
Oreophryne sp. 4 'yellow-spots'	*Oreophryne flavomaculata*	*Oreophryne flavomaculata*
Cophixalus sp. 4'rasping call'	*Oreophryne* sp. 6 'rasping call'	*Oreophryne nicolasi*
Oreophryne notata	*Oreophryne notata*	*Oreophryne notata*
not distinguished in 2015	not distinguished in 2017	*Oreophryne* sp. cf. *notata*
Oreophryne oviprotector	*Oreophryne oviprotector*	*Oreophryne oviprotector*
Oreophryne sp. 3 'slow peeper'	*Oreophryne pseudunicolor*	*Oreophryne pseudunicolor*
Oreophryne sp. 1 'tiny'	removed	removed
Oreophryne sp. 2 'ratchet call'	*Oreophryne* sp. 2 'ratchet call'	*Oreophryne* sp. 2 'ratchet call'

2015	2017	2019
MICROHYLIDAE	**MICROHYLIDAE**	**MICROHYLIDAE**
Sphenophryne cornuta	*Sphenophryne cornuta*	*Sphenophryne cornuta*
Xenorhina sp.	*Xenorhina* sp. 1 'slow call'	*Xenorhina* sp. 1 'slow call'
not distinguished in 2015	*Xenorhina* sp. 2 'fast call'	*Xenorhina* sp. 2 'fast call'
Gen. nov. sp. nov.	Gen. nov. sp. nov.	Gen. nov. sp. nov.

Chapter 2 – Camera trap monitoring of terrestrial mammals and birds

Iain A. Woxvold, Salape Tulai, Samson Yama and Alfred Mani

Ifola (*Dendrolagus* [*dorianus*] *notatus*)

Summary

Background and aims

Terrestrial (ground-dwelling) 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. Wildlife most at risk in Papua New Guinea (PNG) include a variety of medium- to large-bodied species such as echidnas, wallabies, tree kangaroos and cassowaries, many of which are listed by the IUCN as Threatened or Near Threatened with extinction. However, monitoring terrestrial species presents a challenge as 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, as they are effective at detecting rare and elusive species and they provide standardised datasets that can be used to address a variety of ecological questions. Here we present the results of repeat camera trap surveys undertaken in two Biodiversity Assessment Areas (BAAs) in upland sectors of the PNG LNG Upstream Project Area in 2017 and 2019. In each sampling year, 80 camera traps were deployed across four sites (two sites in each BAA) for a period of 89–107 days. Objectives of the camera trap monitoring study are:

1. To improve our understanding of vertebrate diversity in sampling areas.

2. To monitor trends in resident wildlife populations over time.

3. To examine habitat preferences of wildlife in relation to proximity to Project infrastructure ('edge effects').

Major results

Objective 1—To date, more than 94 species have been documented in 11,110 independent photographic events recorded over 13,733 sampling days. Results of the 2019 survey include six species newly reported from the BAAs and one new record for the Kikori Basin – Shaw Mayer's Shrew Mouse (*Pseudohydromys ellermani*). Biennial data are provided for seven IUCN listed species, including: four Threatened species – the Eastern Long-beaked Echidna (*Zaglossus bartoni*), Pademelon (*Thylogale* sp.), Ifola (*Dendrolagus notatus*) and Goodfellow's Tree Kangaroo (*D. goodfellowi*); two Near Threatened species – New Guinea Quoll (*Dasyurus albopunctatus*) and Small Dorcopsis (*Dorcopsulus vanheurni*); and one Data Deficient species – Woolley's Three-striped Dasyure (*Myoictis leucura*). The Small Dorcopsis was the most frequently camera trapped of all species with 1,200 photographic events in 2019.

Objective 2— We used three types of surrogate population estimate to monitor population trends between years (based on data availability, and in decreasing of order of preference) – occupancy estimates, activity rates and naïve occupancy rates. Significant declines in occupancy estimates or activity rates were observed for five bird species at individual sites or BAAs. In addition, naïve occupancy measures fell sharply for three IUCN listed mammals – the Eastern Long-beaked Echidna and Pademelon at Arakubi, and Woolley's Three-striped Dasyure at KP107. An increase in population estimate was recorded for two IUCN listed mammals at KP107 – the Small Dorcopsis and Ifola. The number of days in which humans and/or dogs were detected increased markedly from 2017 to 2019 at BAA 2 sites, but was similar in both years at BAA 1 sites.

Objective 3—Animal activity rate was correlated with distance from infrastructure in 11 species at one or more sites. Edge avoidance patterns were demonstrated by eight species, being strongest at BAA 2 sites for Raffray's Bandicoot (*Peroryctes raffrayana*), Small Dorcopsis, Collared Brushturkey (*Talegalla jobiensis*) and Pheasant Pigeon (*Otidiphaps nobilis*). Six species displayed reverse-pattern edge effects, with higher rates of activity nearer to the forest edge. Reverse edge effects were the most common trend at BAA 1 and were the only patterns observed at the Hides High site.

Conclusions and recommendations

The value of camera traps in detecting rare and elusive species was reinforced during the second full season of camera trap sampling. Deployment time is sufficient to attain a near-complete census of the resident terrestrial bird and medium- to large-bodied mammal faunas in each sampling year.

The 2017–2019 dataset provides a useful baseline against which to measure future population trends. Despite notable changes in population estimates for some species, it is too early to draw conclusions as to the ongoing status of local populations because: (1) data from additional sampling years are required to improve inferential power in light of natural fluctuations in animal populations, and; (2) the 2017 and 2019 surveys were conducted at different times of year, so that seasonal effects may account for some of the observed changes.

The 2019 data consolidate most of the edge-response patterns first observed in 2017 and extend them to a number of additional species. Data collected on nine new environmental covariates in 2019 have improved model performance and our ability to make reliable inferences about behavioural responses to Project infrastructure. Edge avoidance was most clearly demonstrated at BAA 2, where some species may avoid near-edge environments due to the presence of degraded forest near infrastructure (particularly at Arakubi) and/or display an aversion to frequent human activity along roads and the pipeline ROW. The reverse-pattern edge effects commonly observed at BAA 1 are counter-intuitive for interior forest species. Causal factors are likely to be environmental rather than anthropogenic. Regardless of the cause, after two years of camera trap monitoring there is no compelling evidence that any terrestrial mammal or bird species avoid forest edge on Hides Ridge.

We recommend that the camera trapping program continue in 2021, and in subsequent survey years, because it provides a reliable method for detecting changes in population estimates of multiple rare, elusive and hunting sensitive species. However, surveys should take place at the same time of year to control for seasonal effects; we recommend reverting to the 2017 timing (May–August) to test for a potential reversal in the change of population estimates observed for some species. As far as practical, the biennial schedule should be maintained as fewer data points will extend the time before which reasonable inferences can be made about population trends.

The current sampling design – based on the clustering of 20 cameras within sites of c. 70–180 ha – is suitable for modelling edge effects but limits our ability to monitor wildlife population trends because: (1) it is not possible to draw conclusions as to the status of populations beyond the site scale, and; (2) the close spacing of many cameras constrains our ability to use the preferred occupancy modelling approach. Future datasets are likely to yield diminishing returns in terms of revealing novel edge response patterns, particularly on Hides Ridge (BAA 1). We therefore recommend that the sampling design be expanded (using the same number of cameras) within BAAs beyond the site scale, as far as practical, to increase sampling of important local populations and to improve the scope for occupancy modelling. Details are provided regarding possible expansion scenarios.

Introduction

Tropical forest faunas include many ground-dwelling ('terrestrial') species that are vulnerable to anthropogenic change. Population declines have been observed in terrestrial mammals and birds in response to habitat fragmentation and degradation (Michalski and Peres 2007; Burivalova et al. 2014), over-hunting (Bennett and Robinson 2000; Peres and Palacios 2007) and the presence of invasive species such as feral dogs (Cassano et al. 2014; Lessa et al. 2016). Many medium- to large-bodied species are specifically targeted by hunters (Jerozolimski and Peres 2003; Sampaio et al. 2010), and those with low population densities and slow life histories are often the most susceptible to over-harvesting (Bodmer 1995; Peres and Palacios 2007) and to habitat change (Michalski and Peres 2007; Costantini et al.

2016). Although not specifically targeted by hunters, a variety of terrestrial birds are also known to be sensitive to the fragmentation and degradation of tropical forest habitat (Thiollay 1997; Lambert and Collar 2002; Peh et al. 2005).

New Guinea's upland forests support a rich assemblage of endemic terrestrial mammals and birds. Many of the larger species have suffered population declines as a result of hunting and habitat loss (e.g. Johnson et al. 2004; Eldridge and Coulson 2015; Nicol 2015) and are listed as Threatened or Near Threatened on the IUCN *Red List of Threatened Species* (IUCN 2020). However, population status varies markedly at the local scale (species extirpated near some settlements may be fairly common in remote areas) and the response of various species to individual stressors remains poorly known.

Given their susceptibilities, terrestrial species serve as useful surrogate indicators of ecosystem health and connectivity (e.g. Crooks et al. 2011; Peters et al. 2015) and present suitable monitoring targets in the vicinity of anthropogenic development projects. Yet collecting sufficient data to monitor populations presents a challenge – animals are often difficult to census in tropical forest environments (Ahumada et al. 2007) and many terrestrial species are rare or elusive (O'Brien and Kinnaird 2008).

Camera traps are increasingly used as an efficient and non-invasive tool in the study of terrestrial wildlife populations (Burton et al. 2015). Able to run continuously for long periods without human intervention, they are effective at detecting rare and elusive species (e.g. Dinata et al. 2008; Beirne et al. 2017; Thomas et al. 2020) and they provide standardised datasets that can be used to address a variety of ecological questions – among their many applications, camera trap studies have been used to estimate species richness and abundance (O'Connell et al. 2011; Rovero et al. 2014; Li et al. 2018), to examine habitat preferences (Pettorelli et al. 2010; Martin et al. 2015; Zimbres et al. 2017), to monitor population trends over time (Blake et al. 2017; Beaudrot et al. 2019; O'Brien et al. 2019), and to investigate the impacts of roads and forest edges (Srbek-Araujo and Chiarello 2013; Rovero et al. 2017), feral animals (Murphy et al. 2017, 2018) and hunting and disturbance (Rao et al. 2005; Hegerl et al. 2015; Oberosler et al. 2017).

Following a pilot study in 2015 (Woxvold and Aplin 2017), in 2017 a biennial camera trap monitoring program was initiated within two Biodiversity Assessment Areas (BAAs; see Report Summary) in upland sectors of the PNG LNG Upstream Project Area (Woxvold and Legra 2019a). Camera trap arrays were deployed in the vicinity of Project infrastructure to meet three main objectives:

1. To improve our understanding of vertebrate diversity present in sampling areas.

2. To monitor trends in resident wildlife populations over time.

3. To examine habitat preferences of wildlife in relation to proximity to Project infrastructure ('edge effects').

This report integrates and interprets the results of the first two camera trap monitoring surveys undertaken in 2017 and 2019.

Methods

Study sites

Camera traps were deployed at two sites within each BAA (Figures 3–4 & 6–7 of Report Summary):

- BAA 1 – at 'Hides Low' immediately northwest of Wellpad D, and at 'Hides High' between Wellpad E and Wellpad G.

- 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.

The sites differ in altitude, with camera positions spanning an altitudinal range of more than 1,800 m (922–2,731 m; Table 2.1). 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 dolines and valleys. The overlying vegetation is described in detail in Venter and Ona (2017). 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

Twenty white-flash digital camera traps (Reconyx PC850) were deployed at each site in each sampling year. To test for possible edge effects (Objective 3), 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). To maximise inference potential in population monitoring (Objective 2), cameras were placed in the same position in both years wherever possible. Fifteen positions used in 2017 were relocated in 2019 due to security concerns (Hides Low – seven cameras lost) or to site damage resulting from garden construction (Arakubi – 2) or from an earthquake in 2018 (Arakubi – 1, KP107 – 4, Hides High – 1). The position of functioning camera traps (see below for summary of losses and malfunctions) at each site/year is mapped in the Report Summary and in Appendix 2.2. Distance to the nearest camera within sites ranged from 25–365 m. Between sites, camera arrays were separated by a minimum distance of 4.5 km at BAA 1 (Hides Low–Hides High) and 2.7 km at BAA 2 (Arakubi–KP107).

Camera traps operated 24 hours/day, and were programmed to maximum detection sensitivity and to take three photographs at each trigger with the minimum amount of rest time between triggers (<2 seconds). Each camera was fixed to a tree or freshly cut wooden pole 15–25 cm above the ground and directed along an animal trail in an area of flat or gently sloping ground. Most positions were located on ridges/spurs or on hill-slope terraces; valley floors and gullies were avoided as these were often difficult to reach in the steep terrain and in order to minimise variation in detectability associated with local topographic effects. Site disturbance was restricted to removal of low vegetation (herbs, ferns, etc.) from 2–3 m directly in front of the camera. Camera positions 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, and from 10 August to 2 December 2019. Table 2.1 summarises the trapping effort at each site/year. Of 160 cameras deployed across both years, 14 yielded no data due to theft (11 cameras) or malfunction soon after deployment (three cameras). Most of the remaining cameras (2017 – 60/71; 2019 – 65/75) operated for the full deployment period of 89–107 days. However, two types of event limited data availability from 21 functioning units. First, camera malfunction or obstruction of view by fallen or growing vegetation resulted in partial datasets (35–93 days) from 15 cameras (2017 – 9; 2019 – 6). Second, mud splashes during heavy rain led to the accumulation of dirt on the lens covers and infrared detectors of eight cameras (2017 – 3; 2019 – 5; two of which also lost some data under the previous category), thereby lowering detector sensitivity and making it impossible to identify some images. One of these units (at Arakubi in 2019) was affected for the entire sampling period. The remaining seven affected cameras took clear images for periods of 26–77 days. Data collected during periods of reduced camera performance are included in the species summary totals for each site; however, because changes in detectability may influence the interpretation of animal behaviour patterns, data from these periods were excluded from activity rate and occupancy models. The overall trapping effort across all site/years was 13,733 camera days, 13,304 of which were included in statistical models.

Table 2.1. Altitudinal range and camera trapping effort at each site

Site	Elevation (m asl)	No. operating cameras 2017/2019	Camera days 2017/2019*		
			Total	Mean	Range
BAA 1					
Hides Low	2,192–2,389	13/17	1,186/1,735	91.2/102.1	76–97/84–107
Hides High	2,645–2,731	20/19	1,824/1,799	91.2/94.7	62–98/48–103
BAA 2					
Arakubi	922–1,052	19/19	1,729/1,748	91.0/92.0	35–101/38–98
KP107	1,297–1,398	19/20	1,809/1,903	95.2/95.2	40–101/93–98
Total		*71/75*	*6,548/7,185*	*92.2/96.0*	*35–101/38–107*

* Number of days operating, excluding deploy and collection dates and malfunction periods, but including periods of reduced detectability.

Analysis

Data preparation

Data organisation and all analyses were performed in R (R Development Core Team 2015).

All bird and most mammal images were identified by IW. Ken Aplin contributed to the identification of rodent and bandicoot images in 2017. Kristofer Helgen (Australian Museum) and Kevin Rowe (Museums Victoria) assisted with the identification of newly recorded rodent taxa in 2019. Photographs of uncertain identity were excluded from analysis. Images and associated metadata were managed for analysis using the 'camtrapR' package (Niedballa et al. 2016).

For all taxa, we calculated the number of independent photographic 'events' per camera. Within-camera events were considered independent where consecutive pictures of the same species were taken more than 60 minutes apart (Burton et al. 2015). Multiple events were scored within 60-minute periods where more than one individual was seen in a single photograph or sequence.

In order not to over-estimate forest incursions by hunting parties, events for humans and dogs were limited to one record per-site/day regardless of the number of cameras on which they appeared in a single day. Anthropogenic events leading to the loss of cameras or garden construction were not included.

Terrestrial species are the most suitable for monitoring under the current approach, since lower image rates result from incidental trapping of predominantly arboreal species. Analyses addressing Objectives 2 and 3 were therefore limited to terrestrial taxa.

Covariates

In order to examine potential edge effects (Objective 3), we assessed the relationship between animal activity rates and distance from Project infrastructure while controlling for influential environmental covariates. Five measures of distance from Project infrastructure were assessed:

- Distance from the nearest clearing (road, pipeline ROW, wellpad, quarry or sidecast) – as a continuous measure (DClr), or as categorical measures comparing activity within distance classes of <50/>50 m (LT50) and <100/>100 m (LT100).

- Distance from the nearest road – as a continuous measure (DRd), or as a categorical measure comparing activity within <100/>100 m distance classes (LT100Rd).

We measured the following environmental covariates at each camera position. Terrain measures (local relief) – measured as the difference between the highest and lowest elevations present within 20 m, 50 m and 100 m of the camera (LR20, LR50, LR100); elevation data were taken from 5 m LiDAR Digital Elevation Model (DEM). Canopy height (CnpHt) – taken as the average height of the three tallest trees located within 30 m of the camera position, as measured by a Nikon Forestry Pro laser range finder. Remaining covariates were measured within a 20 m x 20 m plot established by arranging two 20 m cords perpendicular to one another in cross-hair fashion with the centre point at the camera position. Tree density – calculated as the number of trees >10 cm (TrSm) and >30 cm (TrLge) diameter at breast height (dbh) within the plot. Understorey density – measured using a 2 m pole with alternating colours in 10 cm segments and held vertically at the four ends of each of the two cords (10 m from the camera position); densities below 1 m (UD1) and below 2 m (UD2) were calculated by counting the number of wholly visible coloured segments in each height class. Leaf litter depth (LfLit) – measured with a ruler as the distance between the leaf litter surface and underlying soil or root mass, at the nearest three 2 m intervals along each of the four cord axes emanating from the camera position (12 measures at each camera position). Proportion of the plot ground surface covered by moss (Moss), rock (Rock) and large woody debris (>10 cm diameter) (Logs) – estimated by eye and ordered categorically as: 0 (none visible), 1 (0–2%), 2 (2–5%), 3 (5–10%), 4 (10–20%), 5 (20–35%), 6 (35–50%), 7 (50–65%), 8 (65–80%), 9 (>80%).

We tested for correlations among all covariates in order to avoid collinear terms appearing together in the same models. Collinearity among numeric variable-pairs was tested using the Pearson Correlation Coefficient (PCC). Correlations between ordinal (ordered categorical) terms, and between ordinal and numerical terms, were examined using Kendall's rank correlation coefficient. Where final models included three or more covariates, we tested for higher-order multicollinearity using the 'mctest' R package.

Activity rates

Photographic rates were used: (1) to monitor population trends by assessing changes in animal activity between years (Objective 2) in cases where occupancy modelling could not be applied (see below), and; (2) to test for edge effects by assessing habitat preferences in terms of spatial proximity to Project infrastructure (Objective 3). For each species of interest, an activity index was calculated from the daily number of events per camera.

Generalised Linear Mixed Models (GLMMs) were used to model activity rates of terrestrial species across their distribution (1–4 sites) where sufficient data were available (generally ≥16–20 events per site/year; models for taxa with fewer events often fail to converge: this study; Martin et al. 2015; Oberosler et al. 2017). Site and camera position were treated as random effects, and because we frequently detected overdispersion, we routinely used a quasi-Poisson model structure that included an additional observation-level random term (camera-year).

Objective 2—To assess trends in activity between years, the dataset was contracted to those camera positions that were sampled in both years (Arakubi – 16, KP107 – 16, Hides Low – 13, Hides High – 18). Environmental covariates were not included in these models as there was assumed to be no change between years in the conditions present at each position.

Objective 3—When assessing habitat preferences and edge effects, data were used from all camera positions at which the full complement of covariates was measured (Arakubi – 18, KP107 – 20, Hides Low – 17, Hides High – 20). Most species' activity was modelled at the site level, as different covariates influence a species' activity rate at each site. In the one exception, Dwarf Cassowary (*Casuarius bennetti*) activity was assessed across both BAA 2 sites to ensure sufficient data for modelling. Models were initially compared using the dredge function in 'MuMIn' (Bartoń 2015). We used a common set of models for each species as determined by all covariate combinations excluding collinear pairs. Models were ranked using Second-order Akaike Information Criterion (AIC_c) and their associated Akaike weights (w_i). 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). Model

averaging was used to assess the 'relative importance' (sum of w_i) of each covariate from a candidate set of models with $\Delta AIC_c < 6$. Covariate coefficient point estimates and standard errors were generated using full model averaging (Grueber et al. 2011; Symonds and Moussalli 2011). Collinear distance and terrain measures compete with one another for weight among the best-ranked models. For each species-site, models were therefore ultimately compared using only the best performing distance and terrain measures, as initially determined by model averaging under the full covariate set. Final models were constructed using the most influential covariates with back-removal of non-influential terms (at $P>0.10$).

Occupancy

Occupancy is the proportion of area or sites that is occupied by a species. Naïve occupancy is the proportion of cameras at each site at which a species is detected.

Model-based occupancy analysis involves the estimation of occupancy (ψ) across sampled positions while accounting for imperfect detection – the possibility that a species is present but remains undetected. This is achieved by creating capture histories for each sampling unit (e.g. camera) by dividing the sample 'season' into a series of sampling 'occasions'. The probability of detection (p) is then estimated and used to inform the occupancy measure. By accounting for variation in p, occupancy estimation is often considered to be a more reliable estimate of population density than are 'relative abundance indices' (RAIs) such as activity rate models based on photographic rates (Burton et al. 2015; Sollmann 2018). Where the data permitted, we therefore prioritised the use of multi-season occupancy modelling (MacKenzie et al. 2006) to monitor population trends between years using the package 'unmarked' (Fiske and Chandler 2011). We used the same dataset that was applied to comparing activity rates between years (cameras sampled in both years). Capture histories for each monitoring year were created by registering presence/absence data (0 or 1) over repeat sampling occasions of 1 day (Rovero and Spitale 2016).

Occupancy modelling assumes that sampling stations are independent. Our sampling arrays violate the assumption of independence as individual animals may be photographed at more than one camera station within a single sampling season (year). To account for this, we grouped cameras within sites into 'areas' whose nearest cameras were no less than 250 m apart (4–5 areas per site, 1–8 cameras per area). We then modelled occupancy trends at the area scale in a subset of species whose home range, based on published estimates, is considered unlikely to span more than one area (based on a circular home range of c. 5 hectares (ha)), including bandicoots (Dickman 2015) and birds with body mass less than c. 100 g (e.g. Jansen 1999; Lindsell 2001). To ensure sufficient sample size, we further restricted our assessment to the BAA level, and thus to species that were present at both sites within a BAA.

For species analysed across both BAAs, occupancy, colonisation and extinction parameters were all modelled for variation at the BAA level. For species analysed in a single BAA, occupancy, colonisation and extinction parameters were all held constant. A default 'Site+Year' structure was applied to the detectability measure; site was removed from the model structure in cases where one or more sites had all areas occupied or unoccupied. We applied a bootstrapped goodness of fit test using 1,000 simulations to test the data-model relationship. Scores with a Chi-squared value outside of the 0.1–0.9 range were rejected, in which case we reverted to activity rate model procedures. Occupancy modelling was applied to two mammal and six bird taxa. Results are reported for four bird species with suitable goodness of fit test results.

P-values were not used to test the significance of change in occupancy between years. Rather, a change in occupancy estimate was considered 'significant' where both the lower and upper bounds of the estimated 'growth' rate's 95% confidence intervals had the same sign (positive or negative).

Conventions

Taxonomic order and nomenclature follow the *Handbook of the Mammals of the World* (Wilson and Mittermeier 2015; Wilson et al. 2017) in most cases and the *IOC World Bird List* (Gill and Donsker 2020). An exception is made for the local

subspecies of Doria's Tree Kangaroo (*Dendrolagus dorianus notatus*), which is assessed separately by the IUCN as the Ifola (*D. notatus*) and classified as Endangered (IUCN 2020). Invasive alien mammals appear after native species in tabulated lists.

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. Scientific names are used 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). The scientific name appears with the English name in photographs, tables and appendices.

Results

Recorded diversity (Objective 1)

A total of 11,110 independent photographic events was recorded over a sampling period of 13,733 camera days (both years). More than 94 vertebrate species have now been documented by camera trap within the BAAs, including 59 bird species, 34 mammal taxa and one reptile. All taxa photographed in 2017 and 2019 under the full sampling program are listed in Appendix 2.1 along with their conservation status and the number of independent photographic events recorded at each site. A selection of taxa is shown in Figures 2.8–2.43. The total number of species photographed is considered to be more than 94 since a number of the mammal taxa are only identifiable to genus level in the images; for example, multiple species of *Murexia*, *Paramelomys* and *Rattus* are known to occur within the study area (Aplin and Opiang 2017), and given changes in community structure with elevation, more than one species in each of these genera is believed to have been photographed.

Four mammal and 11 bird species were newly camera trapped in 2019 (cf. 2017: Table 2.2). Although four of these species (three rodents and one bird) could not be identified to species, none can be confused with taxa recorded in 2017. Most of the newly imaged taxa have been recorded previously within the Kikori Basin and locally within the BAAs.

One species – Shaw Mayer's Shrew Mouse (*Pseudohydromys ellermani*) – is previously unreported from the Kikori Basin (Namo 2004; Crome 2008; Aplin and Opiang 2017). This small rodent was photographed at 2,235 m asl at Hides Low (Fig. 2.26).

Six species are newly reported from the BAAs in which they were photographed. Loria's Tree Mouse (*Pogonomys* cf. *loriae*) is not previously reported from BAA 2.). The remaining five species were previously camera trapped in BAA 2, but new BAA 1 data provide altitudinal range extensions – New Guinea Waterside Rat (*Parahydromys asper*) (at 2,695 m asl; previously to 2,200 m asl), White-tailed Giant Rat (*Uromys caudimaculatus*) (at 2,230 m asl; previously to 1,925 m asl), Collared Brushturkey (*Talegalla jobiensis*) (at 2,325 m asl; previously to 1,950 m asl), New Guinea Bronzewing (*Henicophaps albifrons*) (at 2,325 m asl; previously to 2,150 m asl) and Bare-eyed Rail (*Gymnocrex plumbeiventris*) (at 2,710 m asl; previously to 2,100 m asl) (Beehler and Pratt 2016; Denys et al. 2017).

Appendix 2.1 includes 57 taxa with predominantly or entirely terrestrial habits. Figures 2.1–2.2 show the number of independent photographic events taken for each terrestrial mammal and bird taxon in 2017 and 2019.

Table 2.2. Species newly camera trapped in 2019 and the number of photographic events at each site.

Species	Arakubi	KP107	Hides Low	Hides High
Mammals				
Mountain Cuscus (*Phalanger carmelitae*)				3
Loria's Tree Mouse (*Pogonomys* cf. *loriae*)		1		
New Guinea Waterside Rat (*Parahydromys asper*)				3
Shaw Mayer's Shrew Mouse (*Pseudohydromys ellermani*)			1	
Birds				
Barred Owlet-nightjar (*Aegotheles bennettii*)		2		
Dusky Lory (*Pseudeos fuscata*)		4		
Fan-tailed Berrypecker (*Melanocharis versteri*)			1	
Black Butcherbird (*Melloria quoyi*)	2			
Variable Shrikethrush (*Colluricincla fortis*)	1			
Sooty Thicket Fantail (*Rhipidura threnothorax*)	1			
Dimorphic Fantail (*Rhipidura brachyrhyncha*)			1	
Magnificent Bird-of-paradise (*Diphyllodes magnificus*)		2		
White-winged Robin (*Peneothello sigillata*)				2
Black-throated Robin (*Plesiodryas albonotata*)				1
Blue-faced(/Papuan) Parrotfinch (*Erythrura trichroa(/papuana)*)				2

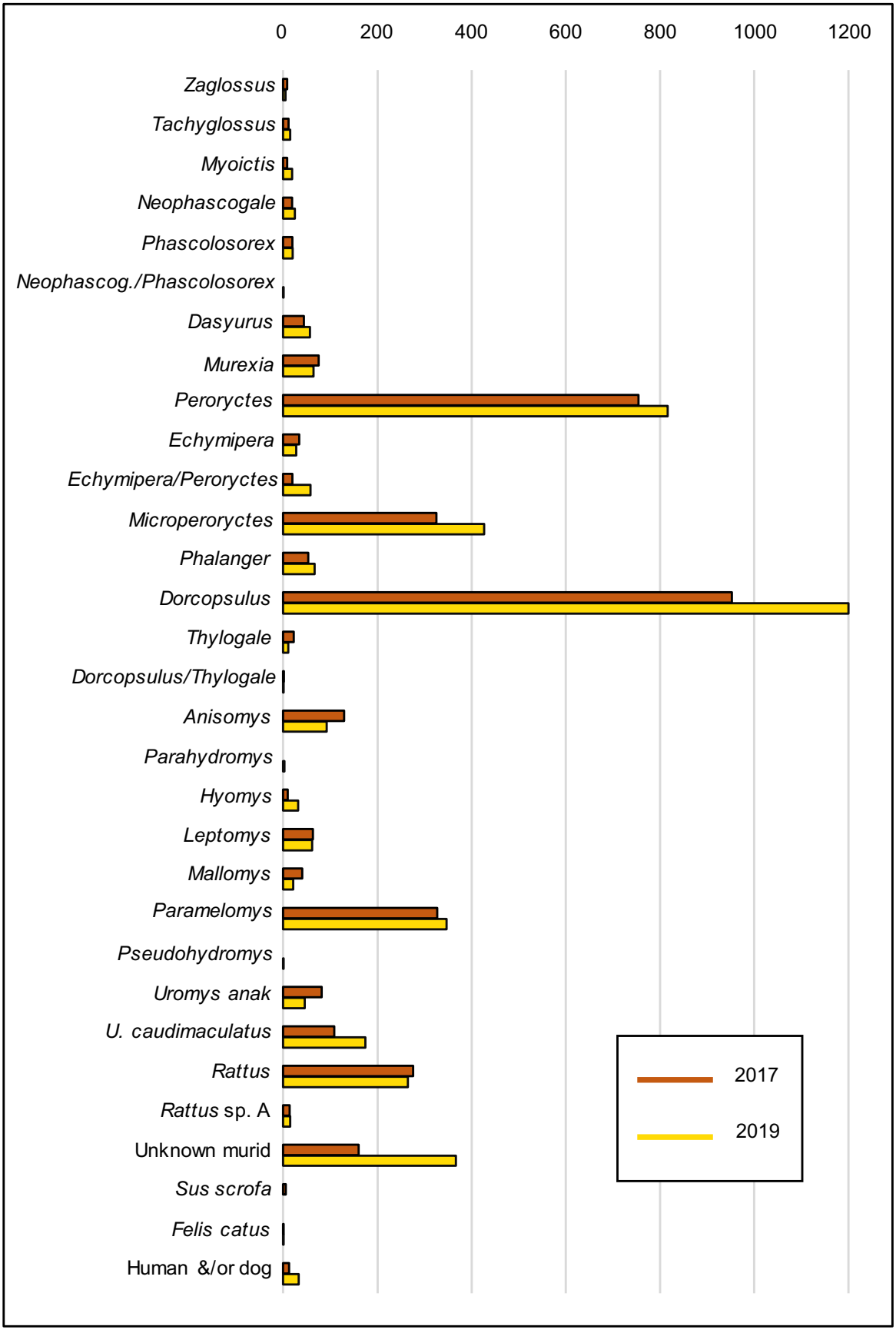

Figure 2.1. The number of independent photographic events of terrestrial mammals recorded in each sampling year.

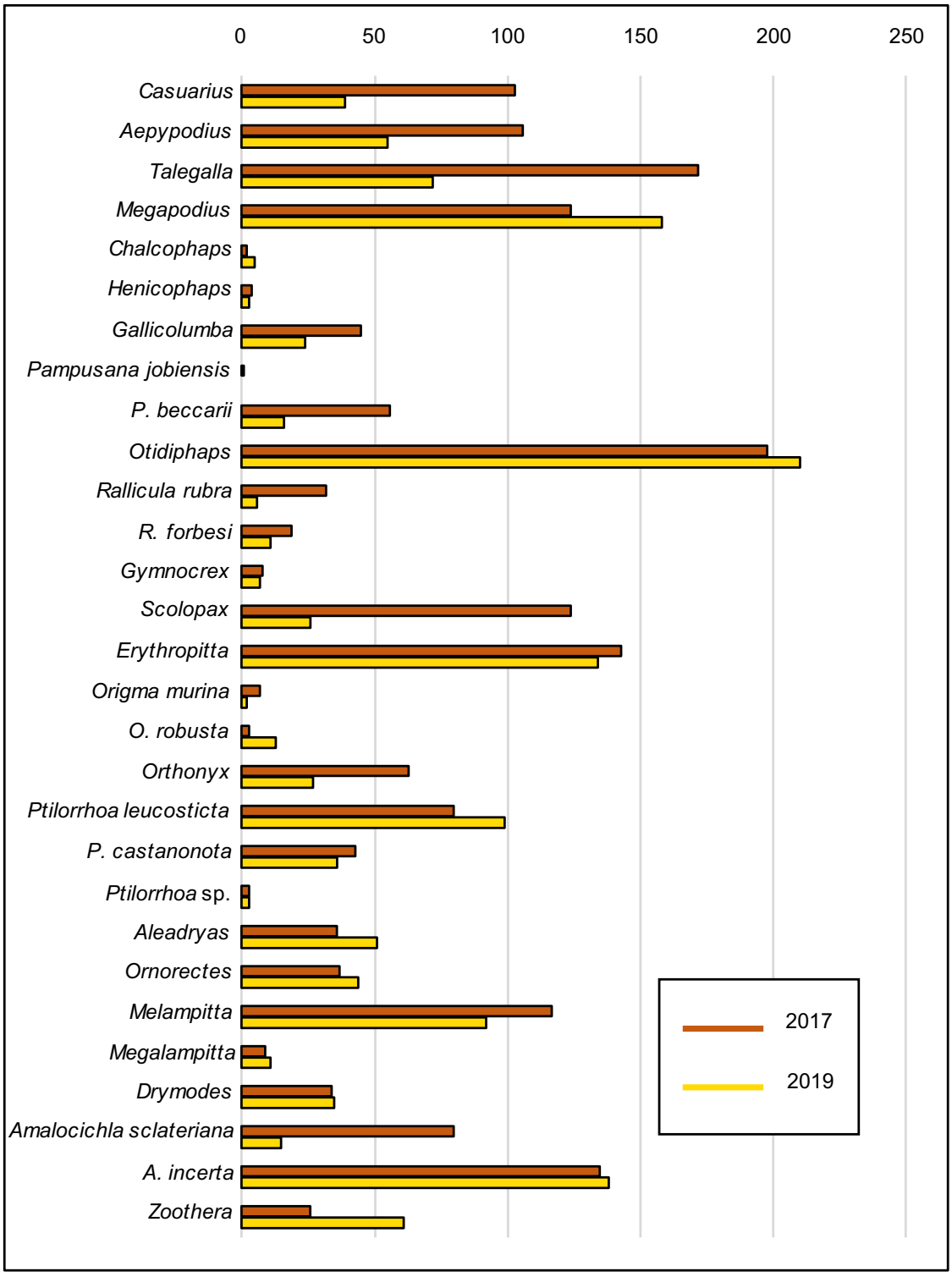

Figure 2.2. The number of independent photographic events of terrestrial birds recorded in each sampling year.

Population monitoring (Objective 2)

Annual model-based occupancy estimates are shown for four species in Figure 2.3. Figure 2.4 shows annual activity indices for 15 species for which model-based occupancy estimates were inappropriate (due to home range size or poor goodness of fit results in occupancy testing). Annual naïve occupancy measures are shown in Figure 2.5 for five species of conservation significance for which too few data were available to generate statistical models of occupancy or activity rate. Significance testing can only be applied to species represented in Figures 2.3 and 2.4.

Observed trends varied both between species and among sites within species. Most comparisons indicate a steady state between years (Figures 2.3–2.5).

One species – the Papuan Logrunner (*Orthonyx novaeguineae*) – showed a significant reduction in occupancy rate at BAA 1 in 2019 (Figure 2.3). This was largely driven by a steep decline of recorded events at Hides High (Appendix 2.1), with a drop in naïve occupancy at that site from 0.45 to 0.05.

Six species showed a significant change in activity rate at one or more sites in 2019. In most cases the change was restricted to a single site. Two species – Ground Cuscus (*Phalanger gymnotis*) and Pheasant Pigeon (*Otidiphaps nobilis*) – showed an increase in activity at KP107. Activity rate declined significantly between years for Collared Brushturkey at KP107, and for the Chestnut Forest Rail (*Rallicula rubra*) and Greater Ground Robin (*Amalocichla sclateriana*) at Hides High. Dwarf Cassowary activity was significantly lower in 2019 at both BAA 2 sites (Arakubi and KP107).

Data were sufficient to model activity rates for two conservation listed species. There was no significant change in the activity rates of New Guinea Quoll (*Dasyurus albopunctatus*) or Small Dorcopsis (*Dorcopsulus vanheurni*) at any site, although there was a trend towards higher dorcopsis activity at KP107 in 2019 (Fig. 2.4; P=0.103). For both of these species, naïve occupancy was also steady between years: site-level measures for New Guinea Quoll ranged from 0.30–0.60 in 2017 and from 0.24–0.58 in 2019.

Among other conservation listed species, in 2019 there were marked declines in naïve occupancy rates for the IUCN Vulnerable Eastern Long-beaked Echidna (*Zaglossus bartoni*) and the Pademelon (*Thylogale* sp.) at Arakubi (Figure 2.5), from records on 32% and 21% of cameras respectively in 2017, to none in 2019. Naïve occupancy of Woolley's Three-striped Dasyure (*Myoictis leucura*) fell sharply at KP107 in 2019. Conversely, naïve occupancy of the Endangered Ifola more than doubled at KP107, where it was recorded on 40% of cameras in 2019.

Maps in Appendix 2.2 show the camera positions at which most conservation listed species were photographed in each site and year. Recorded locations of the Small Dorcopsis are not mapped, as this species was photographed on all cameras in 2019 and on all but two cameras in 2017.

Figure 2.6 shows the total number of days that humans and/or dogs were photographed at each site in each sampling year. The number of incursion days was similar in both years at Hides Low and Hides High (BAA 1), but was much higher at Arakubi and at KP107 (BAA 2) in 2019.

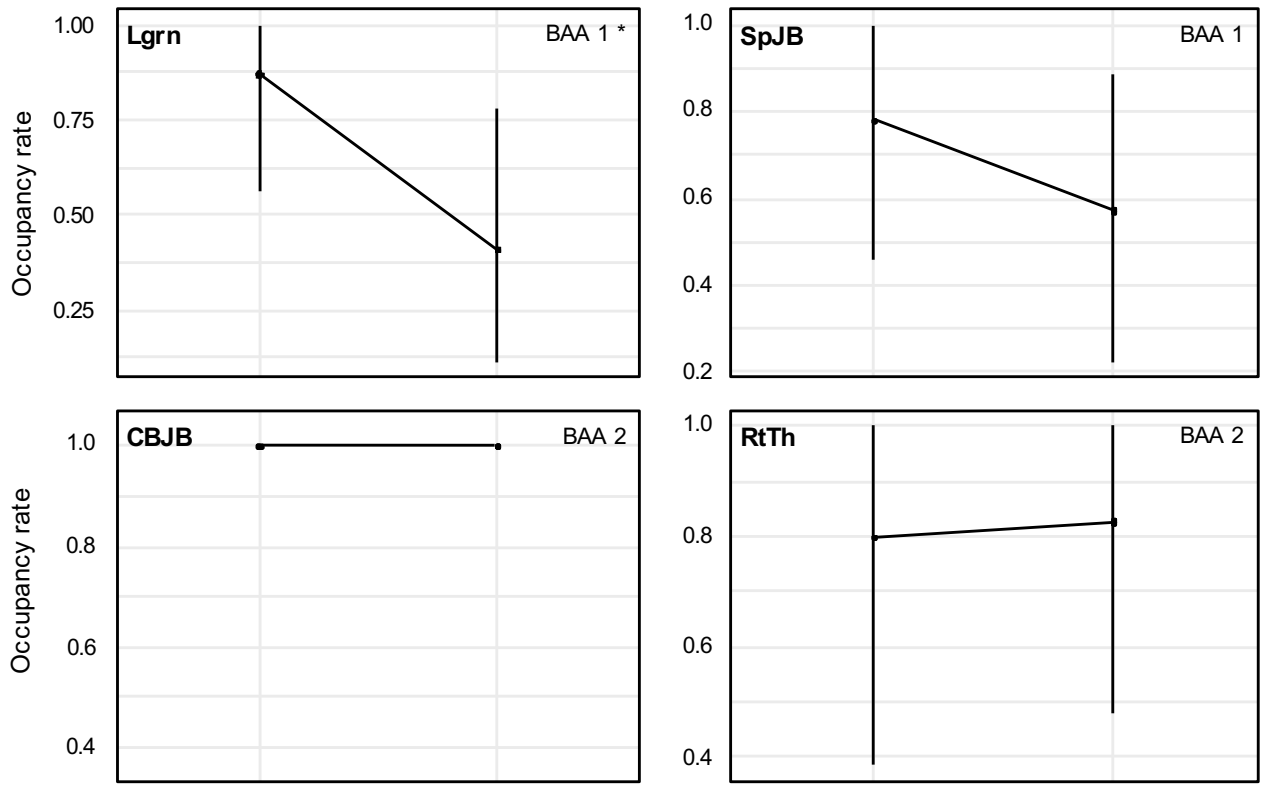

Figure 2.3. Change in occupancy rate between years. Numbers on the Y axis show the proportion of 'areas' occupied within each BAA (see Methods). Significant results are indicated by an asterisk next to the BAA name. Species codes: Lgrn – Papuan Logrunner; SpJB – Spotted Jewel-babbler; CBJB – Chestnut-backed Jewel-babbler; RtTh – Russet-tailed Thrush.

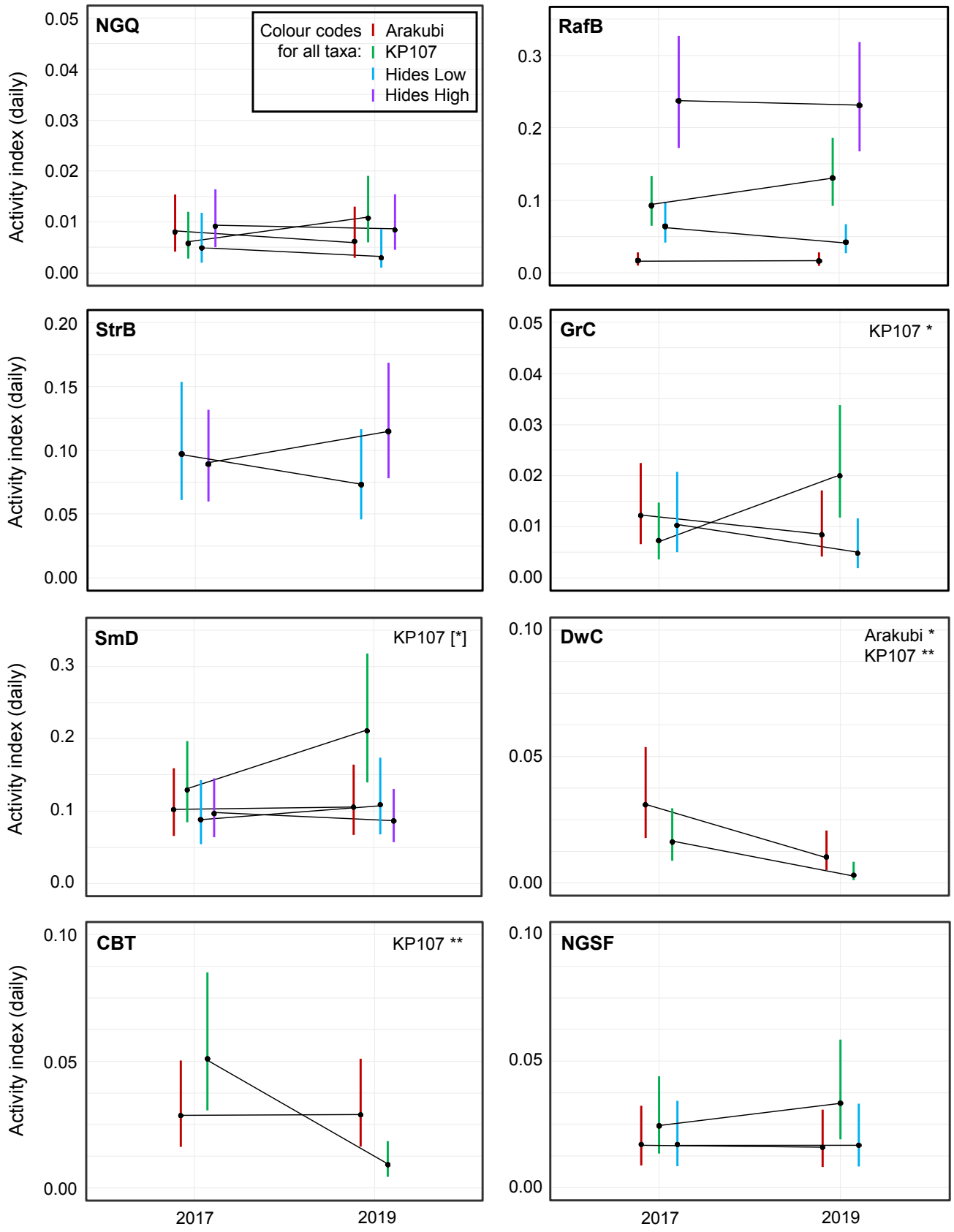

Figure 2.4. Change in animal activity rate between years. Species codes: NGQ – New Guinea Quoll; RafB – Raffray's Bandicoot; StrB – Striped Bandicoot; GrC – Ground Cuscus; SmD – Small Dorcopsis; DwC – Dwarf Cassowary; CBT – Collared Brushturkey; NGSF – New Guinea Scrubfowl; PhP – Pheasant Pigeon; Rail – Forbes's Forest Rail at Hides Low, Chestnut Forest Rail at Hides High; NGW – New Guinea Woodcock; Pitta – Papuan Pitta; LMel – Lesser Melampitta; GGR – Greater Ground Robin; LGR – Lesser Ground Robin. Significance codes: [*] =0.05<P< 0.1; * =P<0.05; ** =P<0.01.

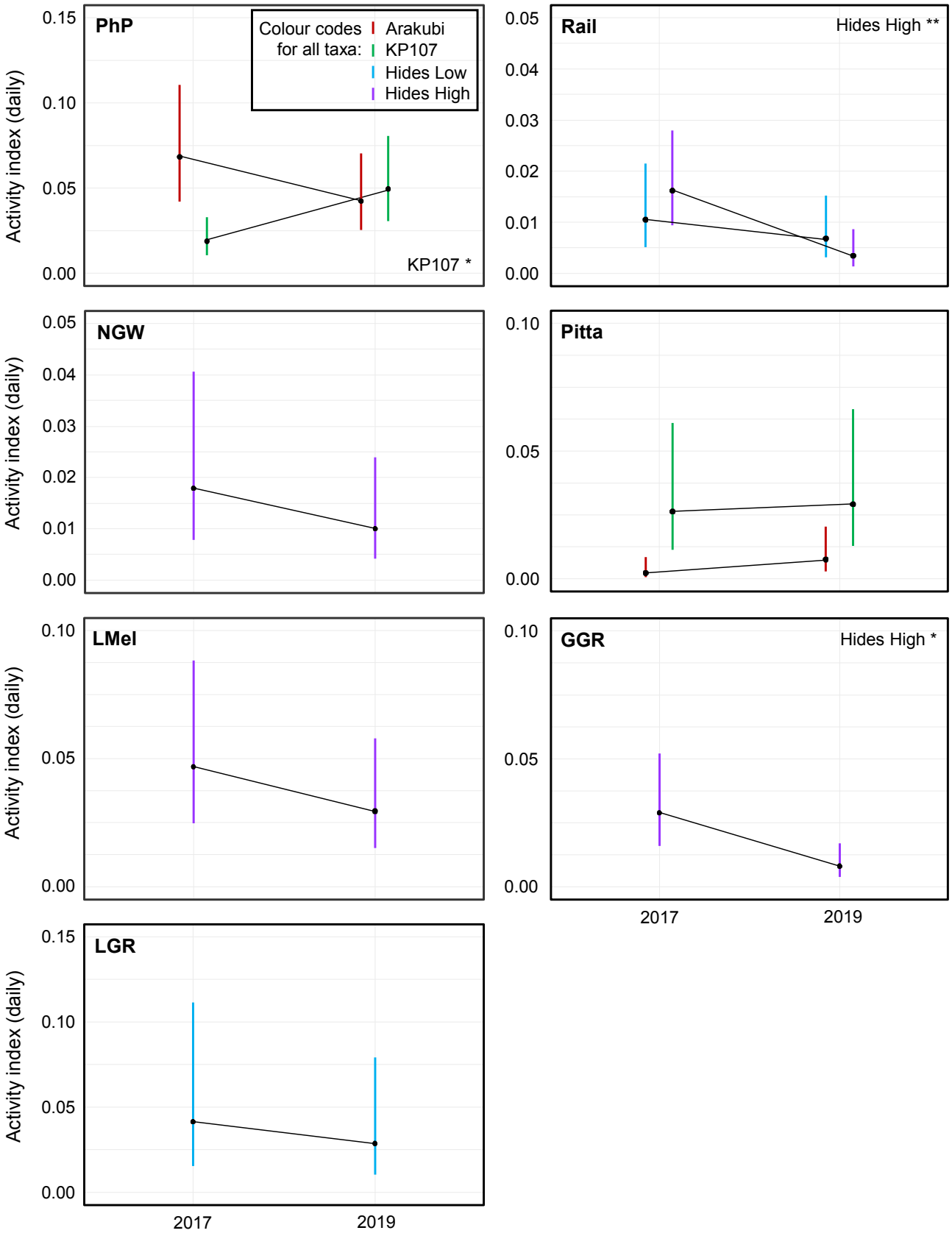

Figure 2.4. continued

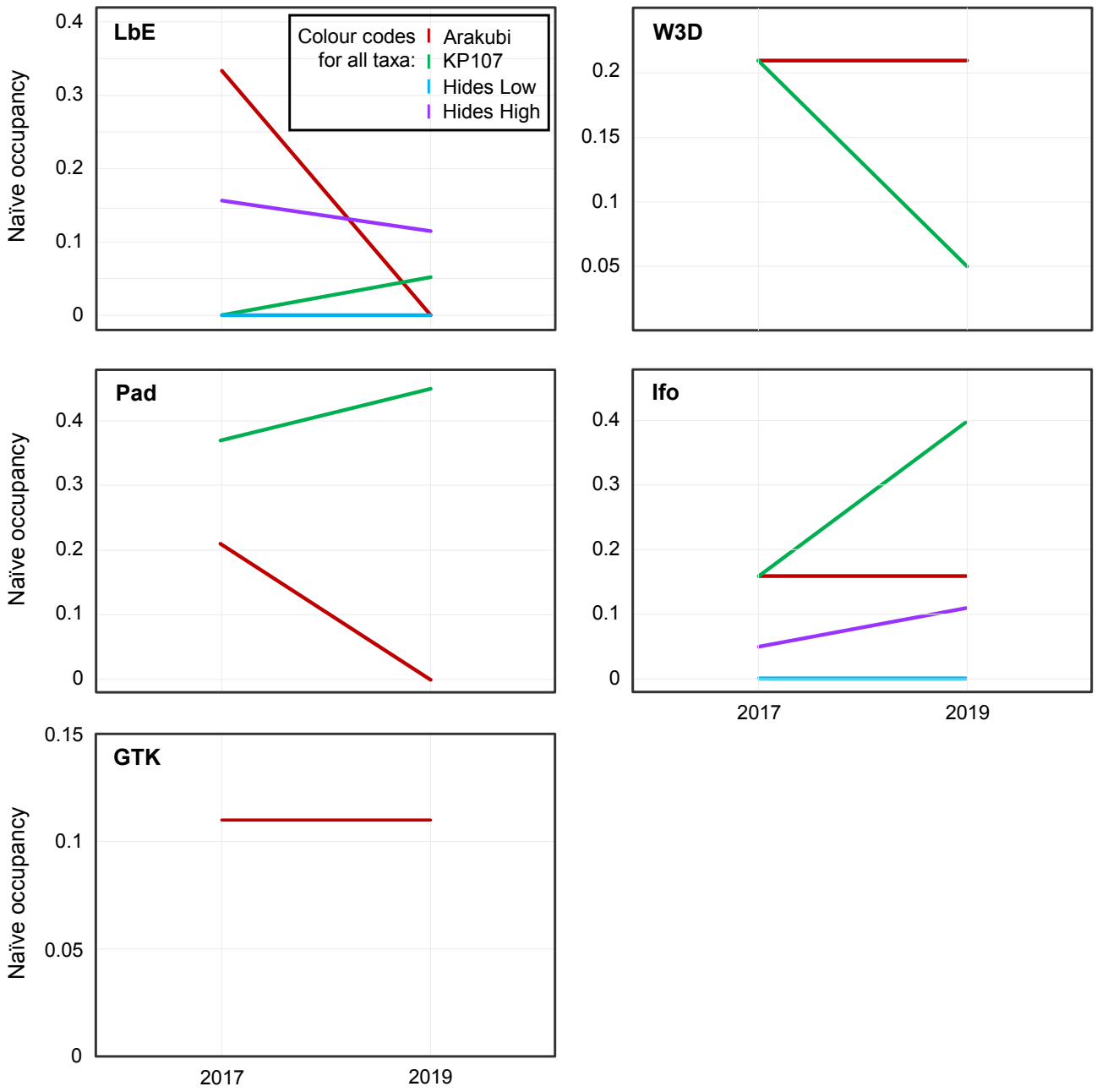

Figure 2.5. Change in naïve occupancy rate between years, for five IUCN listed species for which statistical modelling could not be performed. Species codes: LbE – Long-beaked Echidna; W3D – Woolley's Three-striped Dasyure; Pad – Pademelon; Ifo – Ifola; GTK – Goodfellow's Tree Kangaroo.

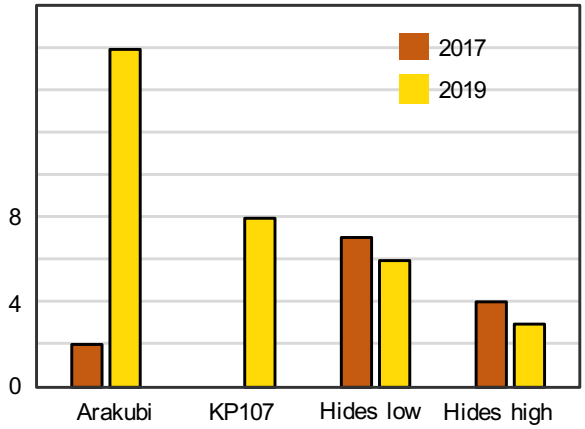

Figure 2.6. Total number of daily incursions by humans and/or dogs.

Edge effects (Objective 3)

Multi-model analyses were successfully run for eight terrestrial mammal and 15 terrestrial bird species (41 site- or BAA-level analyses). We did not analyse rodent data as this family (Muridae) is the focus of a separate study (Chapter 3, this report). For all taxa analysed, Appendix 2.3 shows the model-averaged relative importance of predictor variables with an importance value >0.1, along with their coefficient point estimates and standard errors.

Focusing on edge effects, and considering only those cases where final models ranked higher than the associated null model, distance measures featured in the final models constructed for 11 species (three mammals and eight birds, 16 site/BAA-level models) (Table 2.3, Figure 2.7). In three other cases, the null model ranked higher than the final model which included distance measure as a trending effect ($0.05<P<0.1$) – Ground Cuscus at KP107, Piping Bellbird (*Ornorectes cristatus*) at Arakubi and Papuan Scrub Robin (*Drymodes beccarii*) at KP017; due to the lack of statistical support, these cases are not assessed further in this report.

In each of the models presented in Table 2.3, distance from the nearest road or clearing was either significantly correlated with activity rate ($P<0.05$; 13 sites, nine species) or showed a near-significant trend ($0.05<P<0.1$; three sites, two species). In just over half of the cases (10/16) the observed pattern is consistent with edge avoidance, with less activity recorded nearer to Project infrastructure. Evidence for edge avoidance was strongest at BAA 2, particularly for Raffray's Bandicoot (*Peroryctes raffrayana*) at KP107, Small Dorcopsis at KP107, Collared Brushturkey at Arakubi and KP107, and Pheasant Pigeon at Arakubi and KP107 – these cases comprise all models that were clearly better than the associated null, and in which there was significantly more activity further from Project infrastructure. Similar patterns were observed for Dwarf Cassowary at BAA 2 (sites pooled) and Russet-tailed Thrush (*Zoothera heinei*) at KP107, although statistically these were less compelling (respectively a non-significant trend or the null model was equally well supported; Table 2.3).

There was comparatively little evidence for edge avoidance at BAA 1. In the only relevant cases, activity rates of both the Striped Bandicoot (*Microperoryctes longicauda*) and New Guinea Scrubfowl (*Megapodius decollatus*) were lower within 100 m of clearings at Hides Low, although the observed pattern was either non-significant (Striped Bandicoot, $P=0.075$) or the final model was no better than the null (New Guinea Scrubfowl, $\Delta AIC_c=0.41$).

The remaining models presented in Table 2.3 describe a reverse-pattern edge effect, with higher rates of activity closer to Project infrastructure (Figure 2.7). This pattern was particularly prominent at the Hides High site, where all three cases involve higher rates of activity nearer to clearings (Lesser Melampitta (*Melampitta lugubris*) and Greater Ground Robin) or roads (Striped Bandicoot). Reverse-pattern edge effects are also reported for Papuan Logrunner at Hides Low, Small Dorcopsis at Arakubi and New Guinea Scrubfowl at KP107. Observed effects were significant and in well-supported models (null $\Delta AIC_c>6$) for the Lesser Melampitta and Greater Ground Robin at Hides High, and for Small Dorcopsis at Arakubi.

Table 2.3. Model summaries for 11 species in which distance from clearings or roads was influential in the final model structure, and where the final model ranked higher than the null model. Model estimates and standard errors are shown for each variable. Abbreviated variables (see Methods): DClr – distance from clearing; LT50/LT100 – less/more than 50/100 m from clearing; LT100Rd – less/more than 100 m from road; LR20 – local relief at the 20 m radius scale; CnpHt – canopy height; TrSm/TrLge – density of trees >10/30 cm dbh; UD1/UD2 – understorey density below 1/2 m; LfLit – leaf litter depth; Logs/Moss – proportion of ground covered by large woody debris/moss.

Species, sites, model structure and peformance	**Variable**	**t value**	***P***	**Estimate (±SE)**
Raffray's Bandicoot (*Peroryctes raffrayana*) – KP107				
LT50+Year+CnpHt+Logs	LT50: >50 m	5.51	<0.00001	1.27(0.23)
R^2=0.520, n=36	Year (2019)	2.12	0.042	0.29(0.14)
Null ΔAIC_C=26.74	CnpHt	2.85	0.008	0.06(0.02)
	Logs	-3.61	0.001	-0.41(0.11)
Striped Bandicoot (*Microperoryctes longicauda*) – Hides Low				
LT100+TrSm	LT100: >100 m	1.86	0.075	0.48(0.26)
R^2 =0.156, n=30	TrSm	3.04	0.005	0.05(0.02)
Null ΔAIC_C=7.8				
Striped Bandicoot (*Microperoryctes longicauda*) – Hides High				
LT100Rd+TrLge+CnpHt	LT100Rd: >100 m	-1.72	0.094	-0.58(0.33)
R^2=0.058, n=38	TrLge	-1.76	0.088	-0.09(0.05)
Null ΔAIC_C=1.6	CnpHt	2.57	0.015	0.10(0.04)
Small Dorcopsis (*Dorcopsulus vanheurni*) – Arakubi				
DRd+LR20+TrLge+UD1	DRd	-2.62	0.014	-0.002(<0.001)
R^2=0.409, n=34	LR20	-4.79	<0.0001	-0.10(0.02)
Null ΔAIC_C=15.38	TrLge	3.59	0.001	0.16(0.04)
	UD1	-2.73	0.011	-0.14(0.05)
Small Dorcopsis (*Dorcopsulus vanheurni*) – KP107				
LT50+Year+UD2+TrSm	Year (2019)	2.42	0.022	0.46(0.19)
R^2=0.796, n=36	LT50: >50 m	5.03	<0.0001	1.33(0.26)
Null ΔAIC_C=27.61	TrSm	-2.25	0.031	-0.03(0.01)
	UD2	5.87	<0.00001	0.08(0.01)
Dwarf Cassowary (*Casuarius bennetti*) – BAA 2				
Site+LT50+Year+TrSm	Site (KP107)	-1.64	0.106	
R^2=0.261, n=70	Year (2019)	-3.23	0.002	-0.98(0.30)
Null ΔAIC_C=6.2	LT50: >50 m	1.74	0.087	0.80(0.46)
	TrSm	-1.96	0.054	-0.05(0.02)
Collared Brushturkey (*Talegalla jobiensis*) – Arakubi				
DClr+UD2	DClr	7.69	<0.000001	0.011(0.001)
R^2=0.735, n=34	UD2	-3.58	0.001	-0.08(0.02)
Null ΔAIC_C=31.51				
Collared Brushturkey (*Talegalla jobiensis*) – KP107				
LT50+Year+Logs	LT50: >50 m	2.22	0.034	1.28(0.58)
R^2=0.418, n=36	Year (2019)	-4.55	<0.0001	-1.69(0.37)
Null ΔAIC_C=11.67	Logs	-1.75	0.091	-0.47(0.27)

Species, sites, model structure and peformance	Variable	t value	*P*	Estimate (±SE)
New Guinea Scrubfowl (*Megapodius decollatus*) – KP107				
DRd+UD1+Logs+LfLit	DRd	-2.87	0.007	-0.004(0.002)
R^2=0.082, n=36	UD1	-2.48	0.019	-0.22(0.09)
Null ΔAIC_C=3.12	Logs	2.34	0.026	0.51(0.22)
	LfLit	-2.11	0.043	-0.02(0.01)
New Guinea Scrubfowl (*Megapodius decollatus*) – Hides Low				
LT100+TrLge+Moss	LT100: >100 m	2.16	0.041	0.81(0.37)
R^2=0.008, n=30	TrLge	-1.84	0.078	-0.18(0.10)
Null ΔAIC_C=0.41	Moss	-3.00	0.006	-0.65(0.22)
Pheasant Pigeon (*Otidiphaps nobilis*) – Arakubi				
DRd+Year+LR20+Moss	DRd	2.98	0.006	0.003(0.001)
R^2=0.258, n=34	Year (2019)	-1.95	0.061	-5.78(0.30)
Null ΔAIC_C=6.00	LR20	2.38	0.024	0.06(0.03)
	Moss	-3.22	0.003	-0.44(0.14)
Pheasant Pigeon (*Otidiphaps nobilis*) – KP107				
LT50+Year	LT50: >50 m	3.12	0.004	1.56(0.50)
R^2=0.258, n=34	Year (2019)	3.22	0.003	1.00(0.31)
Null ΔAIC_C=6.00				
Papuan Logrunner (*Orthonyx novaeguineae*) – Hides Low				
LT50+TrLge	LT50: >50 m	-3.81	<0.001	-2.31(0.61)
R^2=0.121, n=30	TrLge	-1.73	0.095	-0.24(0.14)
Null ΔAIC_C=4.46				
Lesser Melampitta (*Melampitta lugubris*) – Hides High				
LT100	LT100: >100 m	-5.90	<0.0001	-1.96(0.33)
R^2=0.496, n=38				
Null ΔAIC_C=24.55				
Greater Ground Robin (*Amalocichla sclateriana*) – Hides High				
LT100+Year+TrSm	Year (2019)	-3.22	0.003	-1.39(0.43)
R^2=0.321, n=38	LT100: >100 m	-2.32	0.027	-0.98(0.42)
Null ΔAIC_C=6.26	TrSm	-2.11	0.043	-0.04(0.02)
Russet-tailed thrush (*Zoothera heinei*) – KP107				
DClr+Year+UD1	DClr	4.09	<0.001	0.009(0.002)
R^2=0.292, n=36	Year (2019)	2.26	0.031	1.11(0.49)
Null ΔAIC_C=1.75	UD1	2.31	0.027	0.22(0.09)

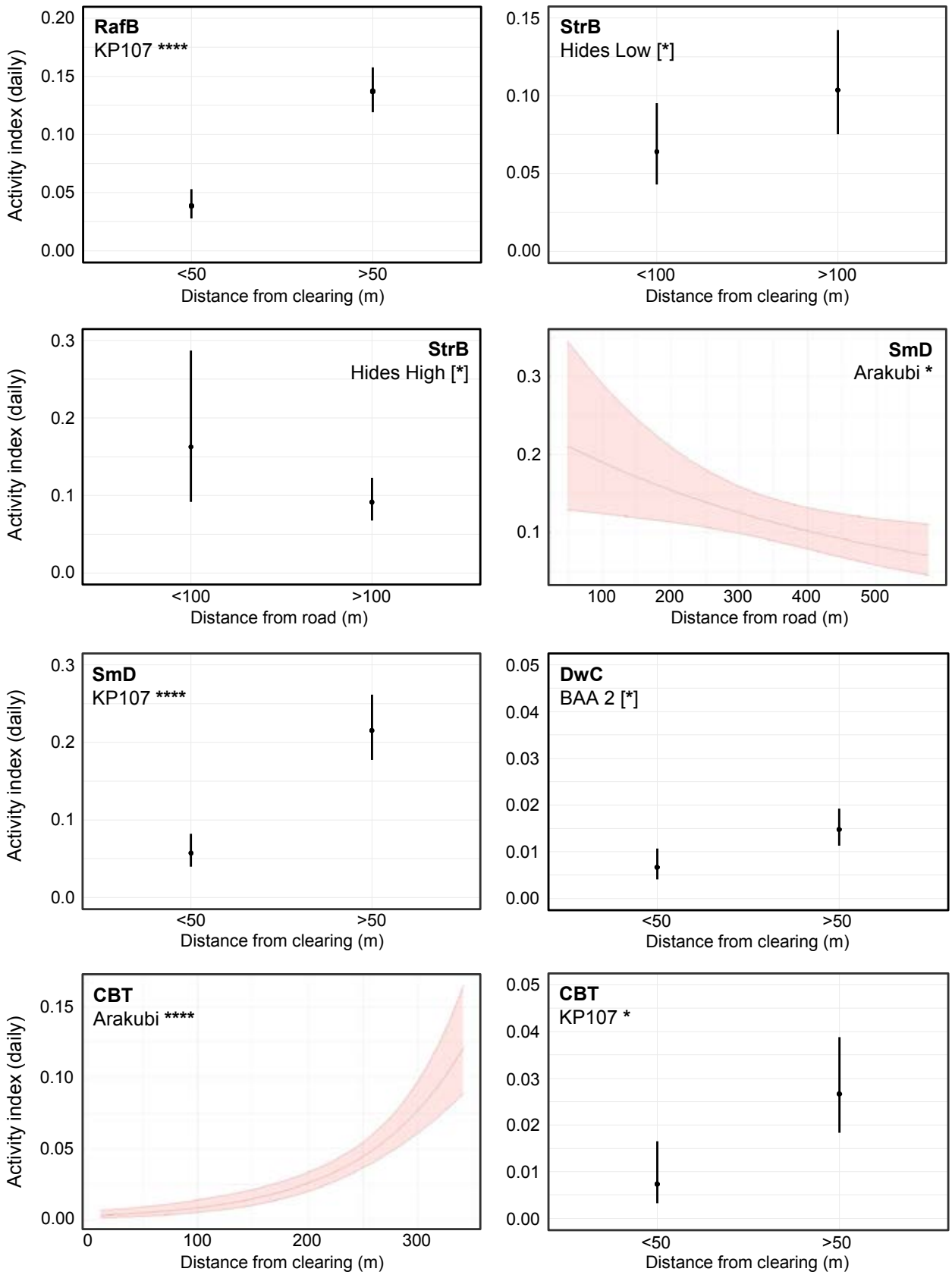

Figure 2.7. The relationship between animal activity rate and distance from project infrastructure for 11 species in which distance measures featured in the final models. Other terms appearing in the final model are held constant (see Table 2.3 for model structures). Species codes: RafB – Raffray's Bandicoot; StrB – Striped Bandicoot; SmD – Small Dorcopsis; DwC – Dwarf Cassowary; CBT – Collared Brushturkey; NGSF – New Guinea Scrubfowl; PhP – Pheasant Pigeon; Lgrn – Papuan Logrunner; LMel – Lesser Melampitta; GGR – Greater Ground Robin; RtTh – Russet-tailed Thrush. Significance codes: [*] =0.05<P<0.1; * =P<0.05; ** = P<0.01; *** =P<0.001; **** =P< 0.0001.

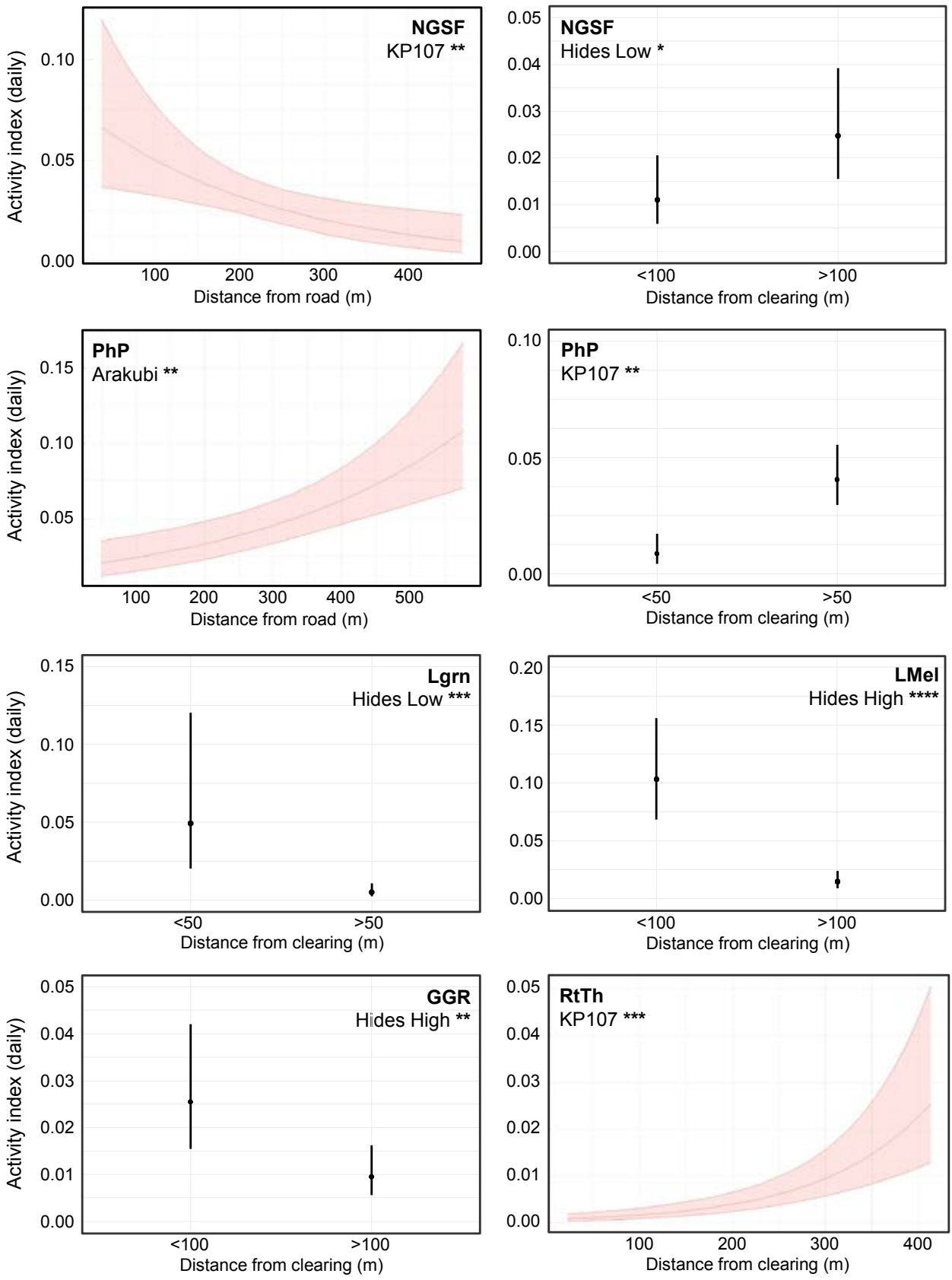

Figure 2.7. continued

Discussion

Species diversity and survey completeness (Objective 1)

The PMA3 camera trapping program has recorded the vast majority of ground-dwelling bird and mammal species expected to reside or regularly occur at sampled sites. Coverage of the terrestrial bird and medium- to large-bodied mammal assemblages appears to be almost complete in each full sampling year (2017 and 2019). No new terrestrial birds were recorded in 2019, and none are expected in subsequent years. Considering mammals larger than 120–200 g, the 2019 photographs of New Guinea Waterside Rat represent a new record for BAA 1.

Most or all unrecorded terrestrial species are likely to be small murid rodents. The only terrestrial species that was certainly newly photographed in 2019 was the small (<30 g) Shaw Mayer's Shrew Mouse recorded at Hides Low. This animal belongs to an endemic New Guinean genus of 12 species, most of which are poorly known and have small geographic ranges (Helgen and Helgen 2009; Denys et al. 2017). A number of other (at least partly) terrestrial, forest-dwelling murid genera are known to be regionally present but are yet to be recorded, including *Coccymys*, *Macruromys*, *Mammelomys*, *Melomys*, *Microhydromys* and *Xenuromys* (Denys et al. 2017). Other predominantly arboreal taxa such as *Abeomelomys* also occasionally come to ground. At least some of these taxa may be recognised in good quality images. Small murid rodents are covered in more detail by the small non-volant mammal monitoring study (Chapter 3, this report).

Additionally, there is almost certainly 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 (e.g. Chapter 3, this report).

In addition to terrestrial species, the camera trapping study continues to provide useful information on a number of arboreal mammals. Most importantly, biennial data on the IUCN Endangered Ifola and Goodfellow's Tree Kangaroo provide the only means of monitoring the local status of these rare and elusive species. A number of other species are not otherwise recorded from the BAAs – Loria's Tree Mouse, the ring-tailed possum *Pseudochirops* sp. (prior data from local informants only), and the Long-fingered Striped Possum (*Dactylopsila palpator*) (Mamu 2008; Aplin and Opiang 2017).

Population trends (Objective 2)

In cases where statistical models could be applied, a significant change in population estimate (occupancy or activity rate) between years was observed for seven species at eight locations (site or BAA). Significant declines were reported for five species – Dwarf Cassowary at BAA 2 (sites pooled), Collared Brushturkey at KP107, Chestnut Forest Rail and Greater Ground Robin at Hides High, and Papuan Logrunner at BAA 1 (predominantly due to decline at Hides High). In most cases where a species' activity was modelled at more than one site, a significant change recorded at one site was countered at other sites by a steady pattern between years, or in some cases a reverse (albeit non-significant) trend; for example, reverse trends among sites were observed for Ground Cuscus and Pheasant Pigeon at BAA 2 (activity rates) (Figure 2.4). By contrast, the decline recorded for Greater Ground Robin at Hides High is of potential significance as this is the only site within the Kikori Basin at which this rare and restricted-range species is known to occur (Woxvold and Legra 2019a,b).

Among conservation listed species, statistical models were run for two IUCN Near Threatened species – the New Guinea Quoll and Small Dorcopsis – neither of which declined at any site. Indeed, the Small Dorcopsis showed a trend towards increased activity at KP107 in 2019, and remains the most frequently detected terrestrial vertebrate across the study area (Figure 2.2) with records from all cameras at all sites (naïve occupancy=1.00) in the most recent sampling year. By contrast, naïve occupancy fell sharply at Arakubi for two IUCN Vulnerable species – the Long-beaked Echidna and Pademelon – from registers on multiple cameras in 2017 (six and four respectively) to none in 2019 (Figure 2.5; Appendix 2.1). Both of these species are susceptible to hunting, particularly where dogs are used (Nicol 2015; Eldridge

and Coulson 2015). In the case of the echidna, whose permanent (no seasonal migration), generally non-overlapping home ranges may exceed 50 hectares (Opiang 2009), the capture of just one or two individuals may result in its long-term absence from the sampled area (c. 70 ha). Interestingly, the decline in records at Arakubi corresponds with a sharp rise there in the number of incursions reported for humans and dogs (Figure 2.6). In addition, since 2017, gardens were constructed along the quarry road and Oil Search had re-established an active camp at the site. However, the co-occurrence of these changes does not prove a link. Further sampling in subsequent years will provide valuable insight into the local status of these high value species.

While the 2017–2019 dataset provides a useful baseline against which to measure future changes, there are at least two reasons why it is too early to draw conclusions as to the ongoing status of terrestrial vertebrate populations.

First, observed changes may be a result of seasonal effects. Photographic rates reflect both animal abundance and behaviour, both of which may be influenced by seasonal factors (Burton et al. 2015) – for example: (1) the presence or departure (dispersal) of a cohort of dependent offspring; (2) changes in resource availability leading to movement into or out of the home range (landscape-level nomadism); (3) changes in foraging/movement rate within a stable home range, for example due to a change in animal density, seasonal food availability or the requirements of dependent offspring, or; (4) a localised increase in resource availability near some camera positions, for example via seed- or fruit-fall. The changes observed in some measures in 2019 may thus in part be attributable to sampling at a different time of year (May–August 2017 vs. August–December 2019). Future sampling should be standardised with respect to seasonal timing. To help unpack the relative influence of seasonal vs. annual changes, we recommend reverting to the 2017 timing to test for reversal in the changes observed for some species.

Second, there may be natural variation in abundance between years, so that longer term studies are required to make reliable inferences about population change. Although previously considered to be relatively stable, recent studies have shown that many tropical animal populations are subject to natural fluctuations (Latta et al. 2011; Blake and Loiselle 2015). For example, annual camera trap monitoring of terrestrial mammals and birds in Ecuador has revealed marked inter-year changes in detection rate and occupancy estimates for multiple species, but no evidence of a consistent change in the status of any species across the full 11-year sampling period (Blake et al. 2017). There are no available data on population dynamics for the species assessed in this study. If natural fluctuations are similar to those observed in lowland Ecuador, then a sampling period of around 20 years would be required to draw similar conclusions under the biennial PMA3 sampling program. However, if the observed changes are more stable across sampling years, then earlier inferences may be possible. Continued sampling will help to determine which pattern is relevant for which species, although the timing with which inferences can be made will depend on the sampling frequency.

Edge effects (Objective 3)

Anthropogenic infrastructure has 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 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). In this study, the activity rates of 11 species (of 23 analysed) were correlated with distance from the nearest clearing or road.

Within species, there was considerable variation in the edge response patterns observed at different sites. Seven species for which a correlation was observed had their activity modelled at multiple sites. Four of these displayed no trend at one or more sites (Raffray's Bandicoot, Small Dorcopsis, New Guinea Scrubfowl, Papuan Logrunner), and three species exhibited a change in the direction of effect between sites, with an edge avoidance pattern displayed at one site and a reverse-pattern edge effect at another (Striped Bandicoot, Small Dorcopsis and New Guinea Scrubfowl) (Table 2.3, Figure 2.7).

Considering patterns across sites, the direction of observed effect tended to vary between BAAs. Edge avoidance patterns were most common at BAA 2 (8/10 models in Table 2.3). By contrast, most models (4/6) in which activity at BAA 1 was correlated with infrastructure distance demonstrated a reverse-pattern edge effect, with higher rates of activity nearer to the forest edge. This was the only pattern observed at the Hides High site, and neither of the two cases consistent with edge avoidance at Hides Low were statistically conclusive (requiring both a significant correlation and a definitive rejection of the null model at $\Delta AIC_c \geq 6$). First observed in 2017 (Woxvold and Legra 2019a), with additional data from 2019 this shift in the direction of effect across BAAs is now demonstrated in more species.

Reverse-pattern edge effects are counter-intuitive for interior forest species. In such cases, we think it unlikely that Project roads and clearings have 'improved' the quality of near-edge habitat. Instead, the causal factors are likely to be environmental rather than anthropogenic. Candidate parameters include those correlated with infrastructure distance at BAA 1, as well as unmodelled factors. Three examples are considered below, with specific reference to animals that showed a reverse-pattern edge effect at BAA 1.

Terrain effects—In both BAAs, most measures of local relief are strongly correlated with distance from clearing, and the direction of this relationship is reversed across BAAs, with steeper terrain closer to clearings at BAA 2 and further from clearings at BAA 1 (Table 2.4). Steepness of terrain is known to influence the abundance and behaviour of a variety of ground-dwelling fauna (e.g. Namgail et al. 2004; Oberosler et al. 2017), and in this study, local relief (20 m radius) was the most important predictor of Small Dorcopsis and New Guinea Scrubfowl activity at Arakubi (the site with steepest terrain) (Appendix 2.3). Could patterns of higher activity nearer to clearings thus be explained by an aversion to steeper ground? Among the four species showing a reverse-pattern edge effect at BAA 1, independent terrain measure models revealed a strong negative relationship between activity and local relief only in the Papuan Logrunner (Hides Low: LR20, P=0.001; LR50, P<0.0001; LR100, P<0.0001). However, evidence for this parameter's influence was weak overall, since (1) the null model ranked higher than the terrain models and (2) terrain measures had low relative importance in the model averaged results (Appendix 2.3).

Table 2.4. The relationship between distance from the nearest clearing and terrain steepness at each BAA and site. Terrain steepness was measured within 20 m (LR20), 50 m (LR50) and 100 m (LR100) radii from each functioning camera position. Numbers show Pearson Correlation Coefficients (PCCs) and associated P-values. The direction of the correlation is indicated by the PCC sign (positive/negative). Significant correlations are shown in bold.

BAA/site	LR20	LR50	LR100
BAA 1	**0.43, *P*=0.009**	**0.59, *P*<0.001**	**0.56, *P*<0.001**
Hides Low	0.41, *P*=0.103	**0.62, *P*=0.008**	**0.57, *P*<0.017**
Hides High	0.45, *P*=0.054	**0.56, *P*=0.013**	**0.56, *P*=0.013**
BAA 2	**-0.47, *P*=0.002**	**-0.39, *P*=0.013**	-0.25, *P*=0.132
Arakubi	**-0.52, *P*=0.024**	**-0.50, *P*=0.031**	**-0.49, *P*=0.033**
KP107	**-0.49, *P*=0.029**	-0.36, *P*=0.119	0.10, *P*>0.6

Understorey density—Understorey density below 2 m was positively correlated with distance from clearings at Hides High (DClr: PCC=0.41, P=0.078; LT50: Kendall's tau=0.43, P=0.035; LT100: Kendall's tau=0.47, P=0.020). In a model including only this term, Lesser Melampitta activity was negatively correlated with understorey density below 2 m (point estimate (standard error)=-0.12(0.04), P=0.002) and this model was clearly better than the null (ΔAIC_c=7.53). Thus, although understorey density had low relative importance after model averaging (Appendix 2.3), there is some evidence that melampittas at Hides High may avoid areas with dense understorey and thereby indirectly prefer habitat nearer to clearings.

Predator avoidance—The pattern may be explained by predator avoidance if predators are more abundant in the forest interior (da Silva et al. 2018). A number of studies have shown that some carnivores are less likely to occur near forest

edge (e.g. Pettorelli et al. 2010; Rich et al. 2016). Relevant predators at BAA 1 include the Papuan Eagle (*Harpyopsis noveaeguineae*) (preying upon Small Dorcopsis) and marsupial carnivores (dasyurids) such as the New Guinea Quoll, Speckled Dasyure (*Neophascogale lorentzii*) and Narrow-striped Dasyure (*Phascolosorex dorsalis*). However, predator avoidance is not considered to be a causal factor, since: (1) the Papuan Eagle almost certainly occurs at densities too low to drive the observed effect for Small Dorcopsis; (2) there was no evidence for higher marsupial carnivore activity further from the forest edge at BAA 1 (Appendix 2.3), and; (3) each of these taxa occurs across more sites than those at which the reverse edge effect was observed.

Overall, there is little evidence that pre-considered parameters are responsible for near-edge habitat preferences observed at BAA 1.

Regardless of the cause, after two years of camera trap monitoring there is no compelling evidence that any terrestrial mammal or bird species avoid forest edge on Hides Ridge. We did not place cameras within 5–10 m of clearings, and it is possible that some animals do avoid these near-edge habitats; for example, along the pipeline ROW at Hides Low where increased sunlight has led to the development of dense tangles of climbing bamboo (*Nastus productus*). However, for most species investigated in this study, these narrow strips of habitat represent only a small proportion of their home range requirement – most occupy home ranges larger than two hectares, and for animals larger than 0.5 kg, including all terrestrial IUCN Threatened and Near Threatened species examined here, the home range is typically in the order of 10s or 100s of hectares. Changes restricted to very near-edge environments are likely to have a minimal impact on such species, and we have therefore elected to investigate habitat effects in the range of 20 to >300 m from the forest edge. While it is possible that edge effects do impact terrestrial vertebrates at the measured scale, the responses on Hides Ridge are evidently negligible, and in some cases appear to have been reversed by the influence of one or more natural (non-anthropogenic) environmental factors.

Edge avoidance was the predominant pattern at BAA 2. Reduced activity near BAA 2 infrastructure was first observed in 2017 for Small Dorcopsis, Raffray's Bandicoot and Collared Brushturkey (Woxvold and Legra 2019a). The 2019 data consolidate these results and extend them to Dwarf Cassowary, Pheasant Pigeon and Russet-tailed Thrush. Observed effects were particularly strong for Raffray's Bandicoot at KP107, Small Dorcopsis at KP107, Collared Brushturkey at Arakubi and KP107, and Pheasant Pigeon at Arakubi and KP107.

Given the likelihood that unmodelled heterogeneity in environmental factors has led to spurious edge response patterns at BAA 1, it is possible that some of the patterns observed at BAA 2 are also environmentally driven. In the absence of pre-construction data, it will be difficult to untangle the effects of infrastructure distance and environmental parameters. Nevertheless, there are a number of reasons why some species may avoid near-edge environments at these sites.

First, forest near infrastructure at the Arakubi site was in many places heavily disturbed. This was most evident at a small number of camera positions along the quarry road. This may partly explain apparent edge avoidance by Dwarf Cassowary, Collared Brushturkey and Pheasant Pigeon at Arakubi. However, forest condition was generally good near roads and the pipeline ROW at KP107, where edge avoidance was most commonly observed (KP107 vs. Arakubi – 6 vs. 3 species).

Second, species may avoid near-edge habitat due to anthropogenic disturbance. 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: Arakubi – 1.7 km, KP107 – 2.7 km, Hides Low – 3.6 km, Hides High – 5.7 km). Consistent with this, the total number of daily incursions by humans and/or dogs was highest at the BAA 2 sites in 2019 (Figure 2.6). However, total incursions were lowest at these sites in 2017, and the number of incursions at KP107 in 2019 was similar to that recorded at Hides Low (BAA 1) in both years. Moreover, these incursions were recorded on

camera traps inside forest environments, and humans and dogs readily travel much further into the forest interior than the distances covered by our camera arrays. Edge effects observed at the measured scale may instead reflect avoidance of frequent human activity along roads and the pipeline ROW.

Sampling design and analytical approach

We have discussed the suitability of our statistical approach to assessing edge effects (Objective 3) in an earlier report (Woxvold and Legra 2019a). We have used the same approach here, but have added sampling year and a number of newly measured environmental covariates which have improved model performance.

In terms of population trends (Objective 2), we have used three types of surrogate population estimate to monitor change between years; in decreasing of order preference, and based on data availability and species-specific life history traits (home range size, see Methods), they are – occupancy estimates, activity rates and naïve occupancy rates.

Photographic rates form the basis for the activity rate response variable used in this study. The use of photographic rates as a surrogate for population density of unmarked species (whose individuals cannot be told apart on camera trap images) has been much criticised (e.g. O'Brien 2011; Sollman et al. 2013; Burton et al. 2015). This is largely because: (1) activity rate models assume constant detection probability, but; (2) a variety of factors unrelated to animal abundance (e.g. seasonal effects, micro-habitat parameters, camera placement) may influence how often animals pass in front of a camera. In some situations, detection rates may underestimate true changes in density due to their failure to account for changes in detectability (Broadley et al. 2019). Occupancy modelling seeks to rectify these problems by estimating rates of spatial occupancy (presence/absence) while separately accounting for variation in the detectability (p) 'nuisance variable' (MacKenzie et al. 2006; O'Brien 2011; Burton et al. 2015).

In species where the occupancy framework could not be applied, we reverted to the use of activity rate models. A number of studies have demonstrated that changes in activity rate do sometimes accurately reflect changes in abundance (Rovero and Marshall 2009; Kuprewicz 2013; Palmer et al. 2018; Broadley et al. 2019). Moreover, with repeat sampling from a standardised design, and where analysis is restricted to comparing activity rates within species and within sites, as done in this study, changes in activity rate are generally considered to provide a reliable indication of the direction of change (increase, decrease) in a species' local population density (O'Brien 2011). This approach is thus considered a suitable next-best option in cases where occupancy modelling cannot be applied.

Naïve occupancy measures are reported for conservation-priority species with too few data to run statistical models (of occupancy or activity rate). This was applied to four IUCN threatened mammal species – the Endangered Ifola and Goodfellow's Tree Kangaroo, and the Vulnerable Long-beaked Echidna and Pademelon – and to the IUCN Data Deficient Woolley's Three-striped Dasyure. Because of imperfect detection ($p<1$), naïve occupancy estimates tend to underestimate true occupancy levels. However, naïve and model-based occupancy estimates are often strongly correlated (Rovero et al. 2014; Hegerl et al. 2015; Blake et al. 2017; Neilson et al. 2018). Naïve estimates therefore present a useful and best-available surrogate for assessing population trends in those priority species for which too few data are available to produce a model-based estimate.

The current sampling design is suitable for activity rate modelling of habitat preferences, such as the approach used in this study to assess potential edge effects. It is also practical in terms of the monitoring program's resource and logistic constraints, and as such has worked well in conjunction with the other PMA3 study disciplines. However, the current camera arrays limit our ability to monitor wildlife population trends in two ways.

First, the clustering of cameras within sites of c. 70–180 ha makes it difficult to draw conclusions as to the overall status of some local populations. For many medium- to large-bodied animals, only a small number of individuals, in some

cases perhaps only one or two (for example, Long-beaked Echidna at Arakubi), may hold territories at each site. Relevant taxa include most terrestrial IUCN listed species recorded in our study. For these species, the localised loss of a small number of individuals – for example due to hunting – may lead to a dramatic decline in recorded observations but a limited ability to assess population trends at a more meaningful scale.

Second, we are constrained in our ability to use the preferred occupancy modelling approach. The relatively close spacing of cameras within sites violates a key assumption of occupancy modelling – that of independence – by allowing individuals of most species to be photographed at more than one camera position. Because of this, we have modelled occupancy among groups of cameras whose units are no less than 250 m apart, reducing the effective per-site sample size from 20 cameras deployed to 4–5 camera groups. Moreover, in order to improve sample size, the occupancy approach is necessarily restricted to a handful of smaller species whose home ranges are unlikely to span more than one camera group, but whose overall population spans both sites within a BAA. Relevant species include a small number of potentially sensitive terrestrial insectivorous birds, but exclude most ground-dwelling non-rodent taxa camera trapped in the study area, including all IUCN listed species.

After two years of edge effect monitoring, improvements in pattern resolution may be expected to diminish in future sampling seasons. Given the proven ability of camera traps to detect the presence of rare and elusive priority monitoring targets, it is therefore timely to consider how camera arrays might be adjusted to maximise return-for-effort and to provide useful data for long-term population studies. An occupancy-based sampling design would involve cameras positioned at 'independent' stations at least 500–1,000 m apart (e.g. Blake et al. 2017; Ehlers Smith 2017; Murphy et al. 2017), thereby sampling more animal territories across a broader area. The Upstream Project Area presents a number of challenges to establishing such arrays, including areas of difficult terrain, land ownership issues and logistic constraints. However, the Hides Ridge landscape presents a good opportunity to apply an occupancy-based design, since: (1) the area supports multiple priority monitoring target species; (2) it already accommodates the camera trap monitoring study, and; (3) a Project-controlled road provides access to more than 14 km of continuous forest above 2,000 m asl. Moreover, we do not expect further sampling with the current arrays to overturn the reverse-pattern edge effects observed on Hides Ridge.

Opportunities to expand the sampling area at BAA 2 are more limited, due in part to higher local human population densities and the overlapping interests of other oil and gas operators. However, any expansion in the number of independent camera groupings would be beneficial, and it may be possible to achieve this in areas along the pipeline ROW north of KP107, and to the southeast between Arakubi and KP107.

Conclusions

1. The following changes were made to sampling arrays and study procedures in 2019:

    - Fifteen camera positions were relocated due to security concerns or to site damage resulting from garden construction or earthquake.

    - Data were collected on nine new environmental covariates at each of the 2019 camera positions. These were included in activity rate modelling procedures used to assess potential edge effects.

    - Inter-year changes in population estimates were monitored for the first time. Occupancy modelling was introduced to maximise inference potential in cases where data availability and species-specific life history traits allowed.

2. Two full seasons of camera trap sampling have improved our knowledge of vertebrate diversity within the study area and across the broader PNG LNG Upstream Project Area. Results of the 2019 sampling year include six species newly reported from BAAs and one new record for the Kikori Basin – Shaw Mayer's Shrew Mouse.

3. The biennial deployment period of 89–107 days is sufficient to attain a near-complete census of the resident terrestrial bird and medium- to large-bodied mammal faunas in each sampling year. Biennial data are provided for a suite of priority monitoring targets, including seven IUCN listed mammal species – Eastern Long-beaked Echidna, Woolley's Three-striped Dasyure, New Guinea Quoll, Small Dorcopsis, Pademelon, Ifola and Goodfellow's Tree Kangaroo.

4. The 2019 data provide the first opportunity to monitor population trends between years. Occupancy estimates and activity rates declined significantly in five bird species at individual sites or BAAs. Naïve occupancy measures fell sharply between years for three IUCN listed mammals – the Eastern Long-beaked Echidna and Pademelon at Arakubi, and Woolley's Three-striped Dasyure at KP107. An increase in population estimate was recorded for a number of taxa, including two IUCN listed mammals at KP107 – the Small Dorcopsis and Ifola. It is too early to draw conclusions as to the ongoing status of local populations; continued sampling, standardised for seasonal effects, is required to make reliable inferences about population trends.

5. The number of incursion days by humans and/or dogs increased markedly at BAA 2 from 2017 to 2019 (Arakubi, 2–16 days; KP107, 0–8 days). The number of incursion days was similar in both years at BAA 1 (Hides Low, 6–7 days; Hides High, 3–4 days).

6. Animal activity rate was correlated with distance from infrastructure in 11 species at 16 sites or BAAs. Final models were consistent with edge avoidance by eight species at 10 sites/BAAs. Evidence for edge avoidance was strongest at BAA 2, particularly for Raffray's Bandicoot at KP107, Small Dorcopsis at KP107, Collared Brushturkey at Arakubi and KP107, and Pheasant Pigeon at Arakubi and KP107. Some species may avoid near-edge environments at these sites due to the presence of degraded forest near infrastructure (particularly at Arakubi) and/or an aversion to frequent human activity along roads and the pipeline ROW.

7. Six species at six sites displayed reverse-pattern edge effects, with higher rates of activity nearer to the forest edge. These were the most common trends observed at BAA 1 (4/6 final models) and were the only patterns observed at the Hides High site. Reverse-pattern edge effects are likely due to unmodelled heterogeneity in environmental factors.

Recommendations

1. We recommend that the camera trapping program continue in 2021 and in subsequent survey years. As far as practical, the biennial schedule should be maintained as fewer data points will extend the time required to make reasonable inferences about population trends. Each monitoring survey should take place at the same time of year to control for seasonal effects; we recommend reverting to the 2017 timing to test for reversal in the potentially seasonal changes observed for some species.

2. We recommend that, as far as practical, the sampling design be expanded (using the same number of cameras) within BAAs beyond the site scale to increase sampling of important local populations and to improve the scope for occupancy modelling. If accepted, a revised design including a set of proposed camera positions will be prepared prior to survey. Additional field assistants may be required to deploy cameras in new positions and to collect environmental covariate data in the time available.

3. The R script used to analyse data in this study was developed in consultation with a biostatistician from the Arthur Rylah Institute (Department of Environment, Water, Land and Planning, government of Victoria). Analysis of future datasets will require expansion of the occupancy modelling procedure to incorporate data from additional years and the influence of environmental covariates (here applied only to activity rate modelling). We recommend funds be made available for additional time with the ARI biostatistician to help expand the analysis protocol. The time required will be considerably less than that used in previous years.

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Plate 1

Figure 2.8. Eastern Long-beaked Echidna (*Zaglossus bartoni*)

Figure 2.9. Short-beaked Echidna (*Tachyglossus aculeatus*)

Figure 2.10. Woolley's Three-striped Dasyure (*Myoictis leucura*)

Figure 2.11. Speckled Dasyure (*Neophascogale lorentzii*)

Figure 2.12. Narrow-striped Dasyure (*Phascolosorex dorsalis*)

Figure 2.13. New Guinea Quoll (*Dasyurus albopunctatus*)

Plate 2

Figure 2.14. *Murexia* sp.

Figure 2.15. Raffray's Bandicoot *(Peroryctes raffrayana)*

Figure 2.16. Striped Bandicoot (*Microperoryctes longicauda*)

Figure 2.17. Ground Cuscus (*Phalanger gymnotis*)

Figure 2.18. Ring-tailed Possum (*Pseudochirops* sp.)

Figure 2.19. Long-fingered Striped Possum (*Dactylopsila palpator*)

Plate 3

Figure 2.20. Small Dorcopsis (*Dorcopsulus vanheurni*)

Figure 2.21. Pademelon (*Thylogale* sp.)

Figure 2.22. Ifola (*Dendrolagus* [*dorianus*] *notatus*)

Figure 2.23. Goodfellow's Tree Kangaroo (*Dendrolagus goodfellowi*)

Figure 2.24. Uneven-toothed Rat (*Anisomys imitator*)

Figure 2.25. White-eared Giant Rat (*Hyomys* sp.)

Plate 4

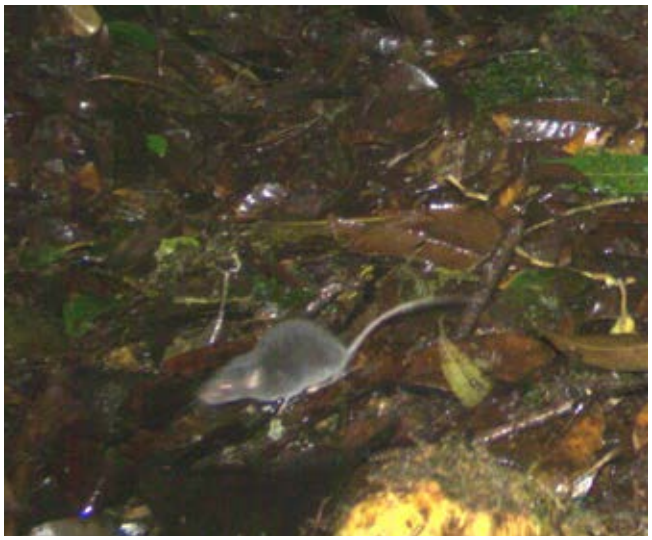


Figure 2.26. Shaw Mayer's Shrew Mouse (*Pseudohydromys ellermani*) camera trapped on Hides Ridge. A new record for the Kikori Basin

Figure 2.27. Dwarf Cassowary (*Casuarius bennetti*)

Figure 2.28. Wattled Brushturkey (*Aepypodius arfakiensis*)

Figure 2.29. Collared Brushturkey (*Talegalla jobiensis*)

Figure 2.30. New Guinea Scrubfowl (*Megapodius decollatus*)

Figure 2.31. Stephan's Emerald Dove (*Chalcophaps stephani*)

Plate 5

Figure 2.32. New Guinea Bronzewing (*Henicophaps albifrons*)

Figure 2.33. Cinnamon Ground Dove (*Gallicolumba rufigula*)

Figure 2.34. Pheasant Pigeon (*Otidiphaps nobilis*)

Figure 2.35. Chestnut Forest Rail (*Rallicula rubra*)

Figure 2.36. New Guinea Woodcock (*Scolopax rosenbergii*)

Figure 2.37. Shovel-billed Kookaburra (*Clytoceyx rex*)

Plate 6

Figure 2.38. Papuan Pitta (*Erythropitta macklotii*)

Figure 2.39. Papuan Logrunner (*Orthonyx novaeguineae*)

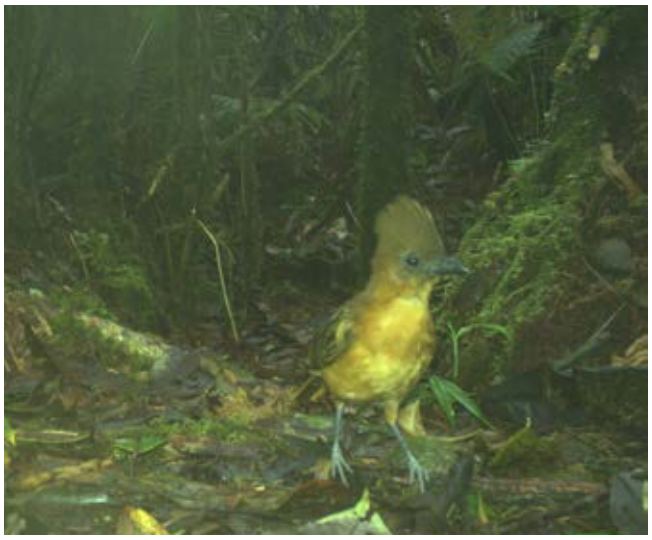


Figure 2.40. Piping Bellbird (*Ornorectes cristatus*)

Figure 2.41. Brown Sicklebill (*Epimachus meyeri*)

Figure 2.42. Domestic Dog (*Canis familiaris*)

Figure 2.43. Hunter at Hides High

Appendix 2.1.

Species recorded on camera traps in 2017 and 2019, their conservation status (Status) and the number of independent photographic events (No. events) at each site. Species with predominantly or entirely terrestrial habits are indicated by (T) after the English name. Conservation status indicates those species listed in the IUCN Red List of Threatened Species (IUCN 2020) 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.

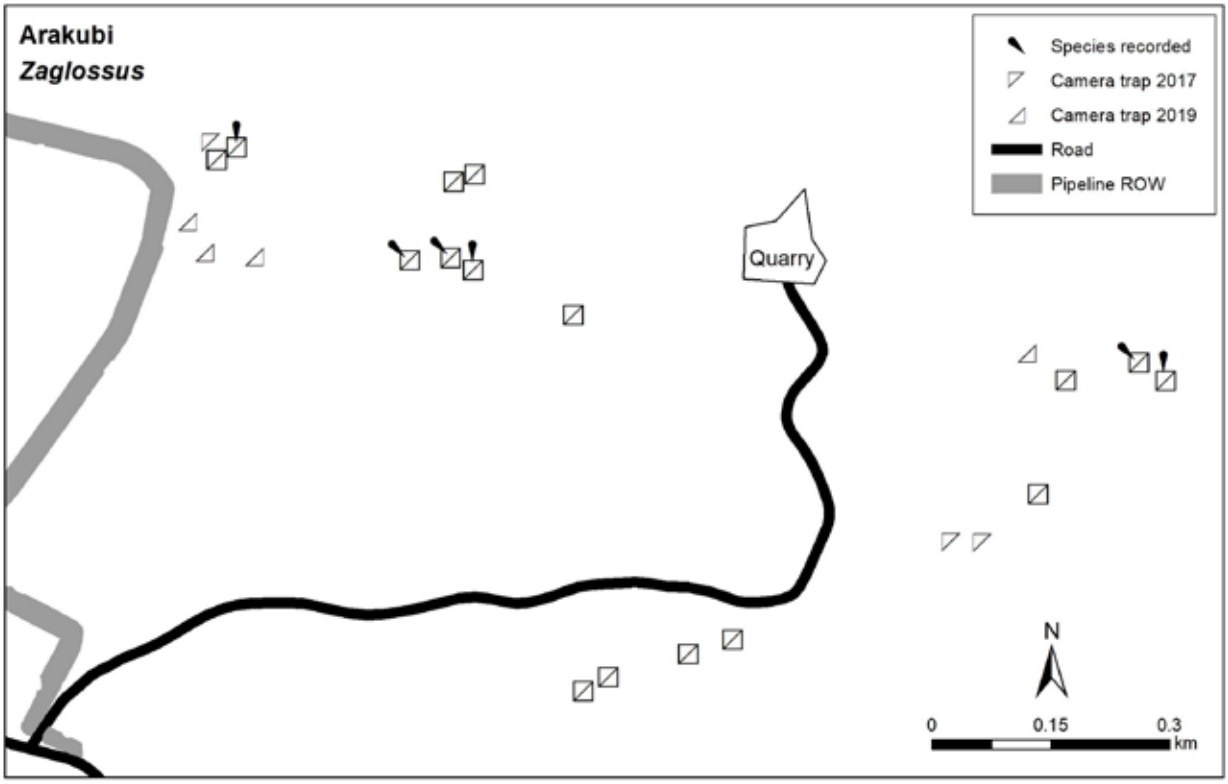
English Name	Scientific Name	Status	No. events				
			Arakubi	KP107	Hides Low	Hides High	Total
Mammals							
Eastern Long-beaked Echidna (T)	*Zaglossus bartoni*	VU, P	6/–	–/1		3/4	9/5
Short-beaked Echidna (T)	*Tachyglossus aculeatus*		10/13	2/2			12/15
Woolley's Three-striped Dasyure (T)	*Myoictis leucura*	DD	4/18	5/1			9/19
Speckled Dasyure (T)	*Neophascogale lorentzii*				9/3	10/22	19/25
Narrow-striped Dasyure (T)	*Phascolosorex dorsalis*				18/19	2/2	20/21
Unidentified dasyure (T)	*Neophascogale/ Phascolosorex*				–/1		–/1
New Guinea Quoll (T)	*Dasyurus albopunctatus*	NT	13/10	9/22	6/8	16/17	44/57
Multiple *Murexia* spp. (T)	*Murexia* spp.		19/30	18/11	25/23	14/1	76/65
Raffray's Bandicoot (T)	*Peroryctes raffrayana*		31/31	167/262	98/79	460/444	756/816
An echymipera (T)	*Echymipera* cf. *kalubu*		30/15	5/13			35/28
Striped Bandicoot (T)	*Microperoryctes longicauda*			7/7	147/158	172/262	326/427
Unidentified bandicoot (T)			1/31	11/13	3/6	5/8	20/58
Ground Cuscus (T)	*Phalanger gymnotis*		21/16	14/38	14/7	5/6	54/67
Mountain Cuscus	*Phalanger carmelitae*					–/3	–/3
A Ring-tailed Possum	*Pseudochirops* sp.				1/5	4/1	5/6
Long-fingered Striped Possum	*Dactylopsila palpator*				1/1	3/5	4/6
Small Dorcopsis (T)	*Dorcopsulus vanheurni*	NT	279/255	337/559	128/220	210/166	954/1,200
A pademelon (T)	*Thylogale* sp.	VU	7/–	16/11			23/11
Dorcopsis/pademelon (T)	*Dorcopsulus/Thylogale* sp.	NT/ VU	1/–	1/1			2/1
Ifola	*Dendrolagus [dorianus] notatus*	EN, P	3/5	3/9		2/4	8/18
Goodfellow's Tree Kangaroo	*Dendrolagus goodfellowi*	EN, P	4/2				4/2
Uneven-toothed Rat (T)	*Anisomys imitator*			49/33	14/31	67/29	130/93
Loria's Tree Mouse	*Pogonomys* cf. *loriae*			–/1			–/1
Water rat/New Guinea Waterside Rat (T)	*Hydromys/Parahydromys asper*					–/3	–/3
A white-eared giant rat (T)	*Hyomys* sp.				2/1	8/31	10/32
Elegant Water Rat (T)	*Leptomys elegans*		16/38	48/24			64/62
A woolly giant rat (T)	*Mallomys* sp.			5/2	9/12	27/8	41/22

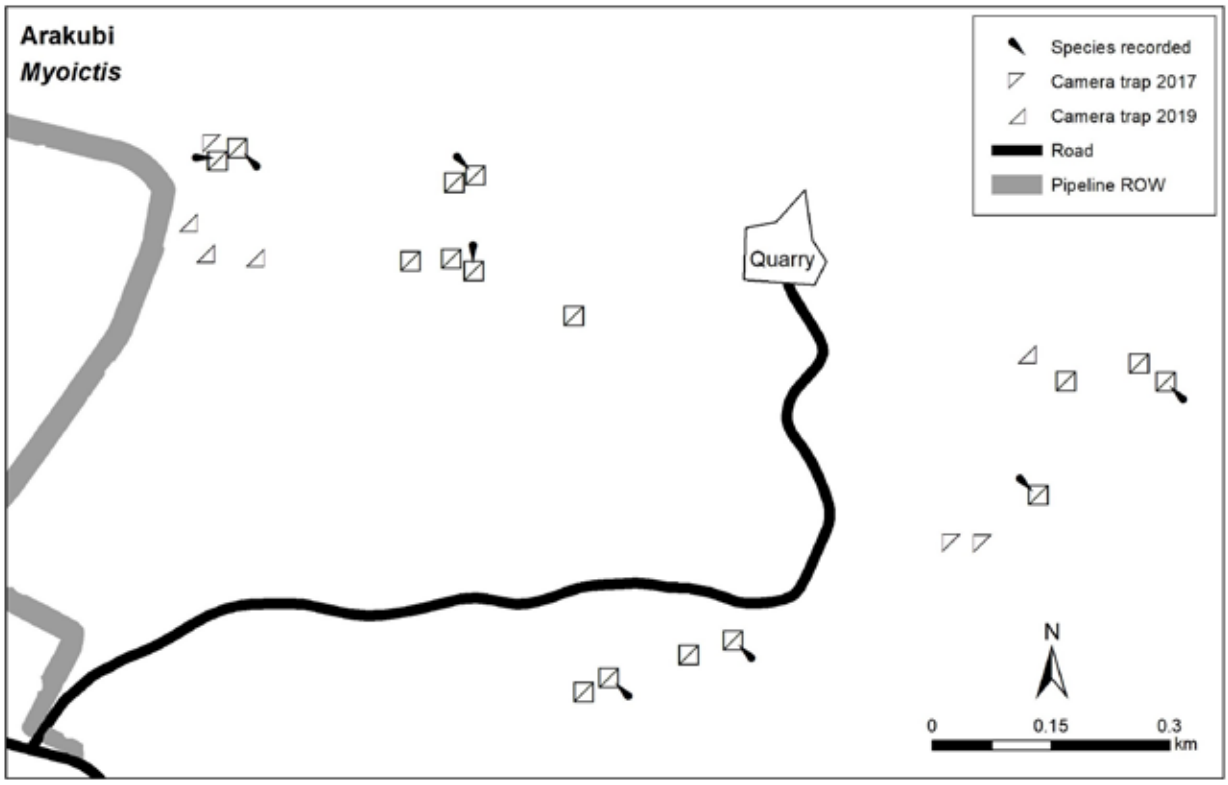
English Name	Scientific Name	Status	No. events				
			Arakubi	KP107	Hides Low	Hides High	Total
Multiple *Paramelomys* species (T)	*Paramelomys* spp.		108/88	81/80	90/137	49/42	328/347
Shaw Mayer's Shrew Mouse (T)	*Pseudohydromys ellermani*				–/1		–/1
Black-tailed Giant Rat (T)	*Uromys anak*		4/1	10/12	26/13	42/20	82/46
White-tailed Giant Rat (T)	*Uromys caudimaculatus*		82/120	27/54	–/1		109/175
Multiple small *Rattus* species (T)	*Rattus* spp.		21/–	2/2	44/78	210/185	277/265
A distinctive large *Rattus (T)*	*Rattus* sp. A		14/15				14/15
Unidentified murids			26/70	35/82	48/97	52/118	161/367
Feral Pig (T)	*Sus scrofa*		2/–	4/–			6/–
Domestic Cat (T)	*Felis catus*		–/1		1/–		1/1
Domestic Dog (T)	*Canis familiaris*		–/16	–/7	3/6	3/3	6/32
Human (T)	*Homo sapiens*		2/–		3/–	–/1	5/1
Human with dog (T)				–/1	1/–	1/–	2/1
Total incursion days, human or dog (T)			2/16	–/8	7/6	4/3	13/33
Birds							
Dwarf Cassowary (T)	*Casuarius bennetti*		70/23	29/15	3/1	1/–	103/39
Wattled Brushturkey (T)	*Aepypodius arfakianus*		2/3	24/42	3/10	77/–	106/55
Collared Brushturkey (T)	*Talegalla jobiensis*		59/51	113/20	–/1		172/72
New Guinea Scrubfowl (T)	*Megapodius decollatus*		41/43	58/69	25/44	–/2	124/158
Barred Owlet-nightjar	*Aegotheles bennettii terborghi*			–/2			–/2
Stephan's Emerald Dove (T)	*Chalcophaps stephani*		2/5				2/5
New Guinea Bronzewing (T)	*Henicophaps albifrons*		1/1	3/1	–/1		4/3
Cinnamon Ground Dove (T)	*Gallicolumba rufigula*		38/15	7/9			45/24
White-breasted Ground Dove (T)	*Pampusana jobiensis*				1/–		1/–
Bronze Ground Dove (T)	*Pampusana beccarii*				10/7	46/9	56/16
Pheasant Pigeon (T)	*Otidiphaps nobilis*		155/88	40/119	3/3		198/210
Papuan Mountain Pigeon	*Gymnophaps albertisii*					1/–	1/–
Chestnut Forest Rail (T)	*Rallicula rubra*					32/6	32/6
Forbes's Forest Rail (T)	*Rallicula forbesi*			5/1	14/10		19/11
Bare-eyed Rail (T)	*Gymnocrex plumbeiventris*			8/7		–/1	8/8
New Guinea Woodcock (T)	*Scolopax rosenbergii*					124/26	124/26
Papuan Eagle	*Harpyopsis novaeguineae*	VU, P	1/–				1/–
Grey-headed Goshawk	*Accipiter poliocephalus*		1/–				1/–
Shovel-billed Kookaburra	*Clytoceyx rex*				3/–	–/3	3/3
Dusky Lory	*Pseudeos fuscata*			–/4			–/4
Papuan Pitta (T)	*Erythropitta macklotii*		4/13	139/121			143/134
Ochre-breasted Catbird	*Ailuroedus stonii*		3/1	–/1			3/2
Black-capped Catbird	*Ailuroedus melanocephalus*			6/–			6/–

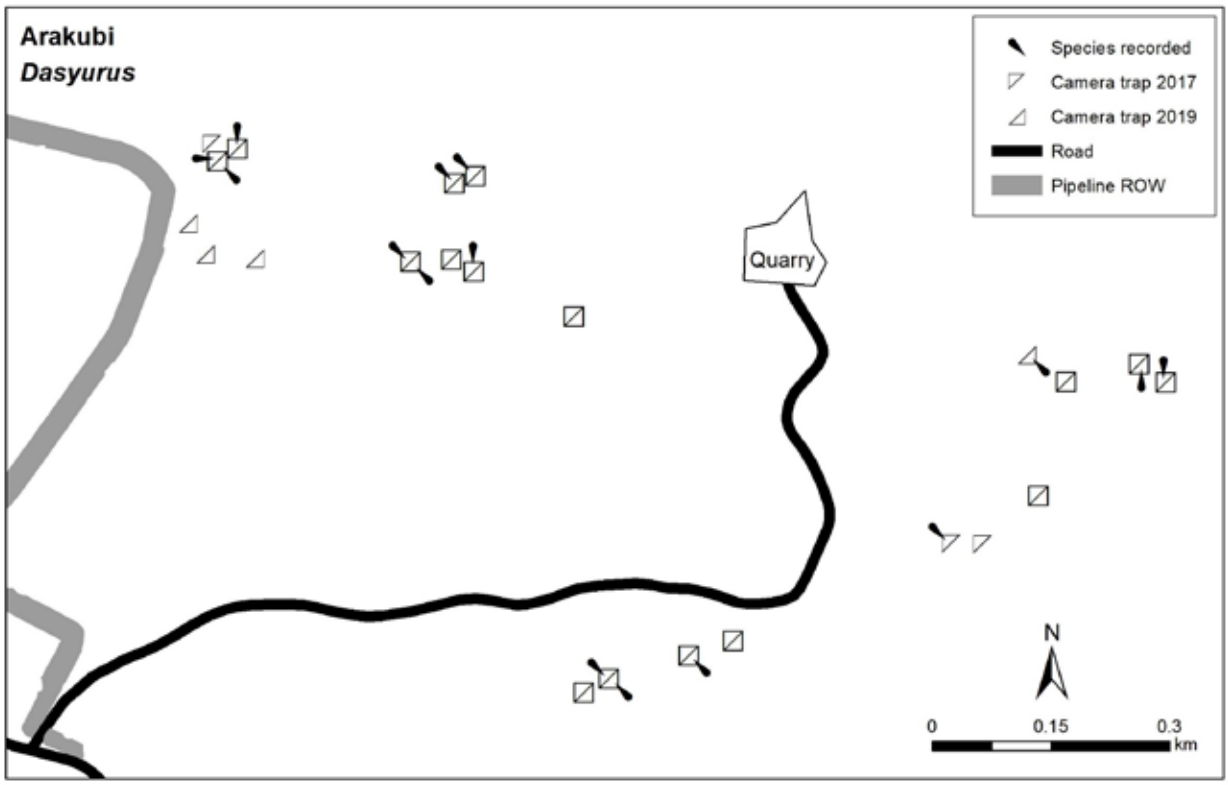
English Name	Scientific Name	Status	No. events				
			Arakubi	KP107	Hides Low	Hides High	Total
Archbold's Bowerbird	*Archboldia papuensis*	NT				1/–	1/–
MacGregor's Bowerbird	*Amblyornis macgregoriae*				–/1	2/–	2/1
Long-billed Honeyeater	*Melilestes megarhynchus*		1/–				1/–
Rusty Mouse-warbler (T)	*Origma murina*		7/2				7/2
Mountain Mouse-warbler (T)	*Origma robusta*				1/2	2/11	3/13
Large Scrubwren	*Sericornis nouhuysi*					1/–	1/–
Papuan Logrunner (T)	*Orthonyx novaeguineae*				35/25	28/2	63/27
Crested Satinbird	*Cnemophilus macgregorii*					3/–	3/–
Fan-tailed Berrypecker	*Melanocharis versteri*				–/1		–/1
Spotted Jewel-babbler (T)	*Ptilorrhoa leucosticta*				62/96	18/3	80/99
Chestnut-backed Jewel-babbler (T)	*Ptilorrhoa castanonota*		22/18	21/18			43/36
Jewel-babbler sp. (T)	*Ptilorrhoa* sp.			3/3			3/3
Black Butcherbird	*Melloria quoyi*		–/2				–/2
Rufous-naped Bellbird (T)	*Aleadryas rufinucha*				19/35	17/16	36/51
Piping Bellbird (T)	*Ornorectes cristatus*		17/18	20/26			37/44
Sclater's Whistler	*Pachycephala soror*				1/–		1/–
Variable Shrikethrush	*Colluricincla fortis*		–/1				–/1
Hooded Pitohui	*Pitohui dichrous*			1/–			1/–
Sooty Thicket Fantail	*Rhipidura threnothorax*		–/1				–/1
Black Fantail	*Rhipidura atra*				1/6		1/6
Dimorphic Fantail	*Rhipidura brachyrhyncha*				–/1		–/1
Lesser Melampitta (T)	*Melampitta lugubris*				1/–	116/92	117/92
Greater Melampitta (T)	*Megalampitta gigantea*		2/1	7/10			9/11
Queen Carola's Parotia	*Parotia carolae*	P		4/–			4/–
Brown Sicklebill	*Epimachus meyeri*	P			3/3	18/4	21/7
Magnificent Bird-of-paradise	*Diphyllodes magnificus*	P		–/2			–/2
White-winged Robin	*Peneothello sigillata*					–/2	–/2
Slaty Robin	*Peneothello cyanus*				1/13		1/13
Black-throated Robin	*Plesiodryas albonotata*					–/1	–/1
Ashy Robin	*Heteromyias albispecularis*				19/4	16/36	35/40
Papuan Scrub Robin (T)	*Drymodes beccarii*		16/7	18/28			34/35
White-eyed Robin	*Pachycephalopsis poliosoma*			3/–			3/–
Greater Ground Robin (T)	*Amalocichla sclateriana*					80/15	80/15
Lesser Ground Robin (T)	*Amalocichla incerta*				135/138		135/138
Russet-tailed Thrush (T)	*Zoothera heinei*		3/11	23/50			26/61
Blue-faced(/Papuan) Parrotfinch	*Erythrura trichroa(/ papuana)*					–/2	–/2
Reptiles							
Monitor species	*Varanus indicus*-group		7/10	1/–			8/10

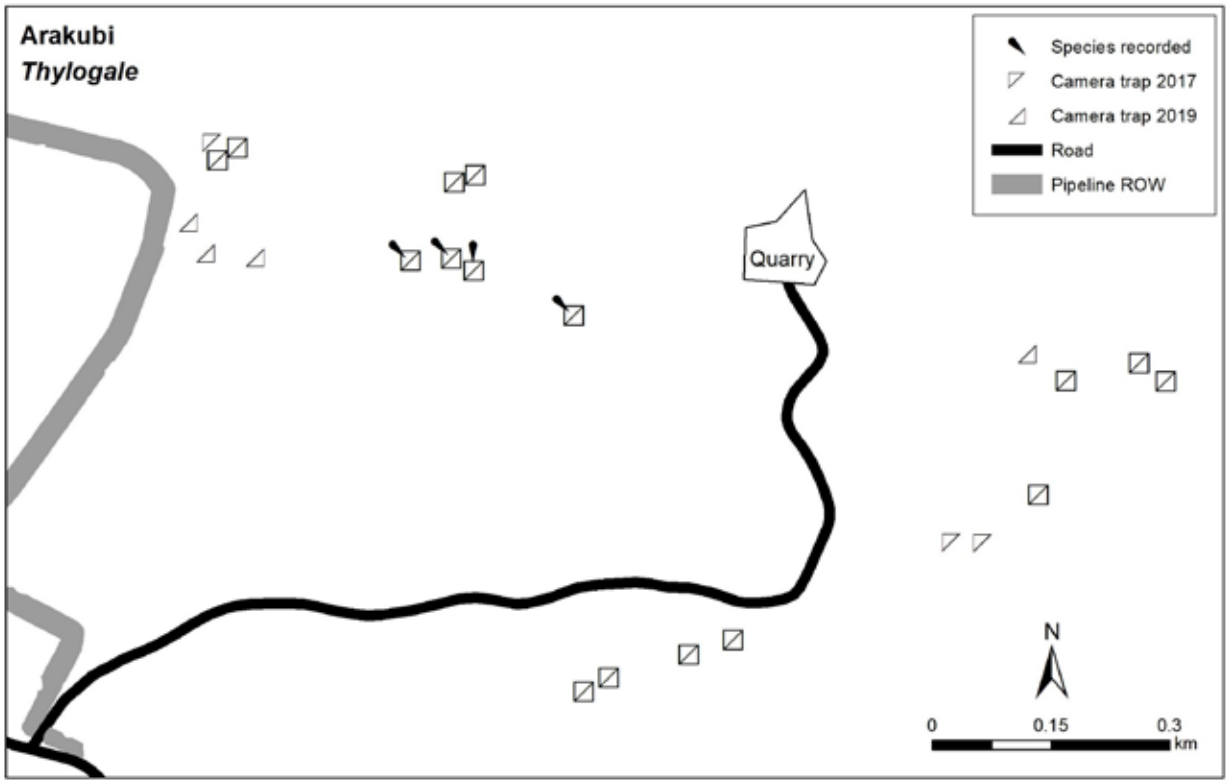
Appendix 2.2.

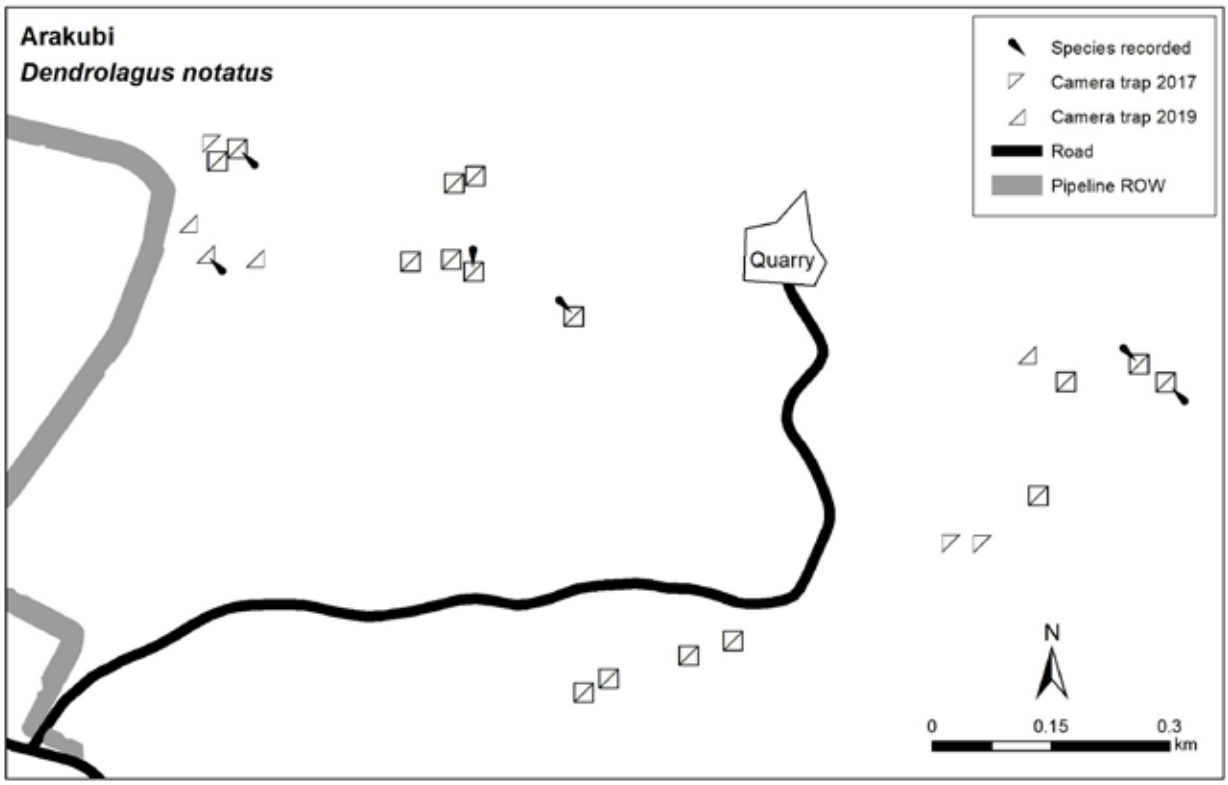
Maps showing the positions at which various priority monitoring target species were camera trapped in 2017 and 2019, grouped by site and taxonomic order. Detections are mapped for most terrestrial IUCN listed species (all except the ubiquitous Small Dorcopsis (*Dorcopsulus vanheurni*)) as well as the isolated population of Greater Ground Robin (*Amalocichla sclateriana*) at Hides High.

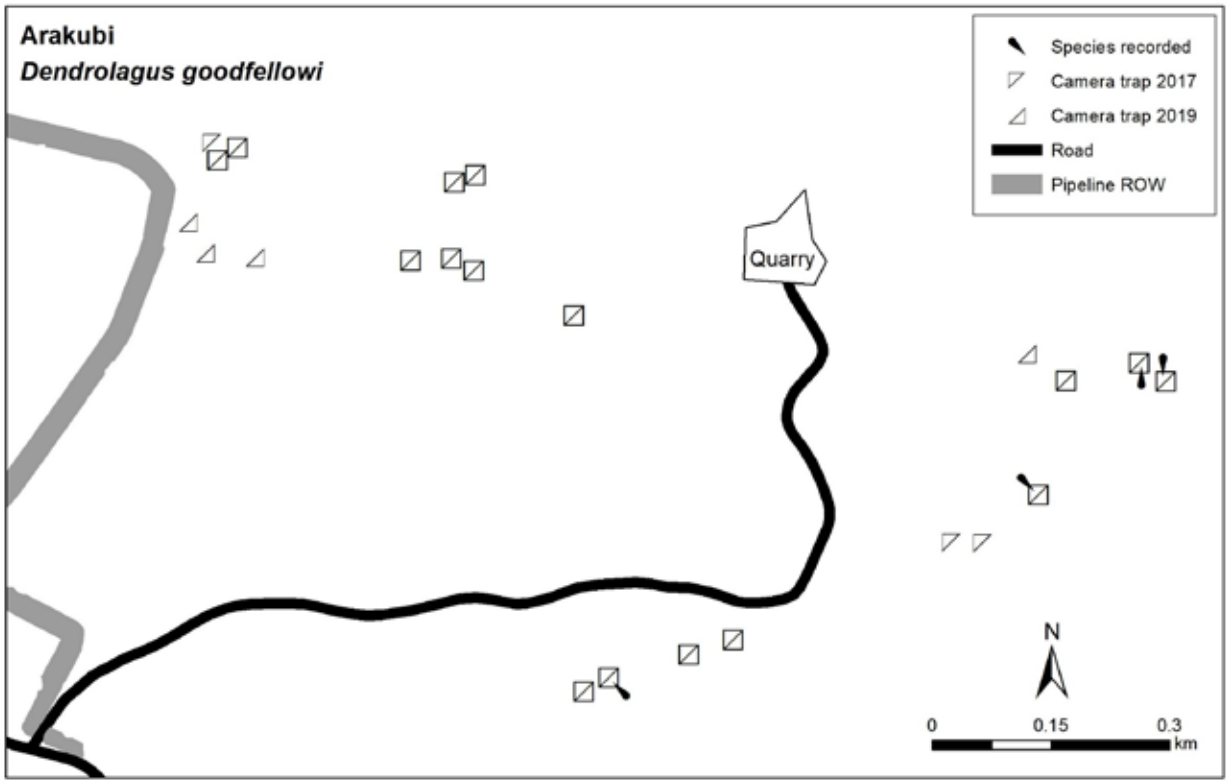





Arakubi
Dasyurus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Quarry
N
0
0.15
0.3
km


Arakubi
Thylogale
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Quarry
N
0
0.15
0.3
km


Arakubi
Dendrolagus notatus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Quarry
N
0
0.15
0.3
km


Arakubi
Dendrolagus goodfellowi
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Quarry
N
0
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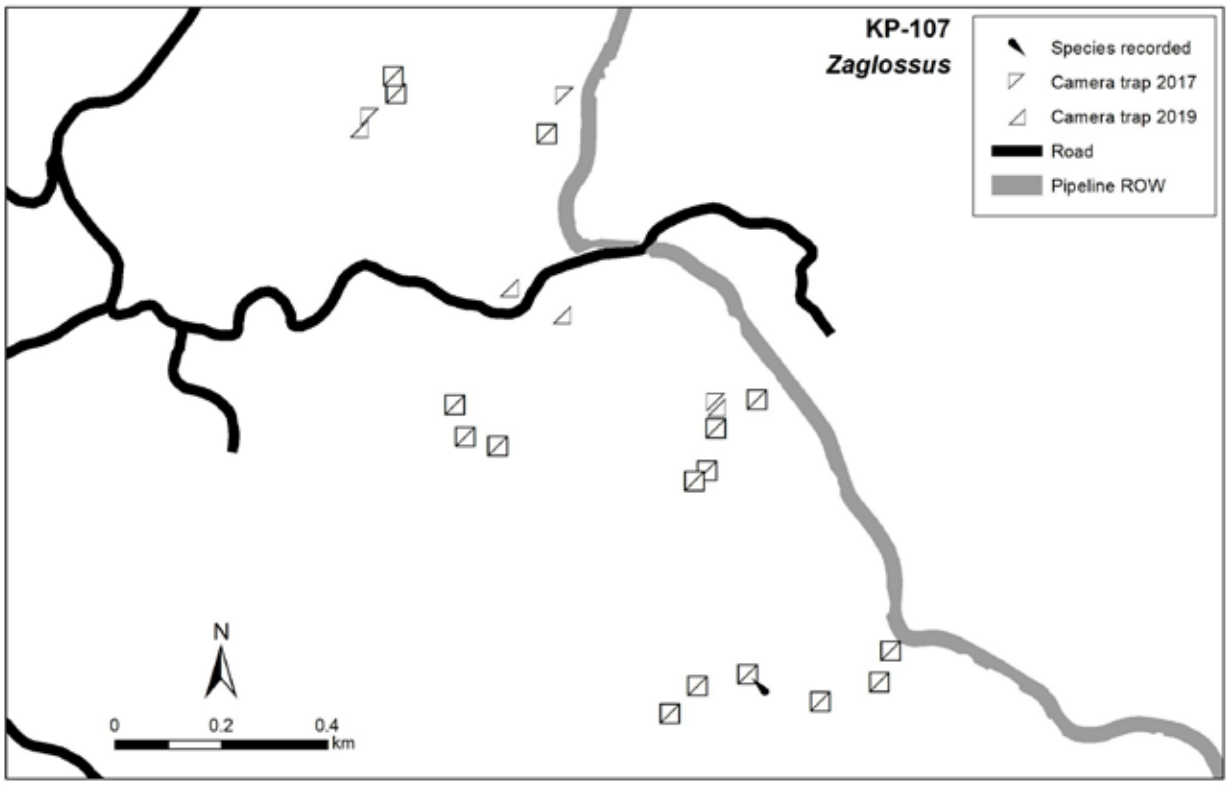
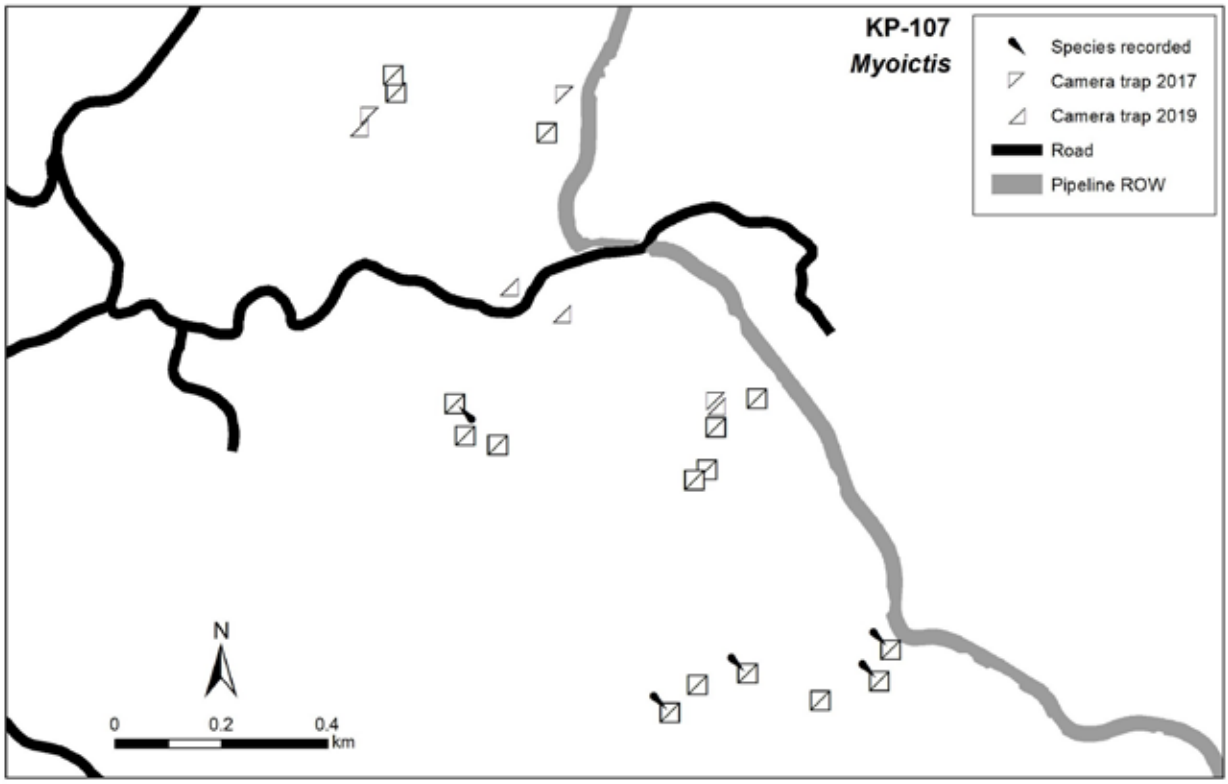
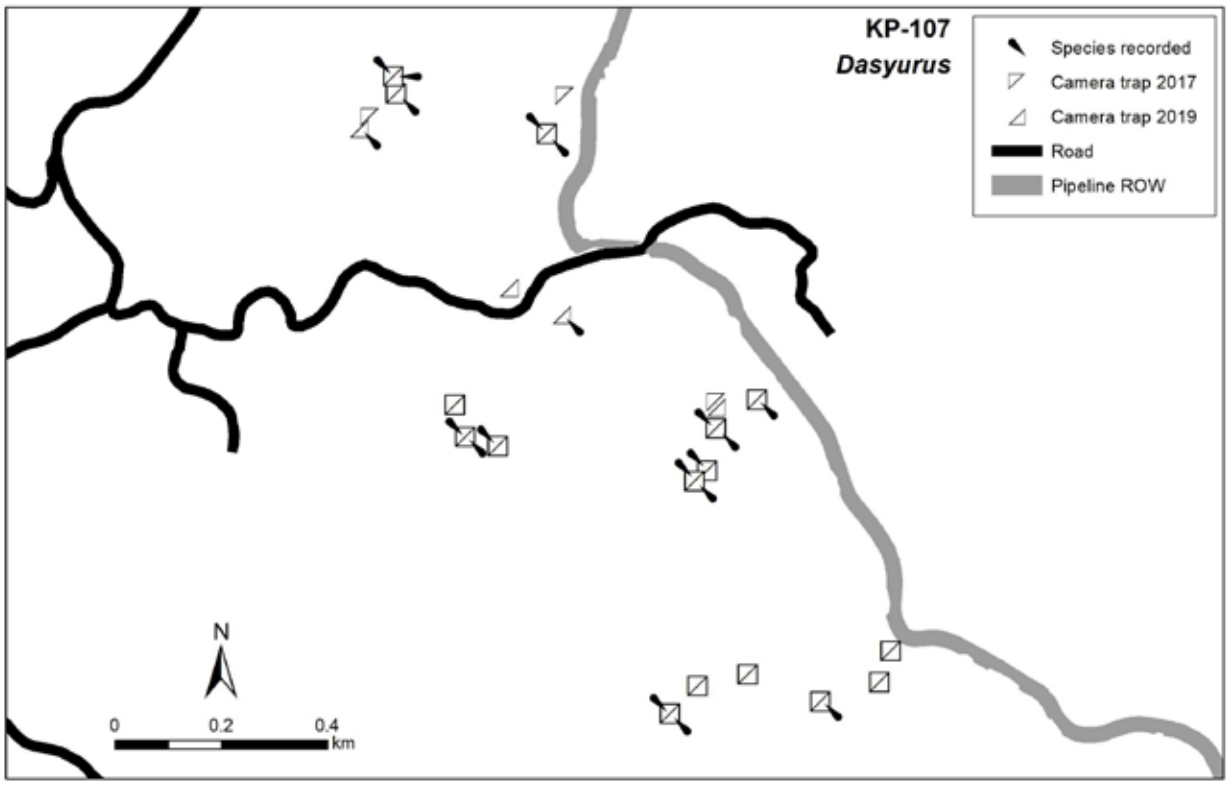
km


KP-107
Zaglossus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
N
0
0.2
0.4
km


KP-107
Myoictis
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
N
0
0.2
0.4
km


KP-107
Dasyurus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
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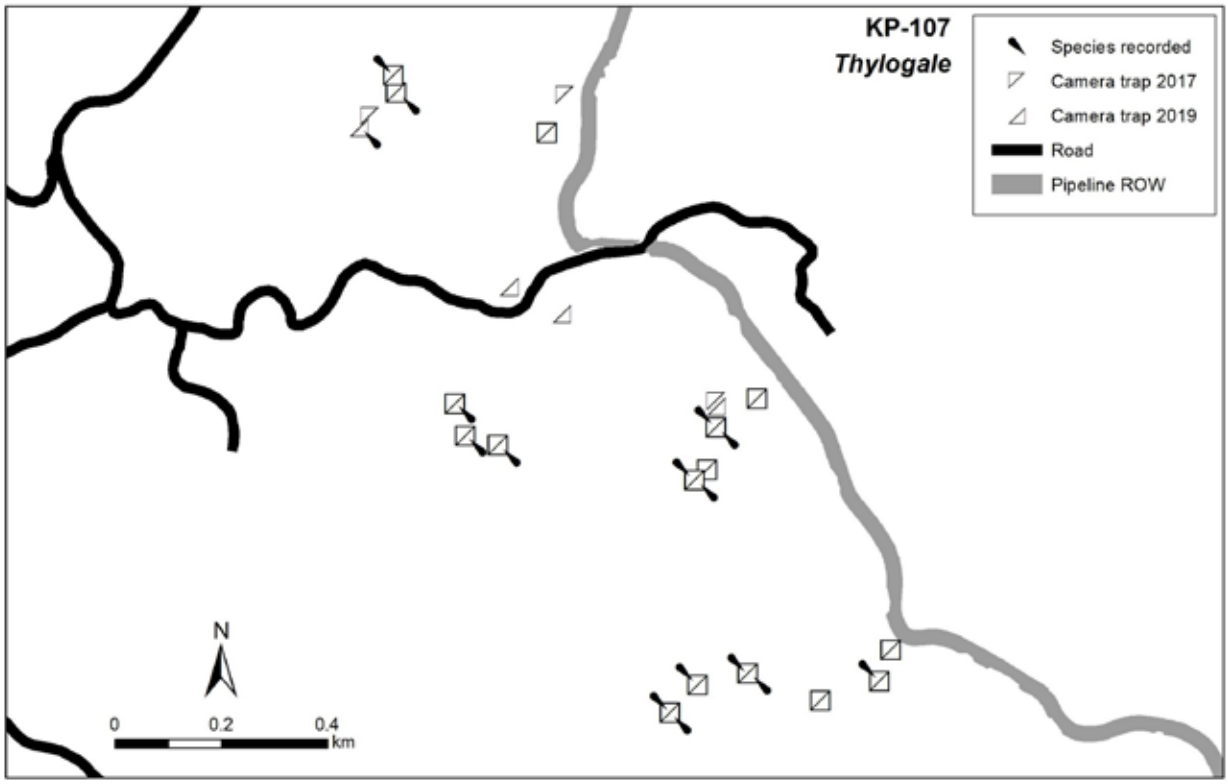
KP-107
Thylogale
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
N
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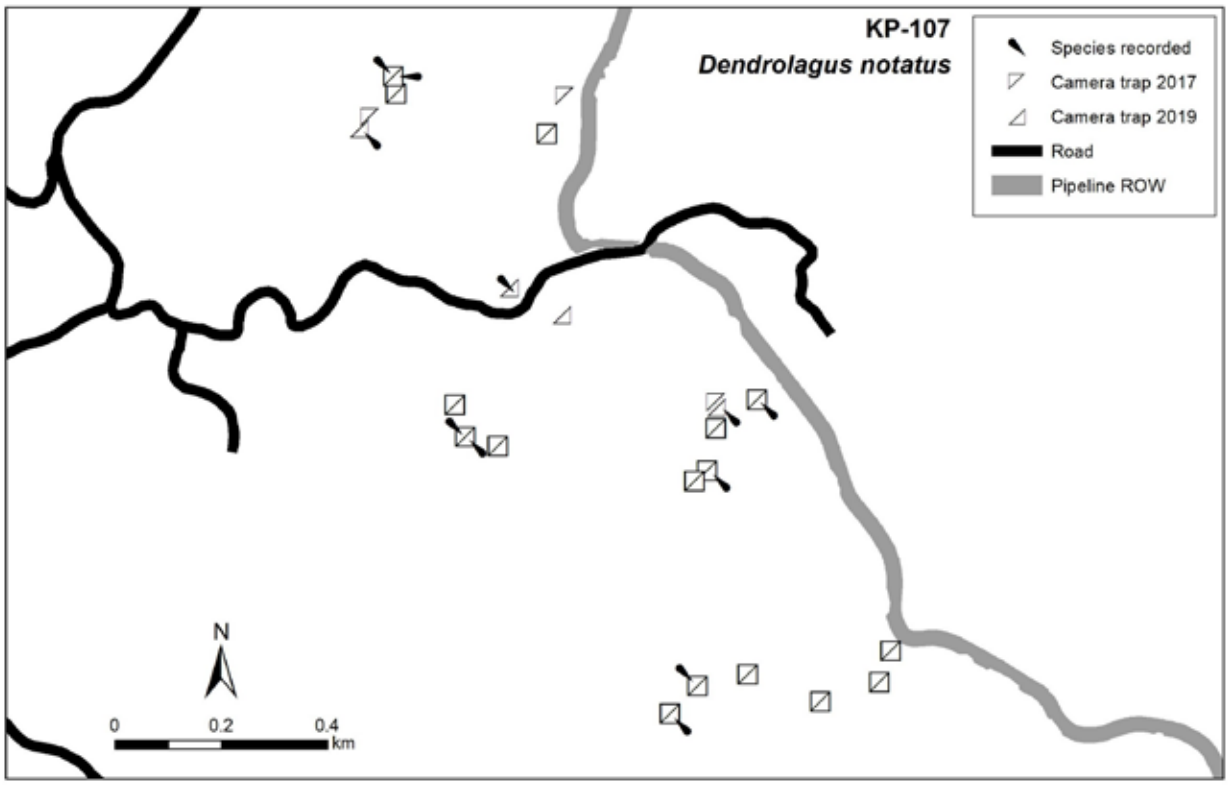
KP-107
Dendrolagus notatus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
N
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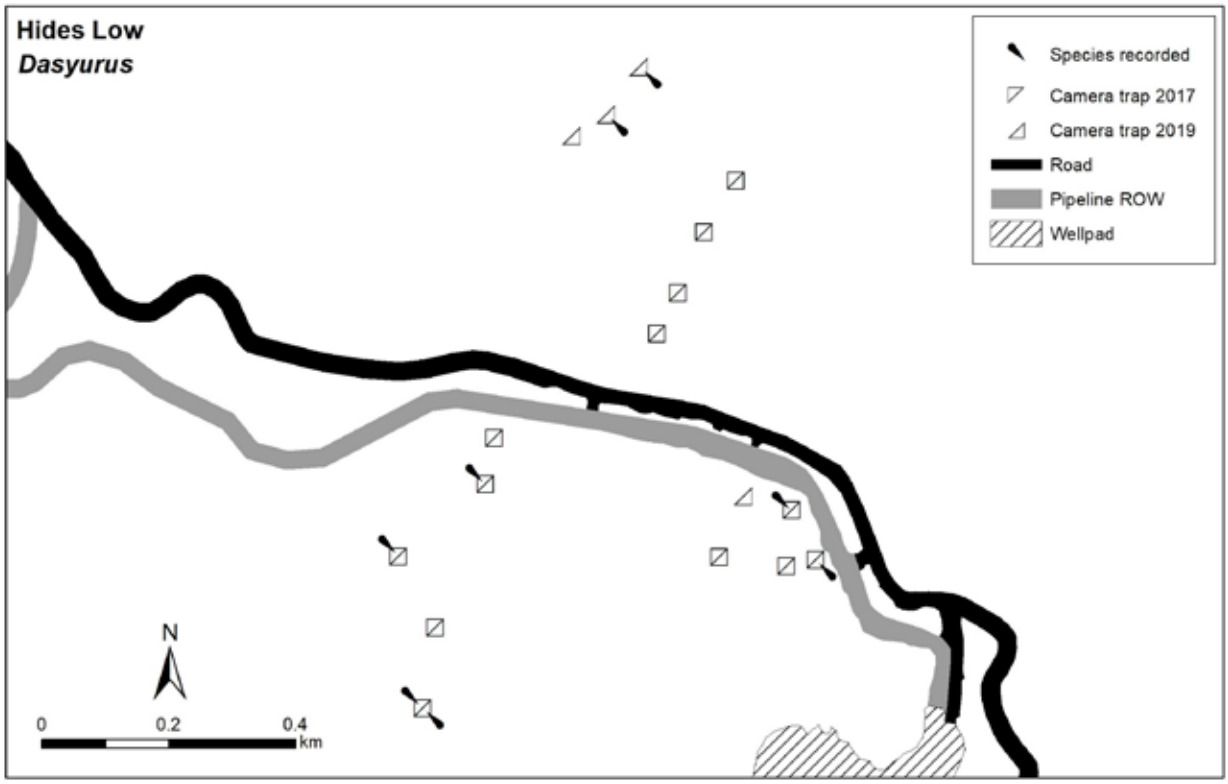
km


Hides Low
Dasyurus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Wellpad
N
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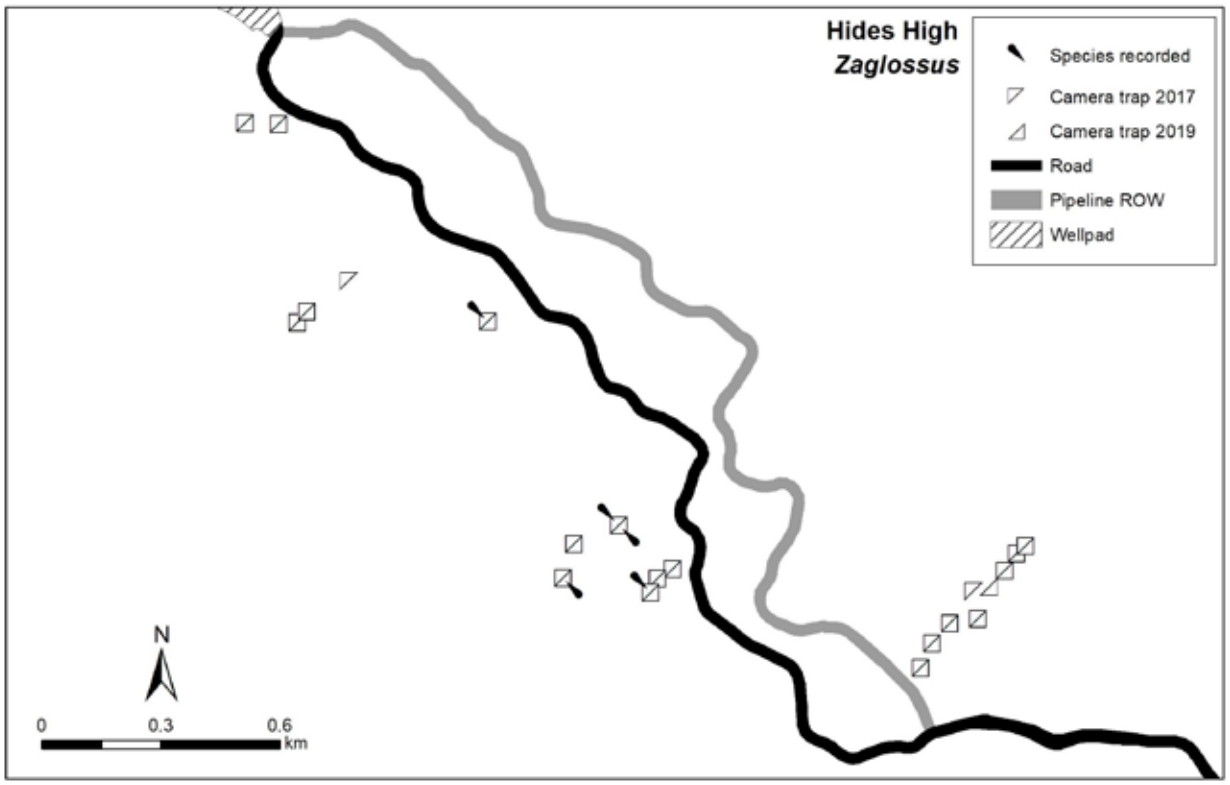
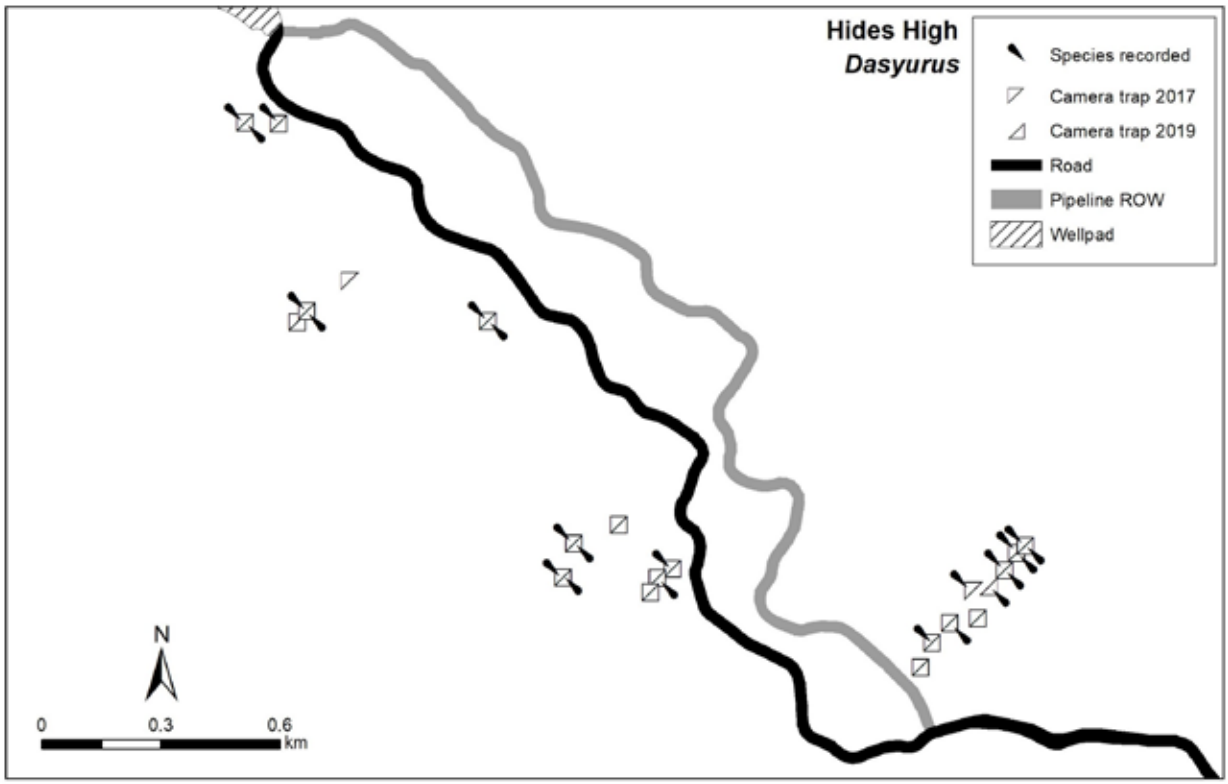
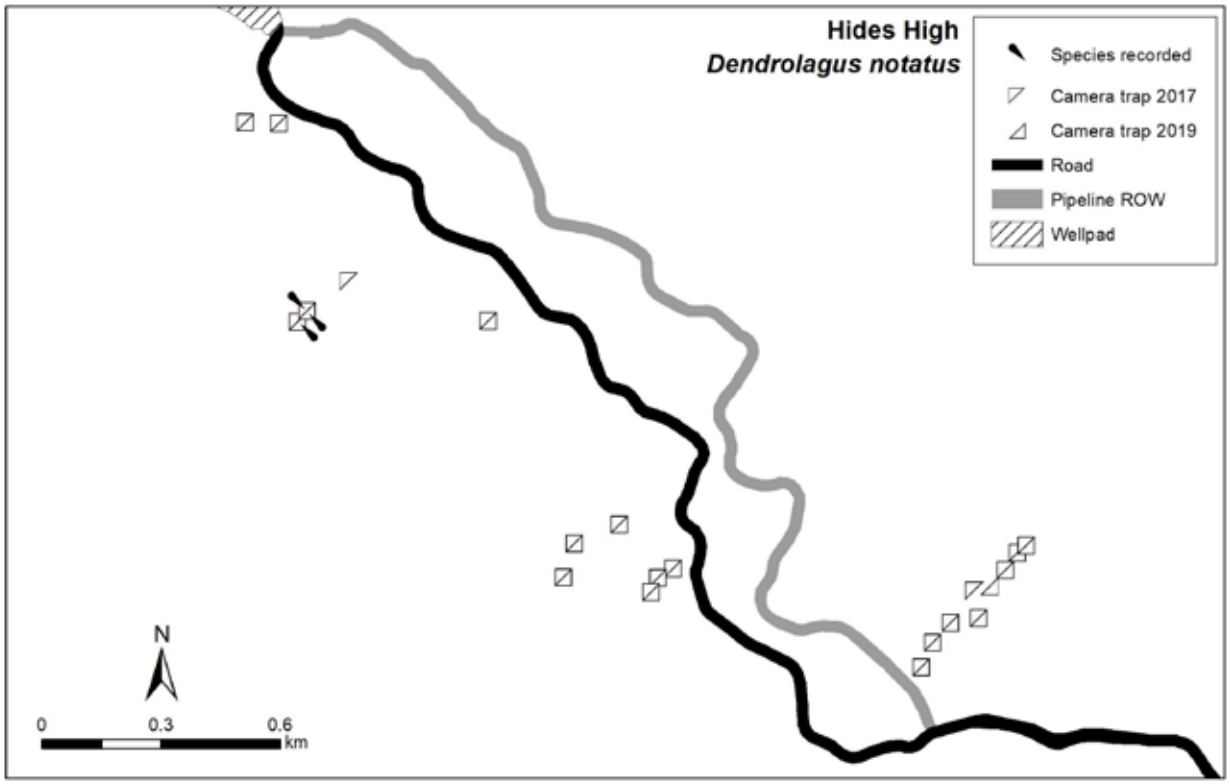
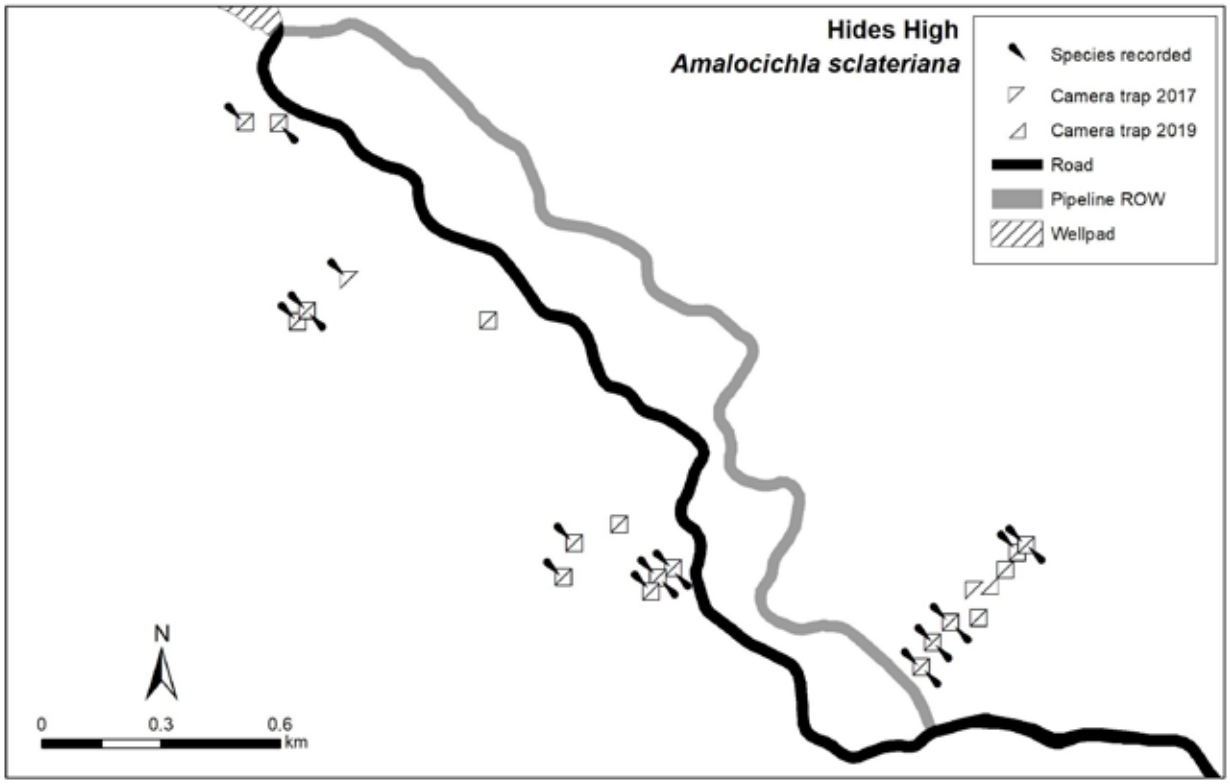
0.2
0.4
km


Hides High
Zaglossus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Wellpad
N
0
0.3
0.6
km


Hides High
Dasyurus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Wellpad
N
0
0.3
0.6
km


Hides High
Dendrolagus notatus
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Wellpad
N
0
0.3
0.6
km


Hides High
Amalocichla sclateriana
Species recorded
Camera trap 2017
Camera trap 2019
Road
Pipeline ROW
Wellpad
N
0
0.3
0.6
km

Appendix 2.3.

Model-averaged coefficient point estimates, standard errors (SE), *P*-values and the relative importance of each of the most influential covariates present in the ΔAIC_c<6 candidate set for each species-site/BAA. The number of models in which each variable appears, and (in brackets) the total number of models in the candidate set, is also shown. Results are presented for all covariates with a relative importance value >0.2, or for the three most important covariates in cases where fewer than three have a relative importance value >0.2. 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; CnpHt – canopy height; TrSm/TrLge – density of trees > 10/30 cm dbh; UD1/UD2 – understorey density below 1/2 m; LfLit – leaf litter depth; Moss/Rock/Logs – proportion of the ground surface covered by moss, rock or large woody debris.

Taxa/sites/covariates	Estimate	SE	*P*-value	Rel. Imp.	No. models
Speckled Dasyure (*Neophscogale lorentzii*) – Hides High					
TrSm	-0.013	0.025	0.624	0.259	45(164)
Moss	-0.093	0.270	0.734	0.253	48
UD1	-0.041	0.103	0.697	0.235	42
Rock	-0.052	0.160	0.750	0.200	44
Narrow-striped Dasyure (*Phascolosorex dorsalis*) – Hides Low					
LT100 (>100)	0.122	0.347	0.731	0.198	13(70)
Logs	-0.022	0.213	0.921	0.175	14
TrLge	-0.019	0.071	0.792	0.134	12
New Guinea Quoll (*Dasyurus albopunctatus*) – Arakubi					
Rock	0.004	0.053	0.946	0.134	9(47)
Moss	0.027	0.103	0.798	0.133	9
CnpHt	-0.003	0.021	0.889	0.125	8
New Guinea Quoll *(Dasyurus albopunctatus*) – KP107					
Year (2019)	0.205	0.399	0.613	0.315	31(85)
TrSm	0.004	0.014	0.778	0.177	
TrLge	-0.025	0.069	0.720	0.172	
New Guinea Quoll *(Dasyurus albopunctatus*) – Hides High					
TrLge	-0.077	0.093	0.414	0.502	68(144)
TrSm	-0.011	0.019	0.573	0.337	49
UD1	-0.009	0.044	0.849	0.169	30
Raffray's Bandicoot (*Peroryctes raffrayana*) – Arakubi					
Rock	**-0.312**	**0.194**	**0.112**	**0.795**	**113(165)**
CnpHt	0.032	0.049	0.517	0.506	75
UD1	-0.046	0.089	0.611	0.262	35
Moss	0.079	0.224	0.726	0.250	40
$Rock^2$	0.013	0.040	0.756	0.236	38
DRd	0.000	0.001	0.741	0.214	35
Raffray's Bandicoot (*Peroryctes raffrayana*) – KP107					
LT50 (>50)	**1.238**	**0.239**	**0.000**	**1.000**	**20(20)**
CnpHt	**0.041**	**0.036**	**0.261**	**0.654**	**10**

Taxa/sites/covariates	Estimate	SE	*P*-value	Rel. Imp.	No. models
Logs	**-0.268**	**0.252**	**0.296**	**0.644**	**10**
Year (2019)	0.183	0.185	0.331	0.603	10
TrLge	0.036	0.053	0.495	0.356	10
Raffray's Bandicoot (*Peroryctes raffrayana*) – Hides Low					
TrSm	0.033	0.034	0.349	0.551	32(98)
Moss	-0.539	0.769	0.488	0.533	50
Year (2019)	-0.277	0.411	0.510	0.451	39
Moss^2	-0.085	0.159	0.595	0.299	27
Raffray's Bandicoot (*Peroryctes raffrayana*) – Hides High					
LfLit	**0.025**	**0.017**	**0.136**	**0.825**	**53(83)**
LR50	-0.016	0.018	0.383	0.512	30
Rock	-0.001	0.157	0.993	0.459	42
LT100Rd (>100)	-0.169	0.304	0.580	0.294	22
TrLge	-0.013	0.028	0.653	0.261	25
TrSm	0.004	0.008	0.644	0.259	17
Striped Bandicoot (*Microperoryctes longicauda*) – Hides Low					
TrSm	**0.040**	**0.023**	**0.082**	**0.841**	**27(38)**
LT100 (>100)	**0.335**	**0.333**	**0.324**	**0.642**	**20**
Moss	-0.104	0.270	0.704	0.328	15
Striped Bandicoot (*Microperoryctes longicauda*) – Hides High					
CnpHt	0.052	0.053	0.326	0.649	167(296)
Year (2019)	0.114	0.227	0.621	0.324	98
TrSm	-0.023	0.048	0.629	0.297	95
TrLge	-0.007	0.013	0.610	0.291	86
LR100	0.007	0.014	0.628	0.291	91
LT100Rd (>100)	-0.126	0.282	0.660	0.269	79
Ground Cuscus (*Phalanger gymnotis*) – Arakubi					
TrLge	0.062	0.107	0.565	0.311	38(107)
LT100Rd (>100)	-0.129	0.385	0.744	0.189	22
Moss	-0.038	0.135	0.782	0.171	22
Ground Cuscus (*Phalanger gymnotis*) – KP107					
Year (2019)	0.461	0.542	0.400	0.483	74(165)
CnpHt	0.037	0.053	0.491	0.427	72
Logs	0.106	0.303	0.731	0.276	45
Small Dorcopsis (*Dorcopsulus vanheurni*) – Arakubi					
LR20	**-0.095**	**0.025**	**0.000**	**1.000**	**9(9)**
TrLge	**0.149**	**0.055**	**0.009**	**0.956**	**8**
UD1	**-0.135**	**0.064**	**0.042**	**0.931**	**7**
DRd	-0.001	0.001	0.378	0.509	2
Moss	-0.071	0.124	0.571	0.293	2
Small Dorcopsis (*Dorcopsulus vanheurni*) – KP107					
LT50 (>50)	**1.285**	**0.281**	**0.000**	**1.000**	**18(18)**
UD2	**0.075**	**0.025**	**0.003**	**0.935**	**16**

Taxa/sites/covariates	Estimate	SE	*P*-value	Rel. Imp.	No. models
Year (2019)	**0.330**	**0.272**	**0.231**	**0.701**	**10**
TrSm	**-0.017**	**0.017**	**0.312**	**0.619**	**9**
Small Dorcopsis (*Dorcopsulus vanheurni*) – Hides Low					
Logs	**-0.172**	**0.167**	**0.312**	**0.630**	**36(76)**
LT100 (>100)	0.331	0.335	0.331	0.627	48
Rock	**0.250**	**0.248**	**0.320**	**0.606**	**34**
UD1	-0.056	0.091	0.543	0.353	22
Small Dorcopsis (*Dorcopsulus vanheurni*) – Hides High					
Logs	**-0.562**	**0.177**	**0.002**	**0.980**	**92(95)**
TrSm	-0.007	0.010	0.481	0.479	46
LR20	-0.004	0.013	0.731	0.204	16
Pademelon (*Thylogale* sp.) – KP107					
Year (2019)	-0.095	0.277	0.736	0.178	12(62)
TrSm	-0.004	0.014	0.803	0.162	11
UD1	-0.017	0.065	0.801	0.146	11
Dwarf Cassowary (*Casuarius bennetti*) – BAA2					
Year (2019)	**-0.836**	**0.482**	**0.085**	**0.826**	**226(329)**
Site	-0.435	0.919	0.638	0.495	152
LT50 (>50)	0.339	0.530	0.524	0.380	106
TrSm	-0.020	0.032	0.539	0.368	106
Wattled Brushturkey (*Aepypodius arfakiensis*) – KP107					
CnpHt	-0.072	0.080	0.374	0.540	53(122)
LR20	0.027	0.037	0.476	0.436	41
TrSm	-0.019	0.029	0.528	0.381	42
UD2	-0.010	0.026	0.719	0.206	33
Collared Brushturkey (*Talegalla jobiensis*) – Arakubi					
DClr	**0.011**	**0.002**	**0.000**	**1.000**	**17(17)**
UD2	**-0.074**	**0.032**	**0.024**	**0.939**	**15**
Logs	0.145	0.728	0.846	0.255	7
Collared Brushturkey (*Talegalla jobiensis*) – KP107					
Year (2019)	**-1.668**	**0.398**	**0.000**	**1.000**	**137(137)**
LT50 (>50)	0.322	0.618	0.606	0.269	36
Logs	-0.121	0.375	0.751	0.262	33
UD2	-0.008	0.020	0.709	0.246	38
LR20	-0.011	0.027	0.693	0.240	32
New Guinea Scrubfowl (*Megapodius decollatus*) – Arakubi					
LR20	**-0.107**	**0.077**	**0.170**	**0.750**	**53(80)**
Logs	1.740	3.359	0.608	0.353	27
LT50 (>50)	-0.444	0.786	0.575	0.315	21
$Logs^2$	0.332	0.620	0.595	0.272	17

Taxa/sites/covariates	Estimate	SE	*P*-value	Rel. Imp.	No. models
New Guinea Scrubfowl (*Megapodius decollatus*) – KP107					
DRd	**-0.004**	**0.003**	**0.158**	**0.809**	**52(74)**
UD1	**-0.153**	**0.140**	**0.280**	**0.665**	**38**
Logs	0.054	0.591	0.929	0.413	24
LfLit	-0.004	0.009	0.662	0.253	16
LR20	-0.013	0.030	0.671	0.217	11
Moss	-0.080	0.234	0.734	0.211	16
New Guinea Scrubfowl (*Megapodius decollatus*) – Hides Low					
LT100 (>100)	**0.571**	**0.519**	**0.280**	**0.683**	**86(142)**
Moss	-0.319	0.543	0.561	0.447	58
Rock	1.032	4.379	0.815	0.188	30
Pheasant Pigeon (*Otidiphaps nobilis*) – Arakubi					
Moss	**-0.504**	**0.278**	**0.077**	**0.992**	**38(39)**
DRd	**0.003**	**0.001**	**0.026**	**0.962**	**35**
LR20	0.023	0.033	0.485	0.417	9
Year (2019)	-0.189	0.314	0.553	0.359	10
Pheasant Pigeon (*Otidiphaps nobilis*) – KP107					
Year (2019)	**1.002**	**0.314**	**0.002**	**1.000**	**31(31)**
LT50 (>50)	**1.572**	**0.515**	**0.003**	**1.000**	**31**
LR50	0.008	0.016	0.636	0.280	7
TrSm	-0.004	0.011	0.746	0.202	8
New Guinea Woodcock (*Scolopax rosenbergii*) – Hides High					
LR100	-0.016	0.034	0.634	0.264	75(242)
Logs	0.013	0.265	0.963	0.262	59
UD2	0.022	0.048	0.650	0.253	63
CnpHt	0.022	0.063	0.739	0.247	59
Year (2019)	-0.124	0.370	0.742	0.225	65
$Logs^2$	-0.274	0.620	0.661	0.200	39
Papuan Pitta (*Erythropitta macklotii*) – KP107					
LT100Rd (>100)	**-1.358**	**1.159**	**0.248**	**0.709**	**42(69)**
Logs	-0.650	0.672	0.338	0.573	39
LR20	-0.047	0.062	0.458	0.504	26
UD1	-0.034	0.095	0.728	0.225	13
Papuan Logrunner (*Orthonyx novaeguineae*) – Hides Low					
LT50 (>50)	**-2.167**	**0.651**	**0.001**	**0.988**	**53(55)**
Year (2019)	-0.325	0.535	0.552	0.394	24
TrLge	-0.046	0.113	0.690	0.206	15
Papuan Logrunner (*Orthonyx novaeguineae*) – Hides High					
LT100Rd (>100)	-0.207	0.543	0.708	0.199	9(47)
Rock	-0.048	0.223	0.831	0.175	10
TrSm	-0.002	0.013	0.901	0.164	9
Sotted Jewel-babbler (*Ptilorrhoa leucosticta*) – Hides Low					
CnpHt	0.050	0.058	0.394	0.487	29(72)

Taxa/sites/covariates	Estimate	SE	*P*-value	Rel. Imp.	No. models
Logs	-0.107	0.235	0.657	0.361	25
LR20	-0.019	0.040	0.641	0.210	14
LT100Rd (>100)	-0.121	0.340	0.729	0.204	17
Chestnut-backed Jewel-babbler (*Ptilorrhoa castanonota*) – Arakubi					
LfLit	-0.002	0.006	0.802	0.153	11(74)
TrLge	0.006	0.035	0.869	0.146	12
LT100Rd (>100)	-0.107	0.336	0.753	0.137	12
Chestnut-backed Jewel-babbler (*Ptilorrhoa castanonota*) – KP107					
Rock	-0.052	0.116	0.118	0.300	53(159)
TrLge	-0.040	0.089	0.091	0.264	46
DRd	0.000	0.001	0.001	0.186	38
Piping Bellbird (*Ornorectes cristatus*) – Arakubi					
Rock	-0.209	0.243	0.397	0.509	42(79)
DRd	0.001	0.002	0.711	0.153	11
Logs	0.032	0.403	0.940	0.127	16
Piping Bellbird (*Ornorectes cristatus*) – KP107					
TrSm	0.014	0.022	0.544	0.343	40(103)
UD2	-0.007	0.021	0.745	0.150	19
CnpHt	-0.008	0.029	0.773	0.145	20
Papuan Scrub Robin (*Drymodes beccarii*) – KP107					
UD1	0.056	0.112	0.621	0.272	22(93)
DRd	0.001	0.002	0.686	0.250	25
LR20	-0.014	0.039	0.722	0.170	15
Lesser Melampitta (*Melampitta lugubris*) – Hides High					
LT100 (>100)	**-2.053**	**0.374**	**0.000**	**1.000**	**84(84)**
TrSm	-0.010	0.015	0.532	0.421	33
LR50	0.007	0.018	0.691	0.275	24
TrLge	-0.021	0.048	0.669	0.265	26
Year (2019)	-0.115	0.264	0.666	0.226	26
Greater Ground Robin (*Amalocichla sclateriana*) – Hides High					
Year (2019)	**-1.328**	**0.495**	**0.009**	**0.974**	**59(63)**
TrSm	-0.025	0.026	0.350	0.615	31
LT100 (>100)	-0.466	0.567	0.417	0.500	24
UD1	0.066	0.104	0.532	0.378	27
Russet-tailed Thrush (*Zoothera heinei*) – KP107					
DClr	0.004	0.004	0.371	0.501	62(144)
Year (2019)	0.380	0.590	0.524	0.363	50
Rock	-0.149	0.251	0.552	0.288	36
TrSm	-0.015	0.034	0.661	0.215	41

Chapter 3 – Small non-volant mammals (Rodents)

Kyle N. Armstrong, Enock Kale, Daniel Okena and George Dahl

Paramelomys sp. cf. *rubex* B

Summary

Background and aims

The aim of this study was to document and interpret observed changes in rodent species diversity and abundance to provide informed advice about potential project-related impacts on forest quality adjacent to linear project infrastructure—the pipeline right-of-way (ROW) and accompanying access roads. The 2019 survey followed the same format as that undertaken in 2017, using the same nine trapping transects that were established in 2015 at two elevations above 2,000 m asl on Hides Ridge (BAA 1) and at two elevations below 1,500 m asl on the Agogo Range near Moro (BAA 2). This report focuses on small to medium-sized rats (Muridae) in two main groups: the tribe Hydromyini (dominated by *Paramelomys* in this study area) and the tribe Rattini (dominated by *Rattus* in this study area). Larger species of rodent and all marsupials were documented in a separate study using camera traps, and those results are presented by Woxvold et al. (this volume).

Major results

The small rodent species assemblage is different in BAA 1 and BAA 2, with no trapped species being present in both BAAs. The total number of captures of small rodents on the 2019 survey (134 individuals) was equivalent to that from 2015 (133 individuals), and over twice that from 2017 (53 individuals). However, statistical tests indicated that Species Richness and the total number of captures were not significantly different amongst the categories defining distance from the ROW, elevation and survey year. The overall patterns in the number of captures are driven by three relatively common species: *Rattus* sp. cf. *niobe* B, *R*. sp. cf. *niobe* D, and *Paramelomys* sp. cf. *rubex* A, which together made up 79.3% of captures in 2019.

Two rodent species were detected for the first time on the 2019 survey (*Lorentzimys nouhuysi* and *Pogonomys macrourus*), both of which are scansorial species that are expected to encounter box traps placed on the ground at a much lower rate than ground-dwelling and semi-fossorial rodent species. Their capture does indicate that the inventory of Muridae for the study area is still incomplete. To date, 16 species have been recorded by box trapping on survey transects, and an additional 12 species are also known from the area based on observations of camera trapping, roadkills, remains in owl pellets, and previous baseline environmental impact assessment studies conducted for the project.

The only invasive *Rattus* species encountered was *R. exulans*. Four individuals of this species were trapped on transects in BAA 2 and, like previous captures of this species during the 2015 survey, all were from trap locations close to the forest boundary or disturbed sections of the transect (as in the first c. 150 m of M4 at Arakubi Quarry). No *Rattus rattus* were detected during the 2019 survey.

Conclusions and recommendations

Genetics-based identification has been the foundation of reliable comparisons among sites, survey years and investigators in this study, and the remarkable results (that have included the discovery of at least two new species not seen elsewhere) are indicative of an under-estimated level of rodent diversity across New Guinea.

The most relevant result documented was the lack of a significant change since 2015 in Species Richness, abundance or species composition at increasing distances from the ROW, in either BAA, indicating that there has been no detectable impact of edge effects from the ROW on these taxa. The populations of native rodents sampled have so far shown good resilience to the removal of adjacent forest for the pipeline and access road, using forest habitat right to the edge. However, the forest edge is still relatively intact, and we may yet see changes that reflect a change in habitat structure and the increased presence of invasive rodents.

We recommend that the live-trapping rodent component of the study continue, that consideration be given to a rapid assessment of the presence of *R. rattus* and *R. exulans* in inhabited areas around the HGCP to provide context on how

common these species are, and how significant a source they might be for invasions along the access road and pipeline along Hides Ridge, and that the project continue to build upon the genetic work that has been initiated because morphologically diagnostic characters for most rodent species in the study area are inadequate for consistently accurate identifications. Effort to document diagnostic morphological characters in past captures and museum specimens that help distinguish the genetic groups will help improve identification in the field. Understanding the special sensitivities of native rodent species, and their interactions with commensal predators such as dogs and competitors such as *Rattus rattus*, also requires further study.

Introduction

Zones of transition between two ecological communities may have increased levels of biodiversity, but also undesirable characteristics (Harris 1988). Disturbed areas and forest edge habitats often have increased species richness relative to undisturbed forest because of the influx of species from other more open habitats, and because of the increased resources that may be present near edges (e.g., Mortellitti and Boitani 2005). By contrast, some species of the forest interior may decline if the amount of edge habitat in forest remnants dominates by proportional area (e.g., Puettker et al. 2008). The present study examines the rodent assemblage adjacent to linear infrastructure in rainforest communities at different elevations in Southern Highlands and Hela Provinces of Papua New Guinea (PNG).

Most of the literature on Papua New Guinean rodents focusses on their discovery by Europeans, their taxonomy and distribution, and their role as disease vectors, with relatively few studies of ecology. The diet of some species has been examined (McPhee 1988; Jackson and Woolley 1994; Elliott and Vernes 2020), and there have also been studies on home range (Dwyer 1978; Berry et al. 1987), and survival rate (Kale et al. 2012). Given that there is still a high level of cryptic diversity in the PNG rodent fauna (Aplin and Opiang 2017; Armstrong et al. 2019), there is a risk that ecological studies might base species-specific conclusions on an incorrectly named taxon, or on more than one taxon. The present study sought to avoid errors with species identification by using genetic markers as the basis for identification. By determining species richness and composition based on genetically-defined groups, we can confidently compare taxa across sites and years, and avoid potential errors derived from having different investigators with different levels of experience involved in the study each year.

In the 2015 survey, cytochrome-*b* mitochondrial DNA markers were used to define these groups, providing a reasonable level of discrimination of 'putative species' and revealing discrete genetic groups at different elevations in the apparently widespread species *Paramelomys rubex* and *Rattus niobe*. It also helped to assign species names to animals that could not be identified in the field. However, while the mitochondrial DNA markers helped to confirm field identifications and contributed to the construction of a working list of taxa present in the study area, some of the relationships amongst samples from the PMA3 study and other geographical regions remained unresolved, and hinted at undocumented cryptic diversity that prevented the accurate application of names to some samples.

In the 2017 survey, we introduced a newer DNA sequencing approach ('DArTseq') to avoid some of the limitations described above, and allow future investigators to allocate consistent names to taxa across survey sites and survey years. This technique provides information from thousands of genic regions, and therefore has better discriminating power than a single mitochondrial gene (Armstrong et al. 2019). Each novel capture (i.e., excluding recaptured individuals) from the 2015 (i.e., these original samples re-sequenced), 2017 and 2019 PMA3 surveys has been sequenced by the DArTseq approach. This has allowed our comparisons to be based on unambiguous identifications of native rodents. Furthermore, detection of incursions by invasive pest species such as *Rattus exulans* and *R. rattus* has become relatively straightforward with genetic markers because they are genetically well-separated from all native New Guinea rodents (e.g., Armstrong et al. 2019).

The first two PMA3 surveys in 2015 and 2017 found no overlap between ground-dwelling rodent assemblages in BAA 1 (transects at 1,000 m asl and 1,400 m asl) and BAA 2 (transects at 2,200 m asl and 2,700 m asl; Armstrong et al. 2019). There were no significant shifts in species richness or capture frequency on transects at increasing distances from the Right of Way (ROW) or its access road in either year (Armstrong et al. 2019). Given that these rodents are short-lived, biennial surveys are unlikely to encounter the same individuals so the results to date have suggested that removal of forest for the ROW has had no detectable effect on native rodent populations.

Aim

The overall aim of this study is to document and interpret observed changes in small, 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 five specific objectives (modified from Aplin and Opiang 2017):

1. Document the diversity of the small rodent assemblage within the two BAAs.

2. Determine whether there has been a significant change since 2015 in the diversity of the small rodent assemblage using the forest adjacent to the Project linear infrastructure (pipeline right-of-way and access roads).

3. Identify species of conservation significance (including new or undescribed species) within each of the BAAs and, where practicable, determine their special sensitivities.

4. Monitor the presence of exotic mammal species in each of the BAAs.

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

Methods

Overview of methods in 2019

The 2019 PMA3 survey was conducted in the same way as the 2017 survey (Armstrong et al. 2019), which departed in several respects from the initial survey in 2015 (Aplin and Opiang 2017)—by splitting the effort for camera trapping into a separate study (see Woxvold et al., this volume) and using a different genetic marker system for confirming identifications. Three main sets of methods are described for the 2019 survey: those pertaining to field sampling, those for making robust identifications using genetic markers, and those used in the statistical analysis of the trapping data.

Field sampling

The 2019 survey used the same nine trapping transects that were established in 2015 by Aplin and Opiang (2017) and operated in 2017 (Armstrong et al. 2019): five transects on Hides Ridge (BAA 1); one transect adjacent to Arakubi Quarry, and three transects at KP107 (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 placed along the transect in a T-shaped configuration (Figure 3.1). Each transect was sampled for at least five nights (Table 3.1) and the total number of trapping nights was 2,207 (one trap-night = one trap set for one night).

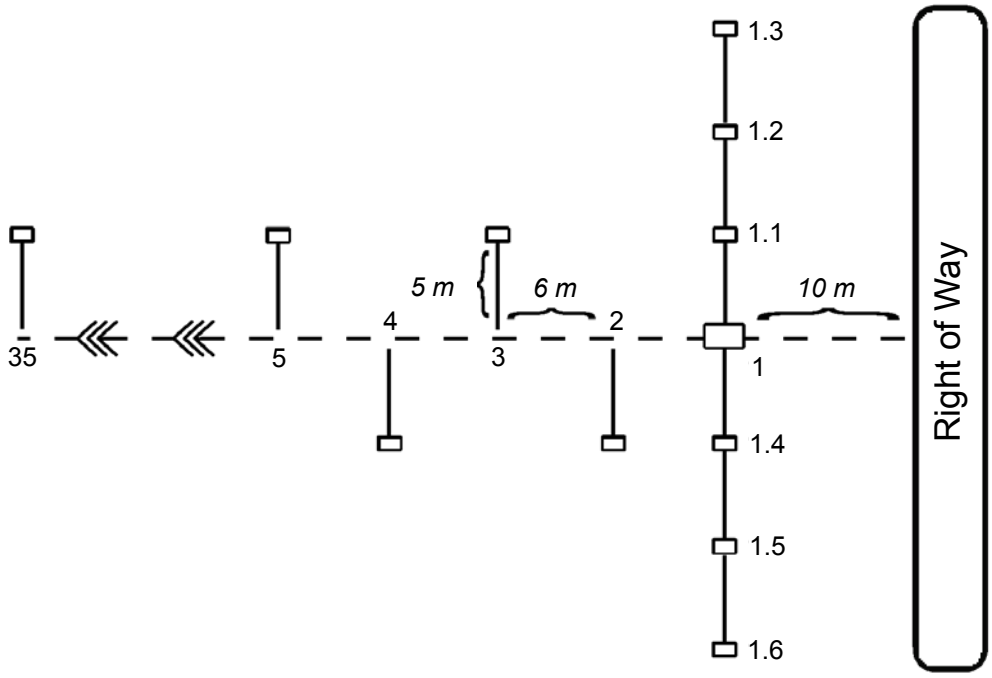


Figure 3.1. Standard design of a 210 m transect trap-line. Large rectangle = large-sized box trap; small rectangle = medium-sized box trap. The central access path is represented by the dashed line. Trap positions were located at 6 m intervals along the transect on alternate sides of the access path, and no more than 5 m to the right or left. Large-sized box traps were placed at positions 1, 11, 21 and 31. Medium-sized box traps were placed at all other positions. An additional six medium-sized box traps were placed along the forest edge parallel to the ROW to provide additional sampling of the most heavily impacted 'edge' habitat.

Table 3.1. Summary of box trap deployments in August 2019 (total number of traps is given as the number of medium-sized traps + number of large-sized traps). Note that some values for total trap nights are lower than might be expected because damage from dogs prevented redeployment of traps on some days.

Elevation (m asl)	Transect	No. traps	Open date	Close date	Total nights	Total trap nights	Elevation totals
1,000	M4	46 (44+4)	22/08/2019	29/08/2019	7	322	**322**
1,400	M1	42 (38+4)	22/08/2019	29/08/2019	7	294	
1,400	M2	41 (37+4)	23/08/2019	30/08/2019	7	287	
1,400	M3	41 (37+4)	24/08/2019	31/08/2019	7	287	**868**
2,200	H1	43 (39+4)	15/08/2019	20/08/2019	5	211	
2,200	H2	40 (36+4)	14/08/2019	19/08/2019	5	176	
2,200	H3	41 (37+4)	13/08/2019	18/08/2019	5	205	**592**
2,700	H5	43 (39+4)	11/08/2019	16/08/2019	5	215	
2,700	H6	42 (38+4)	10/08/2019	15/08/2019	5	210	**425**
						Overall	**2,207**

Trapping results depend heavily on trap condition and placement, and the status of bait. Given that the investigators across all three surveys have been different (with the exception of Enock Kale in 2017 and 2019), it was particularly relevant to ensure that the trapping lines were run with an equivalent level of diligence (see Aplin and Opiang 2017: their Appendix 5.2). Of particular 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. In 2019, the sweet potato bait was supplemented with banana slices.

Captured animals ('novel' or first-time captures) were processed on-site and then released at the point of capture. No animals were intentionally sacrificed as voucher specimens, but inadvertent trap deaths were collected as museum specimens and submitted to the South Australian Museum (Appendix 3.1). To assist with field identifications, each individual was sexed, weighed, measured (lengths of the head-body, tail and pes) and assessed for age (based on body mass and proportions) 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. Animals recaptured on subsequent trapping nights were recognised on the basis of their freshly-snipped tail tips, and re-released near the point of capture.

Genomics-based identification

To ensure that comparisons across transects, elevations and survey years were made on the basis of accurate species identifications, we built further on the accumulating genetic resource of genome-scale genetic markers by submitting a non-lethal biopsy tissue sample from every captured animal for DNA sequencing. This comparative genetic framework is still the most comprehensive ever created for New Guinea native murid rodents.

A 'reduced representation' genome sequencing approach, which generates many thousands of single variable sites (Single Nucleotide Polymorphisms: SNPs) from random locations across the entire chromosome area (the 'genome') was used for DNA sequencing. 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. 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 Technology 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 Diversity Arrays Technology. Individuals and loci that had an excess of missing data were removed. One of the simplest ways to illustrate the results is to produce an ordination plot derived from Principle Coordinates Analysis (PCoA) of the genotypes. 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 geographic origin of samples for each captured individual was coded in PCoA plots so that a species list could be created for each 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 Collection database (South Australian Museum).

Ecological analysis

Basic trapping results including the 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) were calculated. The overall percentage of recaptures (the number of recaptures divided by the number of released individuals; i.e. excluding the small number of inadvertent trap deaths) was also calculated.

The trapping results matrix used in statistical analyses consisted of elevation, transect name, trap position, capture date, field identification, capture type (novel/recapture), plus the survey year. Following genetic analysis, the 'SNP-based identification' was added. Data from 2015 and 2017 were also appended to the 2019 results. Raw data are available in the appendices of Aplin and Opiang (2017), and Armstrong et al. (2019); data from 2019 are presented in Appendix 3.2. Statistical analyses and plotting were conducted on novel captures only. All statistical tests and plots were generated in a custom-written [R] language (R Core Development Team 2020) statistical computing script, which contains a record of all manipulations of the cleaned raw dataset, and all analyses and plot instructions for transparency (script available for future surveys).

Trapping data were pooled into six distance categories, each of which included eight trapping positions (see notes in Appendix 3.3). The categories are defined as representing the immediate edge of the forest adjacent to the ROW ('0–20 metres': one large box trap at position 1, a medium-sized box trap at position 2, and the six medium-sized traps extending in parallel with the ROW either side of position 1) (see Figure 3.1); and up to five distance categories of around 50 metres ('20–70 metres': positions 3–10; '70–120 metres': positions 11–18; '120–170 metres': positions 19–26; '170–220 metres': positions 27–35; '220–370 metres': positions 36–60). Note that Aplin and Opiang (2017) established transect M4 at Arakubi Quarry to be longer than all other transects, and this has been copied in 2017 and 2019. Abundance values in each category were adjusted according to survey effort (number of trap nights per transect) in statistical tests.

Generalised Linear Mixed Models were used to determine whether there were differences in two main dependent variables: 'Species Richness' (total number of species) and 'abundance' for total number of captures from all rodent species; total captures of all Hydromyini rodents combined (genera *Hydromys*, *Leptomys, Lorentzimys, Paramelomys, Pogonomys, Uromys*), and total captures of all Rattini rodents combined (genus: *Rattus*); with three fixed factors: increasing distance from the ROW in the distance categories defined above, elevation category, and survey year; with transect as a random factor. Recapture rates were too low to include this parameter in the models (Appendix 3.4).

Species composition (the relative mix of each species at different sites) was examined by calculating Bray-Curtis Dissimilarity values for sites defined by the five distance categories, four elevations and three survey years. a Non-metric Multidimensional Scaling ordination was then used to summarise the patterns of similarity in a two-dimensional ordination plot.

Usage of scientific names

We followed the scheme established by Aplin and Opiang (2017) for naming undescribed or taxonomically ambiguous taxa. We use 'sp. cf.' to refer to individuals that resemble certain species, but where the identification cannot be confirmed. When there is more than one such taxon, they are given a sequential letter code. The codes used follow Aplin and Opiang (2017) to allow correspondence between the different mitochondrial and genome-scale genetic datasets, but there were some additional codes used in 2019 that are summarised in Appendix 3.5. For the purpose of this report, the words 'taxon' and 'taxa' are interchangeable with 'species'—distinct genetic groups as revealed by the DArTseq are treated as distinct species.

Results

Species identification

The identification framework derived from genetic markers generated during the 2015 and 2017 surveys and from context samples outside the study area permitted unambiguous association of all specimens encountered in 2019 to established genetic groupings. Patterns of species occurrence were examined across elevations (by BAA) and across survey years. Separate PCoA analyses were used to identify species of *Paramelomys* (Figures 3.2–3.4), and species of *Rattus* (Figures 3.5–3.7). Morphologically-based identifications in all surveys years including 2019 suggested that '*Paramelomys rubex*' and '*Rattus niobe*' are found across the elevational range of the study area (1,000–2,700 m asl), but the SNP-based genetic identification method showed unambiguously that there are three elevational forms in '*P. rubex*', and two in '*R. niobe*'.

A comparison of field identifications and SNP-based identification is presented in Appendix 3.2. From an inspection of this list, it is clear that some species are still difficult to identify in the field:

- Identification of *P*. sp. cf. *mollis* AC was correct in some instances, and other individuals were incorrectly attributed to *P. rubex*.
- *P*. sp. cf. *lorentzii* C was misidentified as either *P*. sp. cf. *mollis* or *P*. sp. cf. *rubex*.
- *P*. sp. cf. *rubex* A was not distinguished from *P*. sp. cf. *rubex* F.
- Some field identifications of *R. verecundus* were actually *R*. sp. cf. *niobe* D.
- Some field identifications of *R. verecundus* were also marked as *Rattus* sp.
- Some field identifications of *R. exulans* were marked as *Rattus* sp.

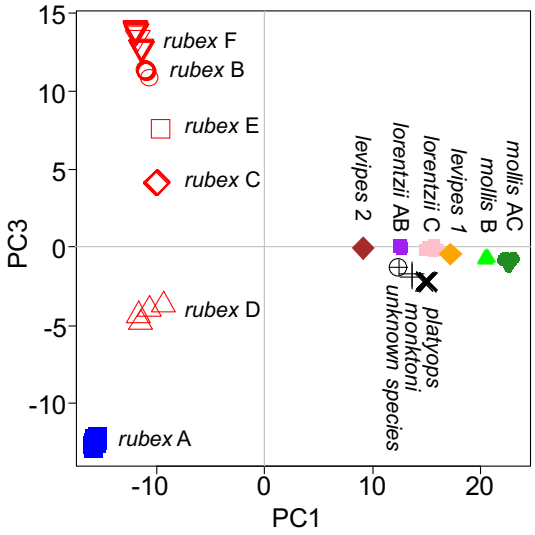


Figure 3.2. Principle Coordinates Analysis (PCoA) of New Guinea *Paramelomys* species (PC1 versus PC3), showing some of the main genetic clusters that correspond to species and species complexes, and illustrating the diversity within the '*rubex*' mitochondrial clade (see Appendix 3.5).

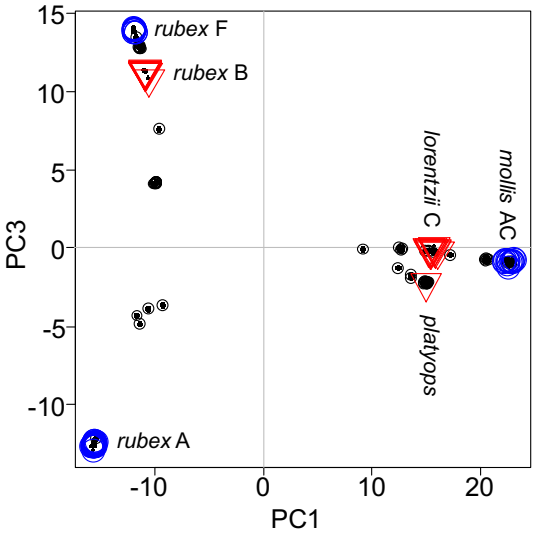


Figure 3.3. Principle Coordinates Analysis of New Guinea *Paramelomys* species (PC1 versus PC3; all samples have small black dots), highlighting those samples from Hides Ridge (BAA 1; blue circles), near Moro (BAA 2; red triangles), and further afield in PNG (smaller black circles).

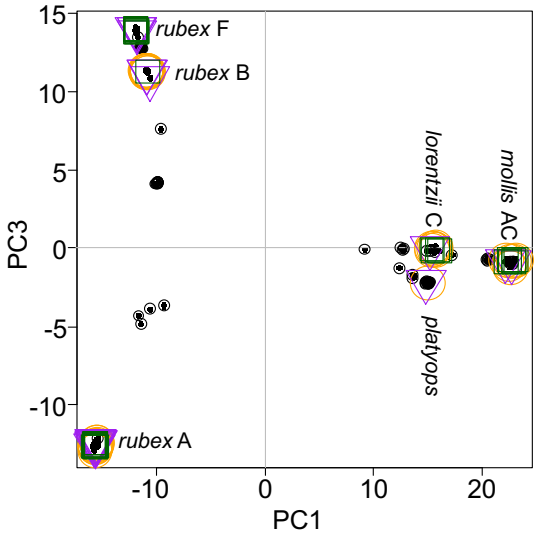
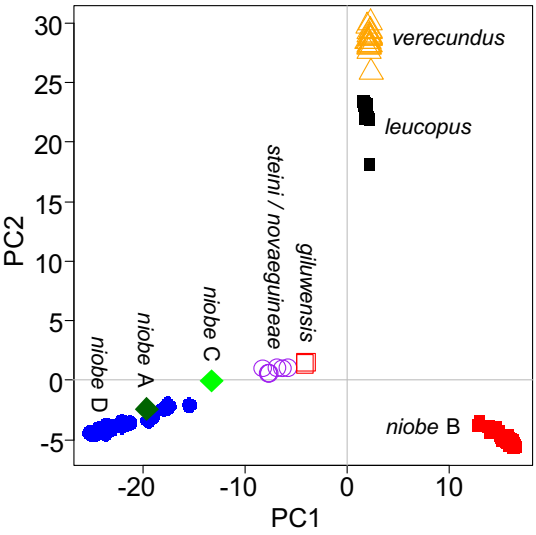


Figure 3.4. Principle Coordinates Analysis of New Guinea *Paramelomys* species (PC1 versus PC3; all samples have small black dots), highlighting those species detected in 2015 (orange circles), 2017 (purple triangles), and 2019 (green squares).



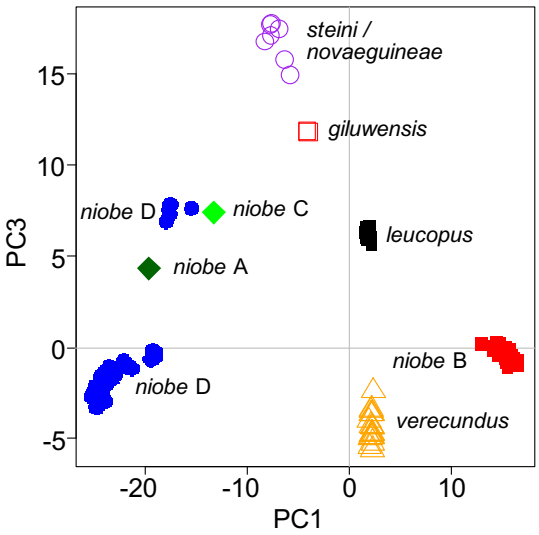


Figure 3.5. Principle Coordinates Analysis of native New Guinea *Rattus* species (left: PC1 versus PC2; right: PC1 versus PC3) showing some of the main genetic clusters that correspond to species and species complexes, and illustrating the diversity within the **'***niobe'* group.

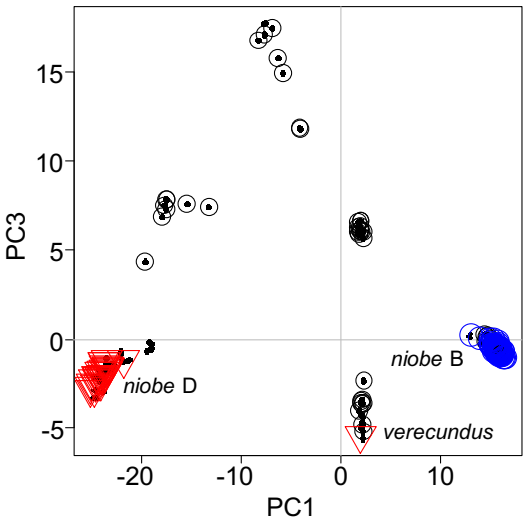


Figure 3.6. Principle Coordinates Analysis of native New Guinea *Rattus* species (PC1 versus PC3; all samples have small black dots), highlighting those samples from Hides Ridge (BAA 1; blue circles), near Moro (BAA 2; red triangles), and further afield in PNG (smaller black circles).

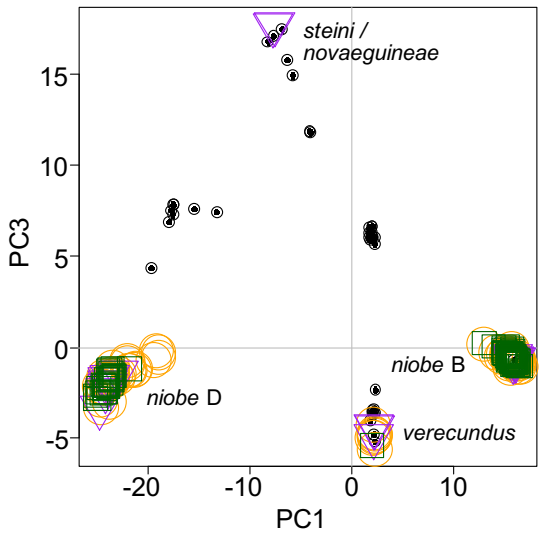


Figure 3.7. Principle Coordinates Analysis of native New Guinea *Rattus* species (PC1 versus PC3; all samples have small black dots), highlighting those species detected in 2015 (orange circles), 2017 (purple triangles), and 2019 (green squares).

Trapping results summary

A total of 16 small to medium-sized rodent taxa have been trapped on the nine transects in both BAAs during the course of the 2015–2019 PMA3 surveys. Eleven of these were captured in 2019, two species of which were trapped for the first time (*Lorentzimys nouhuysi* and *Pogonomys macrourus*, with one and two individuals captured respectively; Table 3.2). In 2019, six rodent taxa were trapped in BAA 2 (with ten taxa now recorded since 2015), and five taxa were trapped at the higher elevations in BAA 1 (with six taxa now recorded since 2015). No taxon was recorded in both BAAs, and there appeared to be a clear difference in species composition amongst the four elevations using Non-Metric Multidimensional Scaling ordination (Figure 3.8).

Trapping with box traps is not an efficient method for detecting all species of PNG rodents, and there are numerous additional species that have been detected in the PMA3 study area with camera traps (Woxvold and Aplin 2017; Woxvold and Legra 2019; Woxvold et al. this volume), from remains found in five owl pellets collected from a cave on Hides Ridge at an elevation of c. 2,065 m asl in 2011 (Aplin and Opiang 2017), from road kills and casual observations made during the PMA3 field surveys, and from the environmental impact assessment work conducted before the construction of the pipeline ROW (summarised in Aplin and Opiang 2017). There are 12 additional species of Muridae identified in these sources (Appendix 3.6). Thus, trapping with box traps has detected 57% of species in the Muridae that are known from the area based on these studies. Of particular note, the camera trapping results show that some species are found in both BAAs, which indicates that the composition of Muridae at different elevations is not mutually exclusive.

The total number of novel captures of rodents in 2019 was 134 individuals (94 captures from BAA 1 and 40 captures from BAA 2), with an additional 35 recapture events (Table 3.3). The total is equivalent to that from 2015 (133 novel captures) and higher than that in 2017 (53 novel captures). There is potential for the capture rate to have been even higher because a total of 59 trap positions/nights on transects H1 (41), H3 (17) and H6 (1) were affected by interference from dogs. By contrast, few traps were disturbed or damaged during the 2015 and 2017 surveys.

Three species accounted for 79.3% of captures: *Paramelomys* sp. cf. *rubex* A (15 individuals; 11.1%), *Rattus* sp. cf. *niobe* B (63 individuals; 46.7%), and *Rattus* sp. cf. *niobe* D (29 individuals; 21.5%). Overall trapping success was 6.1%, and it

ranged from 0.6% at transect M4 to 11.9% at transect H6 (Table 3.3). Thus, while species richness was lowest at 2,700 m asl, the number of individuals trapped was considerably higher than at 1,000 m asl.

There was no obvious pattern of captures by distance category, for any species (Table 3.4; Figure 3.8). No native rodent species was associated unambiguously with either the forest edge, or the forest interior. However, four individuals of the invasive species *R. exulans* were trapped either close to the forest edge, or in an area that had been disturbed previously (the first half of transect M4).

Table 3.2. Summary of captures at each elevation, in each survey year (open circle is an absence of captures; closed circle is at least one capture in that survey year; in each cell the first symbol is from the 2015 survey, the second value from the 2017 survey, and the third from the 2019 survey; the last column is the total number of novel captures across all elevations [m asl], for each year).

	1,000 m	**1,400 m**	**2,200 m**	**2,700 m**	**Novel captures**
HYDROMYINI					
Leptomys elegans	ooo	o●o	ooo	ooo	0,1,0
Lorentzimys nouhuysi	ooo	ooo	oo●	ooo	0,0,1
Paramelomys platyops	●oo	o●o	ooo	ooo	1,1,0
Paramelomys sp. cf. *lorentzii* C	ooo	●●●	ooo	ooo	5,1,4
Paramelomys sp. cf. *mollis* AC	ooo	ooo	●●●	●oo	6,2,6
Paramelomys sp. cf. *rubex* A	ooo	ooo	●●●	●●●	11,12,15
Paramelomys sp. cf. *rubex* B	●oo	●●●	ooo	ooo	14,3,1
Paramelomys sp. cf. *rubex* F	ooo	ooo	o●●	ooo	0,4,9
Pogonomys macrourus	ooo	oo●	ooo	ooo	0,0,1
Uromys caudimaculatus	ooo	●oo	ooo	ooo	1,0,0
RATTINI					
Rattus exulans	oo●	●o●	ooo	ooo	5,0,4
Rattus rattus	ooo	ooo	o●o	ooo	0,1,0
Rattus steini	o●o	ooo	ooo	ooo	0,1,0
Rattus verecundus	●●●	ooo	ooo	ooo	10,5,1
Rattus sp. cf. *niobe* B	ooo	ooo	●●●	●●●	42,11,63
Rattus sp. cf. *niobe* D	o●o	●●●	ooo	ooo	38,11,29
Total novel captures by box trap					**320**
Total Richness each elevation	**6**	**8**	**6**	**3**	***16 spp. total***

Table 3.3. Summary of rodent captures in 2019 (Elev: elevation [m asl]; Tr: transect; TS: trapping success rates of novel captures; Caps: number of novel captures, then number of recaptures in parentheses (RC); SR: species richness).

Tr	TS %	Caps (RC)	SR	*Leptomys elegans*	*Lorentzimys nouhuysi*	*Paramelomys* sp. cf. *lorentzii* C	*Paramelomys* sp. cf. *mollis* AC	*Paramelomys* sp. cf. *rubex* A	*Paramelomys* sp. cf. *rubex* B	*Paramelomys* sp. cf. *rubex* F	*Paramelomys platyops*	*Pogonomys macrourus*	*Uromys caudimaculatus*	*Rattus exulans*	*Rattus rattus*	*Rattus steini*	*Rattus verecundus*	*Rattus* sp. cf. *niobe* B	*Rattus* sp. cf. *niobe* D
BAA1																			
M4	0.6	2 (3)	*2*	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0
M1	5.4	16 (7)	*4*	0	0	2	0	0	1	0	0	0	0	1	0	0	0	0	12
M2	5.2	15 (12)	*4*	0	0	1	0	0	0	0	0	1	0	1	0	0	0	0	12
M3	2.4	7 (1)	*3*	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	5
BAA2																			
H1	10.9	23 (2)	*5*	0	1	0	2	1	0	9	0	0	0	0	0	0	0	10	0
H2	7.4	13 (4)	*2*	0	0	0	3	0	0	0	0	0	0	0	0	0	0	10	0
H3	8.3	17 (3)	*3*	0	0	0	1	6	0	0	0	0	0	0	0	0	0	10	0
H5	7.4	16 (2)	*2*	0	0	0	0	5	0	0	0	0	0	0	0	0	0	11	0
H6	11.9	25 (1)	*3*	0	0	0	0	3	0	0	0	0	0	0	0	0	0	22	0
Elev																			
1,000	0.6	2	*2*	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0
1,400	4.4	38	*5*	0	0	4	0	0	1	0	0	1	0	3	0	0	0	0	29
2,200	9.0	53	*5*	0	1	0	6	7	0	9	0	0	0	0	0	0	0	30	0
2,700	9.6	41	*2*	0	0	0	0	8	0	0	0	0	0	0	0	0	0	33	0
BAA																			
BAA1	7.9	94	*5*	0	1	0	6	15	0	9	0	0	0	0	0	0	0	63	0
BAA2	3.9	40	*6*	0	0	4	0	0	1	0	0	1	0	4	0	0	1	0	29
Total	6.1	134 (35)	*11*	0	1	4	6	15	1	9	0	1	0	4	0	0	1	63	29

Table 3.4. Trapping summary from the 2019 survey (symbols in each cell represent the trapping result from each distance category along the transect, beginning at 0 metres from the left [0–20, 20–70, 70–120, 120–170, 170–220 m for all transects, and additionally 220–370 m for transect M4]; open circle is an absence of captures; closed circle is at least one capture in that distance category; grey shading shows that a species was captured on at least one transect in a particular elevation).

Elevation (m asl)	**1,000**	**1,400**			
Transect	**M4**	**M1**	**M2**	**M3**	
HYDROMYINI					
Leptomys elegans	ooooo	ooooo	ooooo	ooooo	
Lorentzimys nouhuysi	ooooo	ooooo	ooooo	ooooo	
Paramelomys platyops	ooooo	ooooo	ooooo	ooooo	
Paramelomys sp. cf. *lorentzii* C	ooooo	●ooo●	ooo●o	●oooo	
Paramelomys sp. cf. *mollis* AC	ooooo	ooooo	ooooo	ooooo	
Paramelomys sp. cf. *rubex* A	ooooo	ooooo	ooooo	ooooo	
Paramelomys sp. cf. *rubex* B	ooooo	o●ooo	ooooo	ooooo	
Paramelomys sp. cf. *rubex* F	ooooo	ooooo	ooooo	ooooo	
Pogonomys macrourus	ooooo	ooooo	o●ooo	ooooo	
Uromys caudimaculatus	ooooo	ooooo	ooooo	ooooo	
RATTINI					
Rattus exulans	oo●ooo	●oooo	●oooo	●oooo	
Rattus rattus	ooooo	ooooo	ooooo	ooooo	
Rattus steini	ooooo	ooooo	ooooo	ooooo	
Rattus verecundus	●ooooo	ooooo	ooooo	ooooo	
Rattus sp. cf. *niobe* B	ooooo	ooooo	ooooo	ooooo	
Rattus sp. cf. *niobe* D	ooooo	●●●●o	●●●●●	●●o●●	
Elevation (m asl)	**2,200**			**2,700**	
Transect	**H1**	**H2**	**H3**	**H5**	**H6**
HYDROMYINI					
Leptomys elegans	ooooo	ooooo	ooooo	ooooo	ooooo
Lorentzimys nouhuysi	o●ooo	ooooo	ooooo	ooooo	ooooo
Paramelomys platyops	●o●oo	o●●oo	●oooo	ooooo	ooooo
Paramelomys sp. cf. *lorentzii* C	ooooo	ooooo	ooooo	ooooo	ooooo
Paramelomys sp. cf. *mollis* AC	ooooo	ooooo	ooooo	ooooo	ooooo
Paramelomys sp. cf. *rubex* A	●oooo	ooooo	●●o●●	●o●●●	oo●o●
Paramelomys sp. cf. *rubex* B	ooooo	ooooo	ooooo	ooooo	ooooo
Paramelomys sp. cf. *rubex* F	●●●●●	ooooo	ooooo	ooooo	ooooo
Pogonomys macrourus	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●●●	●●●●●	●●●●●
Rattus sp. cf. *niobe* D	ooooo	ooooo	ooooo	ooooo	ooooo

Statistical analyses

Generalised Linear Mixed Models were created to determine if there were statistically significant differences in rodent diversity amongst survey years, at different distances from the ROW, and with elevation. Separate tests were performed on four dependent variables: total Species Richness, total number of captures, total captures of Hydromyini species, and total captures of Rattini species. There were no significant differences in the four tests of Species Richness and abundance at increasing distances from the ROW, among both elevation bands, or across the three years (Appendix 3.7).

An inspection of the means and standard deviations for Species Richness, total number of captures, total captures of Hydromyini species, and total captures of Rattini species reveals how similar these values were across elevation and distance categories (Table 3.5; Figures 3.9–3.12). The only significant result was a barely significant difference in the one-factor comparison of capture rates at different distances from the ROW (Appendix 3.7), but this result was not reflected in any pairwise interactions, and the plots show no strong pattern for differences in capture rates. We therefore consider this result to be an anomaly and it is not considered further. In summary, there has been no detectable change in the overall diversity or population sizes of the rodent assemblage that is attributable to the influence of the ROW.

Table 3.5. Mean ± standard deviation for all distance, elevation and survey year categories.

	Category	Total Species Richness	Total Captures	Total captures Hydromyini	Total captures Rattini
Distance	0–20	1.7±0.8	3.2±2.0	0.8±1.2	2.4±1.8
from ROW (m)	20–70	1.8±1.1	3.3±2.2	1.2±1.1	2.1±1.7
	70–120	1.3±0.6	2.3±1.6	0.5±0.9	1.8±1.5
	120–170	1.5±0.6	2.9±1.5	1.0 ±1.2	1.9±1.4
	170–220	1.8±0.7	3.7±2.6	1.5±1.5	2.2±1.6
Elevation (m asl)	1,000	1.1±0.4	2.0±1.7	0	2.0±1.7
	1,400	1.8±0.9	3.5±1.9	0.9±1.2	2.5±1.5
	2,200	1.7±0.8	2.9±1.9	1.3±1.2	1.6±1.5
	2,700	1.3±0.5	3.0±2.2	0.8±1.2	2.3±1.6
Year	2015	1.7±0.9	3.4±2.2	0.9±1.4	2.5±1.6
	2017	1.4±0.6	2.1±1.3	1.0±1.1	1.1±1.0
	2019	1.6±0.8	3.3±2.0	0.9±1.1	2.4±1.6

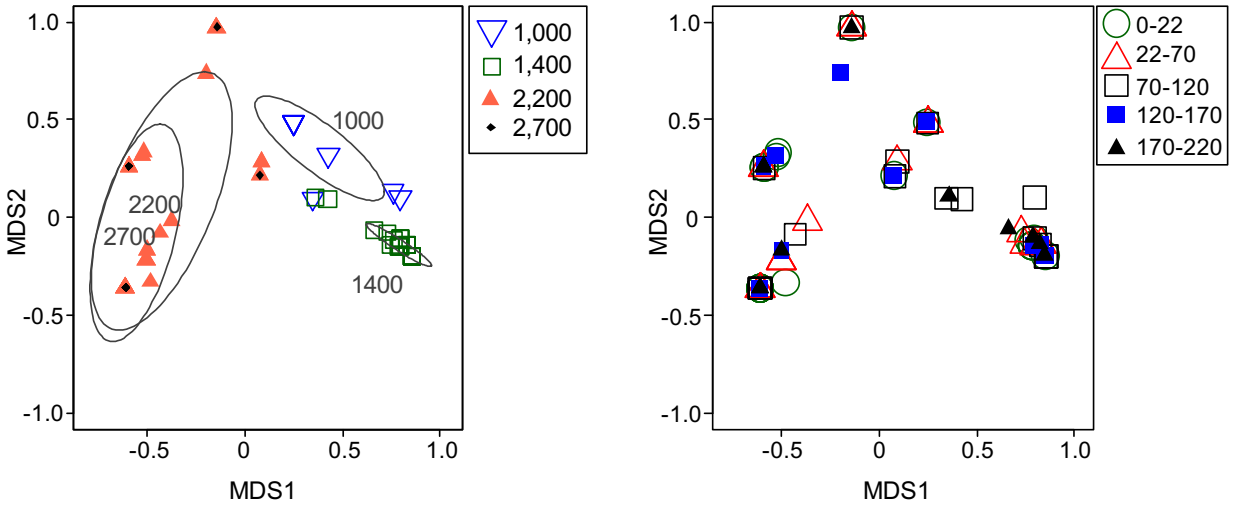


Figure 3.8. Multidimensional Scaling (NMDS) ordinations summarising patterns of species composition (as derived from species lists at each distance category), at different elevations (left), and at increasing distance from the ROW (right), for all survey years combined.

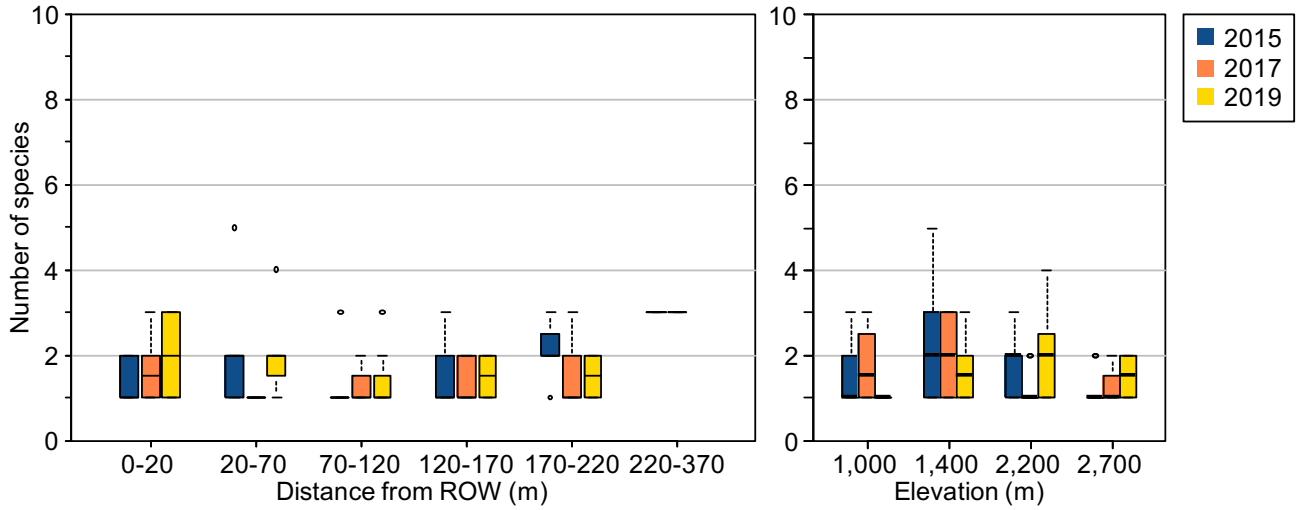


Figure 3.9. Summary of the patterns of Species Richness with increasing distance from the ROW, and with increasing elevation. All sites have been combined for each of the two factors, but segregated by year. [Boxplot components: central bar—median; boxes—inter-quartile range, with second quartile group below median, third quartile group above median; bars—minimum and maximum values; circles—statistical outliers]

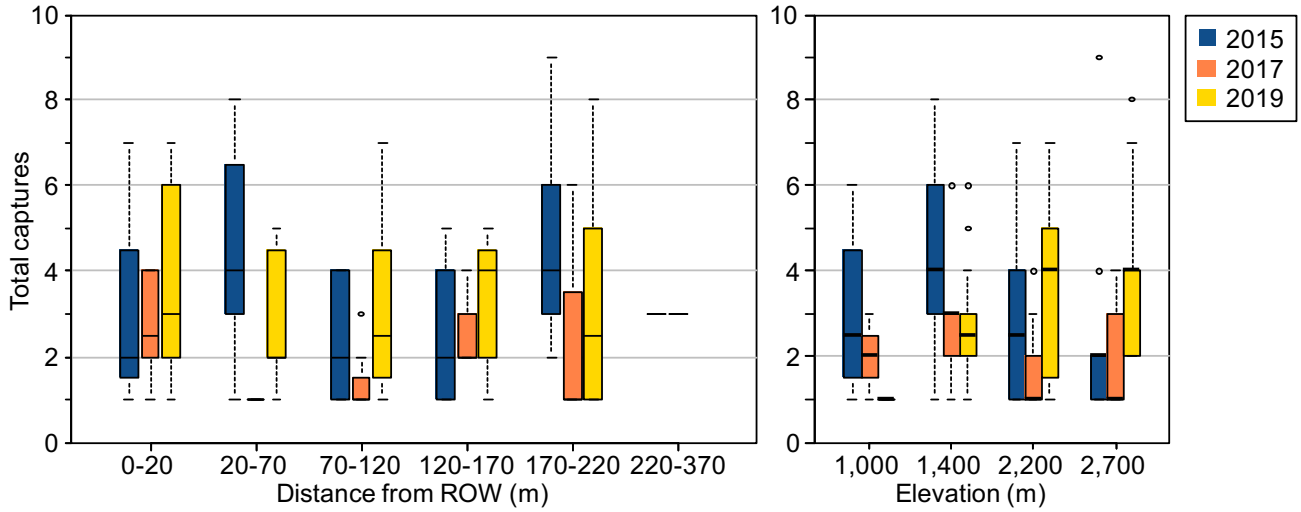


Figure 3.10. Summary plots of the pattern of the total number of captures for all rodent species at increasing distance from the ROW, and with increasing elevation.

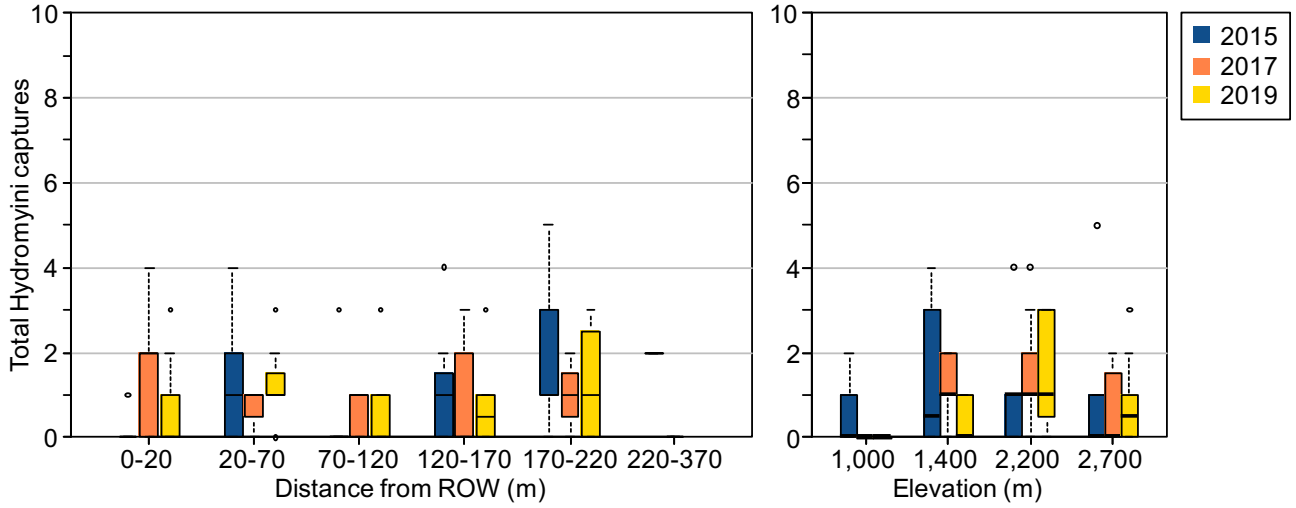


Figure 3.11. Summary plots of the pattern of the total number of captures for Hydromyini rodent species at increasing distance from the ROW, and with increasing elevation.

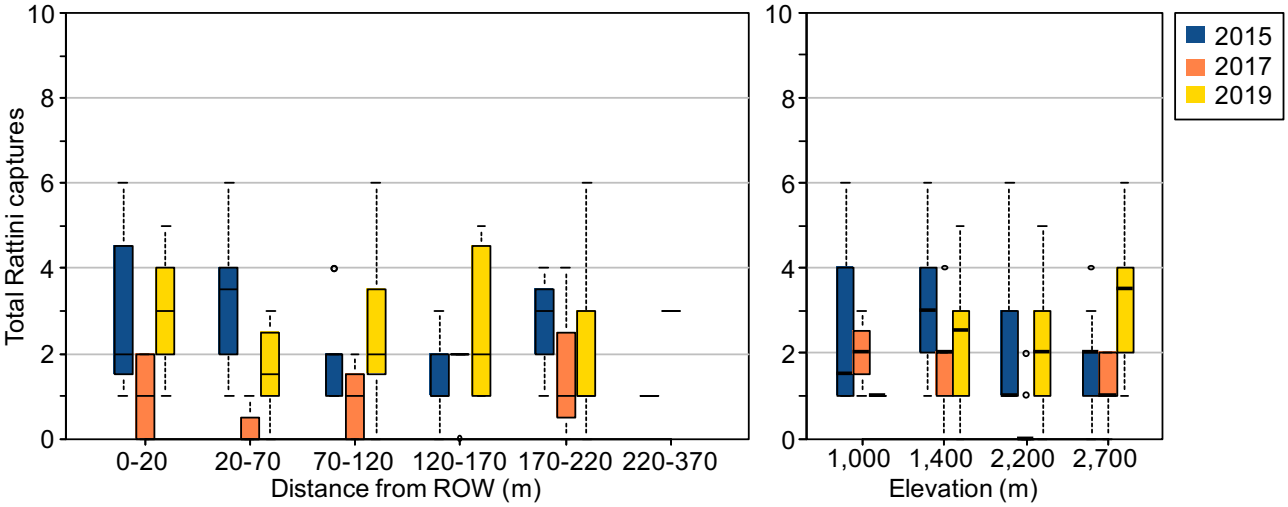


Figure 3.12. Summary plots of the pattern of the total number of captures for Rattini rodent species at increasing distance from the ROW, and with increasing elevation.

Discussion

Patterns of diversity over time

There has been relatively little change in the rodent community adjacent to the ROW throughout the duration of the study. Two species of the Hydromyini were detected by trapping for the first time in 2019: *Lorentzimys nouhuysi* and *Pogonomys macrourus*. Both of these species spend most of their time in trees (Flannery 1995), and it is likely that additional scansorial or arboreal species that are less likely to enter box traps placed on the ground will be encountered in future.

In terms of overall abundance, the rodent community in BAA 1 is dominated by *Rattus* sp. cf. *niobe* B (and to a lesser extent by *Paramelomys* sp. cf. *rubex* A); and the community in BAA 2 is dominated by *Rattus* sp. cf. *niobe* D. Less than half the number of these two species was trapped in 2017 compared to both 2015 and 2019, but statistical tests did not show this to be a significant difference.

However, inspection of Figures 3.10–3.12 does reveal the markedly lower number of captures in 2017 than in 2015 and 2019. The source of this variation might in part reflect the different timing of surveys: 10 June – 8 July 2015; 11 – 30 May 2017; and 11 – 31 August 2019. The highest captures of small ground-dwelling rodents were therefore made between June and August, with fewer captures in May. Relatively little is known about seasonal breeding cycles of rodents in the highlands of PNG, or the relationship of population size and the seasonal availability of food. In the previous report (Armstrong et al. 2019), we stated that the difference in species composition between sampling years shows that 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. It is clear that this notion would need to be demonstrated with a greater level of sampling effort to give greater power to statistical tests.

It is noteworthy that there was an almost identical number of total novel captures for 2015 and 2019. This was despite a difference in the bait used. In 2019, we used slices of plantain banana combined with sweet potato, but in 2015 and 2017 only sweet potato was used. It is not clear from the levels of trapping success whether the addition of banana had a positive influence, especially when the timing of surveys is a confounding factor. However, the continued use of banana in future surveys might help to maximise the capture rate so that a more accurate perspective of abundance might be gained, and also so that statistical tests have increased power. Trap condition has been an important consideration on all three surveys, with care taken to ensure triggers and doors work correctly, which also helps maximise trap success and statistical power.

Edge effects

This study did not detect any shifts in native rodent diversity with increasing distance from the ROW and associated roads (and quarry), suggesting that any effects that might be operating on the forest edge are still having no major impacts on this local fauna. Although no quantitative or qualitative methods have been used to characterise the vegetation along the transects, with the exception of some localised changes (tree falls in the middle of transect H1 and at the beginning of transect H2; the first five metres of forest cover removed from M2 since 2015; of the first 30 m of transect H4 damaged by an earthquake-related treefall in 2019), the forest structure does not appear to have changed significantly across the three survey periods (K.N. Armstrong, personal observation). The trees with metal tags indicating trap locations are still present. Thus, the lack of change in fauna at the forest edge appears to reflect a lack of edge effects relevant to rodents..

The creation of linear infrastructure in both BAA's has increased access for local people, and we documented evidence of hunting along the access road on Hides Ridge and on transects during all three surveys (Aplin and Opiang 2017; Woxvold and Legra 2019; Woxvold et al. this volume). Although small rodents are of less interest to hunters than larger mammals, dogs that accompany them, or that roam freely, probably kill smaller mammal species when they are encountered. Several box traps on transects H1, H3 and H6 were damaged by dogs but it was not possible to determine whether they were attempting to extract trapped rodents or the bait. It is also not known whether predation by dogs has a significant effect on the population sizes of small rodent species but this seems unlikely, at least at current levels of dog presence.

Invasive species

There is one indication of an edge effect, which is the presence of two invasive *Rattus* species. There were five captures of *R. exulans* at KP107 in 2015, one capture of *R. rattus* on Hides Ridge in 2017, and a total of four captures of *R. exulans* at Arakubi Quarry (1 individual) and KP107 (3 individuals) in 2019. *R. exulans* appears to be reasonably well established at KP107, but the lack of detection in 2017 and the capture of one individual at Arakubi Quarry in 2019 might suggest some level of local population fluctuation or movement.

Invasive rodents often gain access to new areas of forest along infrastructure corridors, and all captures during this study were relatively close to the ROW. Seven of the nine *R. exulans* were captured in one of the box traps placed running parallel with the edge of the forest (Figure 3.1). Only two individuals were trapped more than 20 m into the forest: one at each of the 34 m and 82 m positions. The *R. exulans* captured at 82 m into the forest was on transect M4 (BAA 2, Arakubi Quarry). The first c. 150 m of this transect is located in regrowth forest along an old access track. The only capture of *R. rattus* to date was made in BAA 1 at the second trapping position of transect H2, only 16 m from the forest edge.

It is significant that captures of invasive species have not increased during the course of this study. This suggests that incursions from source areas are uncommon, and that populations have not yet expanded significantly in the study areas. Invasive species have the potential to affect resident native species in several ways: by actively excluding them from their territories, out-competing them for resources, and introducing novel pathogens to naïve populations. Studies of pathogens and zoonotic diseases carried by invasive rodents abound in the scientific literature, and the risk to humans of rodent-borne disease is a common theme. However, there is also a growing recognition that wildlife diseases may contribute to population declines of native species (e.g., Begon 2006; Wolf and Edge 2006). The risk of disease transfer from invasive *R. rattus* to native species of rodents has been highlighted (Aplin and Singleton 2006; Aplin and Opiang 2017), but not yet demonstrated.

Preventing the incursion of invasive species on Hides Ridge may not be possible in the long-term. At present, the distance from human occupation that is likely to be a source for commensal rodents is relatively large, but gradually

decreasing with continued encroachment. Continuing the active program of baiting and pest rodent control at the Hides Gas Conditioning Plant and camp will be important for preventing the establishment of a source population that could extend up the spineline over time. However, *R. rattus* is almost certainly established in the surrounding rural areas and villages because it is a successful and pervasive commensal species (e.g. Kale et al. 2018a). Thus, if more people begin to live along the spineline, as was observed in 2019, commensal rodents are likely to follow.

Inventory completeness

A camera trapping program undertaken during the three PMA3 surveys completed to date (Woxvold and Aplin 2017; Woxvold and Legra 2019; Woxvold et al. this volume) documented six species of rodents that were not captured by box-trapping (two of them also documented as roadkill). An additional six species were documented from remains found in five owl pellets collected from a cave on Hides Ridge at an elevation of c. 2,065 m in 2011 (Aplin and Opiang 2017), from road kills and casual observations made during the PMA3 field surveys, and from the environmental impact assessment work conducted before the construction of the pipeline ROW (summarised in Aplin and Opiang 2017) (Appendix 3.6). Thus, box trapping has detected only 57% of the known rodent fauna demonstrated to be in the study area. The potential for encountering additional species in the box trapping effort will likely be dependent on several factors: their ecology (whether they forage on the ground or in trees), their body size, and their general abundance.

Scansorial species of *Chiruromys*, *Melomys* and *Pogonomys* have been detected by camera traps and identified in owl pellet accumulations (Appendix 3.6). Only one individual of a *Pogonomys* species has been captured so far, probably because most of their time is spent foraging in trees. Most species not yet trapped are larger-bodied animals that are too large to enter the medium-sized box traps used on the study transects. However, each transect has four large-sized box traps, which would accommodate species the size of *Hyomys*, *Mallomys* and *Uromys*, and it is unclear why rodents have not been captured in these larger traps. There is also the possibility that rarer species such as *Protochromys fellowsi*, and species of *Parahydromys* and *Pseudohydromys* might be captured using box traps. While there has been three PMA3 surveys to date, greater levels of trapping effort that include more sites might be required to trap these species. Fortunately, most species of rodent not documented by trapping have morphological features that allow them to be identified in camera trap images, which underlines the importance of the camera trapping effort for contributing information on this component of the Muridae. In contrast smaller rodent species are rarely identifiable to species level in camera trap photos (see Woxvold and Legra 2019; Woxvold et al. this volume; also Kale et al. 2018a,b,c).

Making better field identifications

The taxonomy of New Guinea mammals remains incomplete, which has implications for any biological survey on the island, and for 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 (Aplin and Opiang 2017), but 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 the value of including advanced, but cost-effective and practicable, methods to ensure the consistency of identifications among sites, years and investigators. Having now genotyped three sets of captures, and established which genetic groups are present, it is worth considering whether there are sets of morphological characters that can be used to make these same identifications in the field.

In the present survey, field identifications of species that look very similar were not always correct, for example *P*. sp. cf. *mollis* and *P*. sp. cf. *rubex*; and *R. exulans* and *R. verecundus* were also difficult to distinguish from each other (Appendix 3.3). In an effort to determine whether a set of characters could be derived to allow captures to be identified reliably in the field, the limited information on external morphology available from captures in each of the three surveys was combined with information on body size and mammary formula summarised in the individual accounts of Flannery

(1995) (data not shown). Based on this compilation, there appeared to be several issues that currently prevent the derivation of a field-based identification system: the range of external measurements overlaps for many species; fur colour can be variable; information on diagnostic characters (for example, possibly useful features of tail scalation, or those of the skull and teeth) is unavailable or not of practical use for the PMA3 study; and the ability of investigators to make consistent and accurate identifications will vary among individuals. Given the importance of detecting even rare occurrences of invasive species, it does not seem either cost effective or practical to replace the genetics-based identification established over the past three surveys.

Conclusions

The 2019 survey has contributed to each of the five specific objectives of the study:

1. *Document the diversity of the small rodent assemblage within the two BAAs.*

   The trapping effort built further on knowledge of local rodent diversity by adding two species to the overall total, and documented an equivalent level of captures to the study conducted in 2015.

   A greater appreciation of apparent population size change in the three most common rodents (*Rattus* sp. cf. *niobe* B, *R.* sp. cf. *niobe* D, and *Paramelomys* sp. cf. *rubex* A) was gained from comparing the number of captures across the three surveys. 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, and methodological changes such as the addition of banana as bait, and the timing of surveys are confounding factors.

2. *Determine whether there has been a significant change since 2015 in the diversity of the small rodent assemblage using the forest adjacent to the Project linear infrastructure (pipeline right-of-way and access roads)*

   The most relevant result documented to date is the continued lack of a significant shift in Species Richness, abundance or species composition at increasing distances from the ROW, in either BAA, and in any survey year, indicating that there has been no detectable impact of edge effects from the ROW on these taxa.

3. *Identify species of conservation significance (including new or undescribed species) within each of the BAAs and, where practicable, determine their special sensitivities.*

   The genetics-based identification methods used in in all three surveys has helped to identify several likely undescribed species within *Paramelomys lorentzii*, *Paramelomys 'mollis'*, the *Paramelomys 'rubex'* group, and the *Rattus 'niobe'* group. Our results demonstrate that some apparently common and widespread species are complexes of genetic distinct populations with presumably smaller distributions. Species with smaller distributions have greater chance to be affected significantly by anthropogenic development.

   Understanding the special sensitivities of native rodent species, and their interactions with commensal predators such as dogs and competitors such as *Rattus rattus*, requires further study.

4. *Monitor the status of exotic mammal species in each of the BAAs.*

   The invasive species *Rattus exulans* was detected again in 2019 at all transects in BAA 2 (only), but there was no evidence of the use of the ROW by the pest species *Rattus rattus*, which was captured in 2017 at 2,200 m asl in BAA 1.

5. *Assess the usefulness of non-volant mammal communities in each of the BAAs more broadly as potential indicators of change in habitat quality.*

   The populations of native rodents sampled have so far shown good resilience to the removal of adjacent forest for the pipeline and access road, using forest habitat right to the edge. However, the forest edge is still relatively intact, and we may yet see changes that reflect a change in habitat structure and the increased presence of invasive rodents.

Recommendations

It is recommended that the live-trapping rodent component of the study continue, and that the recommendations of Aplin and Opiang (2017; internal version that includes the recommendations) be revisited, with some revision based on our refined understanding of the rodent assemblage in the BAAs:

1. Consideration be given to a rapid assessment of the presence of *R. rattus* and *R. exulans* in inhabited areas around the HGCP to provide context on how common these species are, and how significant a source they might be for invasions along the access road and pipeline along Hides Ridge.

2. Continue to build upon the genetic work that has been initiated here because morphologically diagnostic characters for most rodent species in the study area are inadequate for consistently accurate identifications.

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Appendix 3.1. Summary of whole specimen vouchers taken on the survey, which have been deposited in the South Australian Museum.

Associated tissue number	Verified SNP-based identification	Transect	Sex
MEL01105	*Rattus* sp. cf. *niobe* B	H6-1.2	F
MEL01122	*Rattus* sp. cf. *niobe* B	H6-35	M
MEL01126	*Rattus* sp. cf. *niobe* B	H5-15	F
MEL01156	*Rattus* sp. cf. *niobe* B	H3-35	F
MEL01162	*Rattus* sp. cf. *niobe* B	H5-8	M
MEL01163	*Rattus* sp. cf. *niobe* B	H5-29	M
MEL01166	*Dasyurus albopunctatus*	H3-18	F
MEL01199–MEL01203	*Parahydromys asper*	BAA1 roadkill	M
MEL01216	*Lorentzimys nouhuysi*	H1-5	M
MEL01234, MEL01246–MEL01249	*Rattus exulans*	M4-12	M
MEL01235, MEL01242–MEL01245	*Rattus* sp. cf. *niobe* D	M1-1.6	M
MEL01236, MEL01250–MEL01253	*Paramelomys* sp. cf. *lorentzii* C	M1-1.5	M
MEL01297–MEL01301	*Rattus* sp. cf. *niobe* D	M1-1.2	F
MEL01316–MEL01320	*Pogonomys macrourus*	M2-7	F

Appendix 3.2. Correspondence between morphological-based field identification, and SNP-based identification for all 2019 novel captures sequenced successfully (continued across subsequent pages).

Year	Trap No	Field ID	SNP-based ID	Field No
2019	H6-16	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01101
2019	H6-36	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01102
2019	H6-35	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01103
2019	H6-34	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01104
2019	H6-1.2	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01105
2019	H6-1.5	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01109
2019	H6-5	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01110
2019	H6-12	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01111
2019	H6-16	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01112
2019	H6-32	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01113
2019	H5-1.6	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01114
2019	H5-7	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01115
2019	H5-13	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01116
2019	H5-15	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01117
2019	H6-6	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01118
2019	H6-16	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01119
2019	H6-22	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01120
2019	H6-27	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01121
2019	H6-35	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01122
2019	H6-36	*Rattus niobe*	no genotype	MEL01123
2019	H5-3	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01124
2019	H5-13	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01125
2019	H5-15	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01126
2019	H5-19	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01127
2019	H5-24	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01128
2019	H3-30	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01129
2019	H3-33	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01130
2019	H6-1.5	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01134
2019	H6-12	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01135
2019	H6-16	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01136
2019	H6-20	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01137
2019	H6-27	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01138
2019	H6-32	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01139
2019	H5-6	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01140
2019	H5-20	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01141
2019	H5-23	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01142
2019	H3-1.2	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01143
2019	H3-18	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01144
2019	H3-22	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01145

Year	Trap No	Field ID	SNP-based ID	Field No
2019	H3-25	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01146
2019	H3-33	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01147
2019	H6-1.1	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01148
2019	H6-12	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01149
2019	H6-20	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01150
2019	H6-22	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01151
2019	H5-1.1	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01152
2019	H5-6	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01153
2019	H5-32	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01154
2019	H3-16	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01155
2019	H3-35	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01156
2019	H2-23	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01157
2019	H2-19	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01158
2019	H2-7	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01159
2019	H1-5	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01160
2019	H1-1.6	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01161
2019	H5-8	*Rattus niobe*	no genotype	MEL01162
2019	H5-29	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01163
2019	H3-1.1	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01164
2019	H3-1.3	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01165
2019	H3-18	*Dasyurus albopunctatus*	*Dasyurus albopunctatus*	MEL01166
2019	H3-35	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01167
2019	H2-1.6	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01168
2019	H2-5	*Paramelomys rubex*	*Paramelomys* sp. cf. *mollis* AC	MEL01169
2019	H2-6	*Paramelomys rubex*	*Paramelomys* sp. cf. *mollis* AC	MEL01170
2019	H2-19	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01171
2019	H2-24	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01172
2019	H3-1.2	*Paramelomys* sp. cf. *mollis*	*Paramelomys* sp. cf. *mollis* AC	MEL01191
2019	H3-1.1	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01192
2019	H2-5	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01193
2019	H1-1.3	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01194
2019	H1-5	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01195
2019	H1-35	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01196
2019	H1-30	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01198
2019	H3-1.3	*Hydromys chrysogaster*	no genotype	MEL01199-1203
2019	H3-1.3	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01204
2019	H3-6	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01205
2019	H3-30	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* A	MEL01206
2019	H2-30	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01207
2019	H2-24	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01208
2019	H2-14	*Paramelomys rubex*	*Paramelomys* sp. cf. *mollis* AC	MEL01209
2019	H2-4	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01210
2019	H1-1.3	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01211

Year	Trap No	Field ID	SNP-based ID	Field No
2019	H1-3	*Paramelomys mollis*	*Paramelomys* sp. cf. *mollis* AC	MEL01212
2019	H1-5	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01213
2019	H1-13	*Paramelomys mollis*	*Paramelomys* sp. cf. *mollis* AC	MEL01214
2019	H1-26	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01215
2019	H1-5	*Lorentzimys nouhuysi*	*Lorentzimys nouhuysi*	MEL01216
2019	H1-28	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01217
2019	H1-16	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01218
2019	H1-36	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01219
2019	H1-1.3	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01220
2019	H1-1.6	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01221
2019	H1-17	*Paramelomys rubex*	*Paramelomys* sp. cf. *rubex* F	MEL01222
2019	H1-1.6	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01223
2019	H1-1.5	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01224
2019	H1-13	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01225
2019	H1-16	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01226
2019	H1-26	*Rattus niobe*	*Rattus* sp. cf. *niobe* B	MEL01227
2019	H1-35	*Rattus niobe*	no genotype	MEL01228
2019	M4-1.6	*Rattus* sp.	*Rattus verecundus*	MEL01229
2019	M1-1.4	*Rattus* sp. cf. *verecundus*	no genotype	MEL01230
2019	M1-1.6	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01231
2019	M1-10	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01232
2019	M1-22	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01233
2019	M4-12	*Rattus sp.*	*Rattus exulans*	MEL01234, MEL01246, MEL01247, MEL01248, MEL01249
2019	M1-1.6	*Rattus* sp. cf. *niobe*	*Rattus* sp. cf. *niobe* D	MEL01235, MEL01242, MEL01243, MEL01244, MEL01245
2019	M1-1.5	*Paramelomys* sp. cf. *mollis*	*Paramelomys* sp. cf. *lorentzii* C	MEL01236, MEL01250, MEL01251, MEL01252, MEL01253
2019	M1-1.4	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01237
2019	M1-26	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01238
2019	M2-1.3	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01239
2019	M2-18	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01240
2019	M2-28	*Rattus* sp. cf. *niobe*	*Rattus* sp. cf. *niobe* D	MEL01241
2019	M1-9	*Paramelomys* sp. cf. *rubex*	*Paramelomys* sp. cf. *rubex* B	MEL01263
2019	M2-18	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01264
2019	M2-22	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01265
2019	M3-1.2	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01266
2019	M3-4	*Rattus* sp. cf. *verecundus*	no genotype	MEL01267
2019	M3-1.4	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01293
2019	M2-20	*Rattus* sp. cf. *niobe*	*Rattus* sp. cf. *niobe* D	MEL01295

Year	Trap No	Field ID	SNP-based ID	Field No
2019	M1-1.5	*Rattus* sp.	*Rattus exulans*	MEL01296
2019	M1-1.2	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01297-1301
2019	M1-19	*not recorded*	*Rattus* sp. cf. *niobe* D	MEL01302
2019	M1-34	*Paramelomys* sp. cf. *mollis*	*Paramelomys* sp. cf. *lorentzii* C	MEL01303
2019	M2-22	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01304
2019	M3-4	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01305
2019	M3-25	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01306
2019	M2-27	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01307
2019	M1-12	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01308
2019	M1-19	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01309
2019	M1-13	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01310
2019	M1-19	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01311
2019	M2-1.5	*Rattus* sp. cf. *exulans*	*Rattus exulans*	MEL01312
2019	M2-4	*Rattus* sp. cf. *verecundus*	no genotype	MEL01313
2019	M2-8	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01314
2019	M2-18	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01315
2019	M2-7	*Pogonomys macrourus*	no genotype	MEL01316-1320
2019	M2-1.5	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01321
2019	M2-22	*Paramelomys* sp. cf. *mollis*	*Paramelomys* sp. cf. *lorentzii* C	MEL01322
2019	M2-27	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01323
2019	M3-1.5	*Rattus* sp. cf. *exulans*	*Rattus exulans*	MEL01324
2019	M3-3	*Paramelomys* sp. cf. *rubex*	*Paramelomys* sp. cf. *lorentzii* C	MEL01325
2019	M3-33	*Rattus* sp. cf. *verecundus*	*Rattus* sp. cf. *niobe* D	MEL01348

Appendix 3.3. Summary of how the traps across each transect were pooled for statistical analyses.

Trap number	Distance from ROW (m)	Stated interval	Analysis bin	No. traps
1	10	0–20	1	8
2	16			
3	22	20–70	2	8
4	28			
5	34			
6	40			
7	46			
8	52			
9	58			
10	64			
11	70	70–120	3	8
12	76			
13	82			
14	88			
15	94			
16	100			
17	106			
18	112			
19	118	120–170	4	8
20	124			
21	130			
22	136			
23	142			
24	148			
25	154			
26	160			
27	166	170–220	5	9
28	172			
29	178			
30	184			
31	190			
32	196			
33	202			
34	208			
35	214			
36–60	220–364	220–370	6	13–25

Notes

1. Stated interval is given for ease of comprehending the categories in the plots, but the actual distances and trap numbers are given in the table above.

2. Aplin and Opiang (2017) recorded the origin of captures in the traps at the beginning of the transect that followed the ROW as 2.1–2.6 (see examples in their Appendix 5.4), even though the transect diagram in their Figure 5.1 labelled these as 1.1–1.6. The 2017 and 2019 survey trap positions were numbered according to the scheme presented in Figure 3.1. There is no implication for the statistical analyses because the same number of traps is contained in the first bin for all survey years.

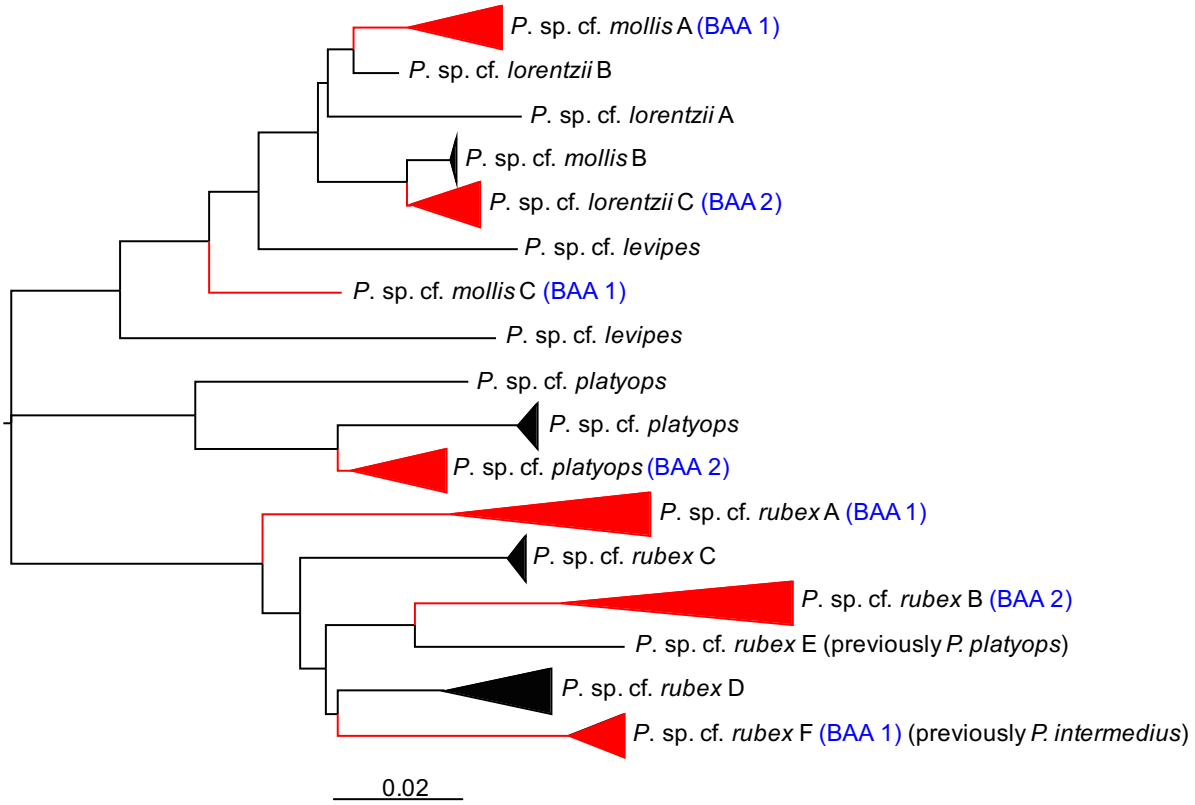
3. For all transects (except M4, and excluding the six traps at the beginning parallel to the ROW): The total number of traps run along the transect perpendicular to the ROW by Aplin and Opiang (2015) was 40 (total length 240 m). In the two subsequent surveys, the maximum number of traps was 34–37. For statistical analyses, the maximum length of transects has been standardised at 35 traps, and three captures made at trap numbers greater than this have been recoded at 'trap 35': position 40 at H5 in 2015; one each from position 36 at H1 and H6 in 2019.

4. Aplin and Opiang (2015) were not able to sample transect M5 that was used for the frog and bat recordings because if its distance from vehicular access. Instead, transect M4 was extended from 240 m to 336 m. This was continued in 2017 and 2019, though to a maximum of 48 trap positions rather than 60. For plotting purposes only, all trap positions for transect M4 between 36–60 were combined into a single category, and this category ('bin 6') was not used in statistical analyses.

Appendix 3.4. Summary of recaptures.

BAA	Trap	Field identification
BAA 1	H1-5	*Paramelomys rubex*
BAA 1	H1-35	*Paramelomys rubex*
BAA 1	H2-6	*Rattus niobe*
BAA 1	H2-7	*Rattus niobe*
BAA 1	H2-19	*Rattus niobe*
BAA 1	H2-30	*Rattus niobe*
BAA 1	H3-6	*Rattus niobe*
BAA 1	H3-25	*Paramelomys rubex*
BAA 1	H3-30	*Paramelomys rubex*
BAA 1	H5-23	*Rattus niobe*
BAA 1	H5-28	*Rattus niobe*
BAA 1	H6-1.2	*Rattus niobe*
BAA 2	M1-1.2	*Rattus* sp. cf. *verecundus*
BAA 2	M1-1.3	*Rattus* sp. cf. *verecundus*
BAA 2	M1-1.4	*Rattus* sp. cf. *verecundus*
BAA 2	M1-1.5	*Rattus* sp. cf. *verecundus*
BAA 2	M1-1.6	*Rattus* sp. cf. *verecundus*
BAA 2	M1-16	*Rattus* sp. cf. *verecundus*
BAA 2	M1-22	*Rattus* sp. cf. *verecundus*
BAA 2	M2-1.2	*Rattus* sp. cf. *verecundus*
BAA 2	M2-4	*Rattus* sp. cf. *verecundus*
BAA 2	M2-8	*Rattus* sp. cf. *verecundus*
BAA 2	M2-13	*Rattus* sp. cf. *verecundus*
BAA 2	M2-15	*Rattus* sp. cf. *verecundus*
BAA 2	M2-18	*Rattus* sp. cf. *verecundus*
BAA 2	M2-18	*Rattus* sp. cf. *verecundus*
BAA 2	M2-19	*Rattus* sp. cf. *verecundus*
BAA 2	M2-19	*Rattus* sp. cf. *verecundus*
BAA 2	M2-20	*Rattus* sp. cf. *verecundus*
BAA 2	M2-23	*Rattus* sp. cf. *verecundus*
BAA 2	M2-28	*Rattus* sp. cf. *verecundus*
BAA 2	M3-1.4	*Rattus* sp. cf. *verecundus*
BAA 2	M4-1.2	*Rattus* sp.
BAA 2	M4-1.4	*Rattus* sp.
BAA 2	M4-1.5	*Rattus* sp.

Appendix 3.5. Revision and correction of *Paramelomys* taxon designations based on the mitochondrial DNA tree from the 2015 survey (with major clades collapsed), and the DArTseq Principle Coordinates Analyses of 2017 and 2019. Red colour indicates that at least one sample collected in 2015 from either BAA1 or BAA2 was present (modified from Aplin and Opiang 2017: figure A5.3.4).



Notes

1. *'P. mollis'* is split into three groups: A, B and C. All individuals affiliated with '*P. mollis'* that were captured on all three surveys group together using genome-scale DNA markers. In 2015, five captures were of *P.* sp. cf. *mollis* A and one capture of *P.* sp. cf. *mollis* C from Hides Ridge. The mitochondrial haplotypes of '*P. mollis'* captured in 2017 and 2019 are unknown because the cytochrome-*b* gene was not sequenced from individuals captured in those years. The designation '*P.* sp. cf. *mollis* AD' was incorrectly used in Armstrong et al. (2019)—the correct designation is *P.* sp. cf. *mollis* AC.

2. Letter designations were not applied by Aplin and Opiang (2017) to the three clades affiliated with '*P. lorentzii'*, nor were they applied by Armstrong et al. (2019), though reference was made to *P. lorentzii* '1' in the Results section of that report for animals captured in the study area. All captures from the three surveys to date have been designated in the present report as *P.* sp. cf. *lorentzii* C.

3. The major clade containing individuals affiliated with *P. intermedius*, *P. platyops*, and *P. rubex* is assigned in the present report in its entirety to '*P. rubex'*. In 2017, four individuals were captured from BAA1 that grouped with context samples (from Bobole and Pn'yang) that comprise the '*P. intermedius'* mitochondrial clade in the tree above. A further nine individuals were captured in 2019 from BAA1 that grouped with these samples, and they have been renamed in the present report as *P.* sp. cf. *rubex* F.

4. Representatives of only one mitochondrial DNA clade of '*P. platyops'* have been recorded in the study area to date, and the membership of this clade extends across a wide area of Papua New Guinea.

Appendix 3.6. Summary of species of Muridae that have been recorded from the PMA3 study area at different elevations [m asl] with camera traps (Woxvold and Aplin 2017; Woxvold and Legra 2019; Woxvold et al. this volume); plus 'Additional species': from remains found in five owl pellets collected from a cave on Hides Ridge at an elevation of c. 2,065 m asl in 2011 (Aplin and Opiang 2017), from road kills and casual observations made during the PMA3 field surveys, and from the environmental impact assessment work conducted before the construction of the pipeline ROW (summarised in Aplin and Opiang 2017). For camera traps, in each cell the first symbol is from the 2015 survey, the second value from the 2017 survey, and the third from the 2019 survey; open circle is an absence of observations, closed circle is at least one observation in that survey year; *** denotes not yet encountered with box trapping; NYS: not yet seen on camera traps or in box traps.

	1,000 m	**1,400 m**	**2,200 m**	**2,700 m**
Camera traps				
****Anisomys imitator*	ooo	●●●	●●●	o●●
Chiruromys / Pogonomys sp.	ooo	oo●	ooo	ooo
****Hyomys* sp.	ooo	ooo	●●●	●●●
Leptomys elegans	o●●	●●●	ooo	ooo
****Mallomys* sp.	●oo	o●●	o●●	o●●
****Parahydromys asper*	ooo	●oo	ooo	oo●
Paramelomys spp.	●●●	●●●	●●●	●●●
****Pseudohydromys* sp.	ooo	ooo	oo●	ooo
Rattus spp.	●●●	●●●	●●●	●●●
****Uromys anak*	o●●	o●●	o●●	o●●
Uromys caudimaculatus	●●●	●●●	oo●	ooo
Additional species				
Abeomelomys sevia	NYS			
Chiruromys vates	NYS			
Lorentzimys nouhuysi	Trapped in 2019			
Melomys sp. cf. *dollmani*	NYS			
Melomys sp. cf. *rufescens*	NYS			
Protochromys sp. cf. *fellowsi*	NYS			
Pogonomys sp. cf. *macrourus*	Trapped in 2019			
Pogonomys sp. cf. *loriae*	NYS			

Appendix 3.7. Summary of the Generalised Linear Mixed Model testing that examined the effect on small rodent Species Richness and abundance (four separate test on dependent variables (dv): total Species Richness , total number of captures, total captures of Hydromyini species and total captures of Rattini species) of the factors 'Distance' from the ROW, 'Elevation', and survey 'Year' (values from the Analysis of Deviance table; Type III Wald chi-square tests; Significance codes: '*' <0.05; the model fit used was: glmer(dv ~ dist + elev + year + dist*elev + elev*year + dist*year + dist*elev*year + (1 | transect), data = y).

Species Richness	**Chi-square**	**df**	**P**	**Pairwise**
Distance	0.73	4	0.94 NS	—
Elevation	1.11	3	0.77 NS	—
Year	0.12	2	0.94 NS	—
Elevation*Year	4.48	6	0.61 NS	—
Distance*Year	2.63	8	0.95 NS	—
Distance*Elevation	12.0	11	0.36 NS	—
Distance*Elevation*Year	15.18	16	0.51 NS	—
Total captures	**Chi-square**	**df**	**P**	**Pairwise**
Distance	9.88	4	0.042*	NS
Elevation	2.47	3	0.48 NS	—
Year	0.65	2	0.72 NS	—
Elevation*Year	3.12	6	0.79 NS	—
Distance*Year	10.03	8	0.26 NS	—
Distance*Elevation	13.49	11	0.26 NS	—
Distance*Elevation*Year	15.58	16	0.48 NS	—
Hydromyini captures	**Chi-square**	**df**	**P**	**Pairwise**
Distance	5.30	4	0.26 NS	—
Elevation	0.31	3	0.96 NS	—
Year	0.24	2	0.89 NS	—
Elevation*Year	1.10	6	0.98 NS	—
Distance*Year	2.75	8	0.95 NS	—
Distance*Elevation	14.25	11	0.22 NS	—
Distance*Elevation*Year	13.32	16	0.65 NS	—
Rattini captures	**Chi-square**	**df**	**P**	**Pairwise**
Distance	8.79	4	0.07 NS	—
Elevation	3.28	3	0.35 NS	—
Year	0.89	2	0.64 NS	—
Elevation*Year	5.32	6	0.50 NS	—
Distance*Year	12.0	8	0.15 NS	—
Distance*Elevation	8.42	11	0.67 NS	—
Distance*Elevation*Year	12.8	16	0.69 NS	—

Chapter 4 – Bats

Kyle N. Armstrong, Alfred Mani and Elizah Nagombi

Nyctophilus microdon from Hides Ridge

Summary

Background and aims

The bat component of the PMA3 monitoring study seeks to determine whether ExxonMobil PNG Limited's pipeline right-of-way (ROW) and Project roads are causing changes in the adjacent bat communities. The August 2019 survey used the same acoustics-based survey approach to detect echolocating bat species, and the same 66 recording sites that were established in 2015 on Hides Ridge (BAA 1) and adjacent to Arakubi Quarry and KP 107 (BAA 2) on the Agogo Range near Moro. The primary aim of the 2019 survey was to determine if there had been a significant change in the diversity and composition of bat communities at increasing distance from the ROW and at different elevations since 2015.

Major results

A total of 20 species was detected in the acoustic recordings, slightly less than previous surveys (2015: 21 spp.; 2017: 20 spp.). No trapping was conducted in 2019. Based on both captures and acoustic recordings from the 2015 and 2017 surveys, and on acoustic recordings from the 2019 surveys, a total of 27 bat species has now been documented in the PMA3 study area.

Two species were encountered for the first time in 2019: Maggie Taylor's Leaf-nosed Bat *Hipposideros maggietaylorae*, and the New Guinea Free-tailed Bat *Austronomus kuboriensis*.

No species of conservation significance (classified in a threatened category or as Data Deficient by the IUCN) have been detected on any of the PMA3 surveys conducted to date.

The bat communities within each of the BAAs have not changed during the monitoring period. However, the number of bat species present was significantly greater below 2,000 m (over three surveys: total 22 species in BAA 2 compared with 8 species in BAA 1). This was due mainly to a greater number of species that forage in Edge habitats (small Emballonuridae) and a greater number of species that forage in Clutter in the forest interior (Hipposideridae and Rhinolophidae) in BAA 2.

This study did not detect a gradual change in the bat community with increasing distance from the forest edge during any of the three surveys, but it has identified that the forest edge (0–20 m) has a significantly higher number of species than the remainder of the transect (20–220 m). For both BAAs combined, the highest proportion of species that forage in Edge habitats was recorded at a distance of 0 m, with higher proportions of species that forage in Clutter at distances within the forest interior.

Conclusions and recommendations

While there is a clear pattern of difference in the presence of foraging bats between the forest interior and the open space/forest edge of the linear corridors, this study has to date detected no spatial or temporal shifts in bat diversity or composition in either BAA since 2015 that is attributable to the construction of linear infrastructure. The combined results from the 2015, 2017 and 2019 surveys suggest that the forest adjacent to the ROW has so far retained its value for a diverse community of bats.

It is recommended that the acoustic bat monitoring component should be continued in future surveys because of a demonstrated ability for detecting bat responses to open areas and the forest edge.

Further effort should be made on future surveys to capture the putative 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 KP 87 adjacent to Lake Kutubu.

Future trapping effort should also target species of *Pipistrellus* that are expected to occur, but have not yet been detected acoustically, because of the similarity of their calls with those of medium- and small-sized *Miniopterus*.

Although abundance data is not available from bat detector recordings, relative levels of activity might reveal more detail about changes in forest usage over time than presence/absence data can suggest. Further consideration could be given to quantifying activity levels of particular species identified in the Indicator Species analysis as Edge and Clutter species, including from past recordings.

Introduction

Background

Papua New Guinea (PNG) retains around 70% of its natural forest cover (Shearman and Bryan 2015), with broad expanses relatively undissected by linear infrastructure corridors for roads, power transimission and pipelines. As a consequence, the effects of linear habitat disturbance on PNG fauna have not been well documented. Studies within broad areas of intact habitat have the potential to be informative about the responses of animals to a single 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 a linear infrastructure corridor on closed forest ecosystems in Southern Highlands and Hela Provinces, by periodically measuring the diversity and composition of selected major vertebrate groups, including bat communities.

Upon first consideration, the effects of road and pipeline construction on bats in PNG forests might not be apparent. Bat species might readily fly over narrow 'canyon-like' breaks in natural habitat, and the ability to fly also gives bats the potential to respond relatively quickly to changes in their habitat by changing where they forage. The first PMA3 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). That study detected a marginally significant higher diversity of bat species assemblages immediately adjacent to the open areas of the PNG LNG pipeline right- of-way (ROW) and access road, but only at the lowest elevation (1,000 m asl.). Several species appeared to benefit from having increased access to open foraging areas and vegetation edges. Sampling two years later (Armstrong et al. 2019) provided greater statistical power when comparing bat diversity along the sampling transects that extend into the forest, and this revealed a moderately but significantly greater bat diversity (Species Richness) within the first 20 metres of the forest edge at elevations of 1,000 and 1,400 m asl.

Edge effects of linear infrastructure corridors on bats

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. Edge effects have been studied for decades (Harris 1988), but there are few long-term studies of bat communities occupying forest edge habitats. Most short-term studies derive from temperate habitats in Europe where landscapes have been subject to modification for hundreds of years, where the landscape is a mosaic of different landuses, and where patches of vegetated habitat may bear little resemblance to the condition before widespread anthropogenic influence. In this landscape, roads increase connectivity for people but can 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 the 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).

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 typically decline, and generalist species that forage in more open habitats become more common (Kingston 2013).

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 simplistic 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; or 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 2019 PMA3 bat study

This study addresses the primary 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 third survey in the program were to:

1. Document the diversity of bats in the PMA3 study areas using the same recording sites as in 2015 and 2017;

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

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.

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 permanent transects established and used in 2015 and 2017. Field sampling was undertaken between 10 and 31 August 2019, later than both previous surveys (June–July 2015; May 2017).

Permanent transects are located within two narrow elevational ranges in each BAA (Table 4.1): approximately 2,200 m asl and 2,700 m asl in BAA 1 on Hides Ridge in Hela Province; and approximately 1,000 m asl (Arakubi Quarry) and 1,400 m asl (KP107) in BAA 2 on the Agogo Range near Moro in Southern Highlands Province.

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, 10–17 August 2019) and BAA 2 (M1–M5; total 30 recording nights over eight sampling nights, 22–29 August 2019) (Table 4.1). A total of 66 full-night recordings was collected in 2019.

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 a potentially decreasing edge effect.

Recordings were made in high quality full spectrum format with either a Pettersson Elektronik D500X bat detector (protected in a plastic box and a waterproof bag), or a Titley Scientific Anabat Swift bat detector. Microphones on a 2–3 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 4.11). Both bat detector types allow automated recordings, have similar detection range and the recording quality is equivalent (500 kHz sampling rate, 16 bit resolution).

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

Area	Elevation (m asl)	Replicate (m asl)	Distance from ROW (m)						Total
			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	
	(KP107)	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

During the 2015 and 2017 surveys effort was made to capture bats to help associate echolocation calls with species. However, no trapping was conducted in 2019.

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 types. 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; Kale et al. 2018a,b,c; 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 species names on the basis of updated information, and a comparison of diversity across sites and studies that is independent of taxonomic allocations.

Data analysis

A comprehensive description of the data analysis is presented in Armstrong (2017) and a brief overview is provided here. 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 among survey years in terms of the number of species ('Species Richness'), the breadth of their evolutionary relationships and ecological roles ('Phylogenetic Diversity', 'Functional Diversity', respectively), 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 have been derived from more than one species (e.g. some calls associated with medium- and small-sized *Miniopterus* could have also been derived from

a species of *Pipistrellus* or *Nyctophilus*; *Kerivoula muscina* and *Murina florium* could not be distinguished reliably from each other), 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 (GLMM) to a site-by-species matrix. Prior to analysis, a check was made to determine which distribution best fit data, and data were transformed.

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. To better understand this measure, consider that sites with five species from five different families will have higher Phylogenetic Diversity, and thus higher value in terms of diversity, than sites with five species from the same family. 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 two additional species recognised in the study area (though since DNA sequences for these species were not obtained in the field, and are not available on Genbank, the sequence from a closely-related congener was used instead). 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 an 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' (representing distinct 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 at 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 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 combinations 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 a Non-metric Multidimensional Scaling ordination. 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).

All analyses were conducted using a custom-written [R] statistical computing language (R Core Team 2020) 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 and 2017 surveys was modified to allow for the incorporation of data from the third sampling year.

Results

Acoustic detections

A total of 20 echolocation call types was recognised from the recordings, which probably represents one species in almost every case (Tables 4.2 and 4.3; Figure 4.1). A 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 three surveys is compiled in Appendix 4.1. A raw site-by-species matrix showing results from each recording site from the 2019 survey is presented in Appendix 4.2.

From a simple inspection of the tabulated presence/absence data at each recording site in 2019 (Tables 4.2 and 4.3), it is clear that species composition differs between the two BAAs. Species Richness is also substantially higher at the lower elevations in BAA 2, where 17 species were recorded (vs seven species in BAA 1).

Two species were encountered for the first time in 2019: Maggie Taylor's Leaf-nosed Bat *Hipposideros maggietaylorae* (call type *125 sCF*); and the New Guinea Free-tailed Bat *Austronomus kuboriensis* (=*Tadarida kuboriensis*) (call type *13 cFM*). However, four species encountered in 2015 and 2017 were not detected in 2019. These were the New Guinea Sheath-tailed Bat *Emballonura furax* (call type *52 i.fFM.d*), Bare-rumped Sheath-tailed Bat *Saccolaimus saccolaimus* (call type *25 sFM*), Fawn Leaf-nosed Bat *Hipposideros cervinus* (call type *140 sCF*) and the unidentified leaf-nosed bat *Hipposideros* sp. cf. *ater* (call type *172 sCF*).

Table 4.2. Summary of species/call type detections at each sampling position in BAA 1 on Hides Ridge in 2019. 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. 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	**Sheath-tailed bats**						
Emballonura dianae	*35 i.fFM.d*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Emballonura furax	*52 i.fFM.d*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Emballonura raffrayana	*45 i.fFM.d*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Mosia nigrescens	*65 i.fFM.d*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Saccolaimus saccolaimus	*25 sFM*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
HIPPOSIDERIDAE	**Leaf-nosed bats**						
Aselliscus tricuspidatus	*120 sCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Hipposideros cervinus	*140 sCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Hipposideros diadema	*58 mCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Hipposideros maggietaylorae	*125 sCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Hipposideros wollastoni	*88 mCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Hipposideros sp. cf. *ater*	*172 sCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
RHINOLOPHIDAE	**Horseshoe bats**						
Rhinolophus euryotis	*52 lCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Rhinolophus mcintyrei	*70 lCF*	○●●○●○	●●○○○○	○●○○○○	○○○○○○	○○○○○○	○○○○○○
Rhinolophus megaphyllus	*65 lCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Rhinolophus sp. cf. *robertsi*	*33 lCF*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
MINIOPTERIDAE	**Bent-winged bats**						
Miniopterus sp. 1 'large'	*38 st.cFM*	●●●○●●	●●○○○●	●●●○○○	●○○○○○	●●○○○○	●○○○○○
Miniopterus sp. 2 'medium'	*45 st.cFM*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Miniopterus sp. 3 'small'	*53 st.cFM*	○○●○○○	●●○○○○	○○○●○○	●●●●●○	○○●○○●	●○○●●●
VESPERTILIONIDAE	**Vesper bats**						
Kerivoula muscina / Murina florium	*80 bFM*	○○○○○○	○○○○○○	○●○○○○	○○●○○○	○○○○○○	○○○●○○
Nyctophilus sp.	*50 bFM*	○○●○●○	○●○○○○	○○○○○○	●○○○○○	○○○○○○	○○○○●○
Philetor brachypterus	*30 cFM*	○○○○○○	○○○○○○	●○○○○○	○○○○○○	○○○○○○	○○○○○○
MOLOSSIDAE	**Free-tailed bats**						
Austronomus kuboriensis	*13 cFM*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○●○○○○	○○●○○○
Chaerephon jobensis	*20 cFM*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Otomops sp.	*30 sFM*	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○	○○○○○○
Total Species Richness		**4**	**4**	**5**	**4**	**3**	**5**

Table 4.3. Summary of species/call type detections at each sampling position in BAA 2 on the Agogo Range near Moro in 2019. Symbols and other explanations as for Table 4.2.

	Elevation	1,000 m		1,400 m		
	Transect	M4	M5	M1	M2	M3
Scientific name	**Call type**					
EMBALLONURIDAE	**Sheath-tailed bats**					
Emballonura dianae	*35 i.fFM.d*	●ooooo	ooooo	ooooo	ooooo	ooooo
Emballonura furax	*52 i.fFM.d*	ooooo	ooooo	ooooo	ooooo	ooooo
Emballonura raffrayana	*45 i.fFM.d*	●ooooo	●●oooo	●oo●oo	ooooo	●ooooo
Mosia nigrescens	*65 i.fFM.d*	●●oooo	●●ooo●	ooooo	ooooo	ooooo
Saccolaimus saccolaimus	*25 sFM*	ooooo	ooooo	ooooo	ooooo	ooooo
HIPPOSIDERIDAE	**Leaf-nosed bats**					
Aselliscus tricuspidatus	*120 sCF*	o●●o●o	o●oooo	ooooo	o●oooo	ooooo
Hipposideros cervinus	*140 sCF*	ooooo	ooooo	ooooo	ooooo	ooooo
Hipposideros diadema	*58 mCF*	ooooo	●ooooo	ooooo	ooooo	ooooo
Hipposideros maggietaylorae	*125 sCF*	oooo●o	ooooo	ooooo	ooooo	ooooo
Hipposideros wollastoni	*88 mCF*	●ooooo	●●o●●●	oo●oo●	oo●●oo	ooooo
Hipposideros sp. cf. *ater*	*172 sCF*	ooooo	ooooo	ooooo	ooooo	ooooo
RHINOLOPHIDAE	**Horseshoe bats**					
Rhinolophus euryotis	*52 lCF*	o●●●●●	o●●●o●	ooooo	o●o●oo	ooo●oo
Rhinolophus mcintyrei	*70 lCF*	ooo●oo	●●oooo	ooooo	ooooo	ooooo
Rhinolophus megaphyllus	*65 lCF*	o●oooo	●ooooo	ooooo	ooooo	ooooo
Rhinolophus sp. cf. *robertsi*	*33 lCF*	oo●ooo	ooooo	ooooo	ooooo	ooooo
MINIOPTERIDAE	**Bent-winged bats**					
Miniopterus sp. 1 'large'	*38 st.cFM*	●●oooo	●●oooo	●ooooo	●●oooo	●ooooo
Miniopterus sp. 2 'medium'	*45 st.cFM*	●ooooo	ooooo	ooooo	●ooooo	ooooo
Miniopterus sp. 3 'small'	*53 st.cFM*	●●o●●o	●●ooo●	●o●ooo	●●●oo●	●o●ooo
VESPERTILIONIDAE	**Vesper bats**					
Kerivoula muscina / Murina florium	*80 bFM*	ooooo	ooooo	ooooo	ooooo	o●oooo
Nyctophilus sp.	*50 bFM*	ooooo	ooooo	ooooo	ooooo	ooooo
Philetor brachypterus	*30 cFM*	ooooo	ooooo	ooooo	ooooo	ooooo
MOLOSSIDAE	**Free-tailed bats**					
Austronomus kuboriensis	*13 cFM*	ooooo	ooooo	ooooo	ooooo	ooooo
Chaerephon jobensis	*20 cFM*	ooooo	ooooo	ooooo	●ooooo	ooooo
Otomops sp.	*30 sFM*	●ooooo	●●oooo	ooooo	ooooo	ooooo
Total Species Richness		**14**	**11**	**4**	**7**	**5**

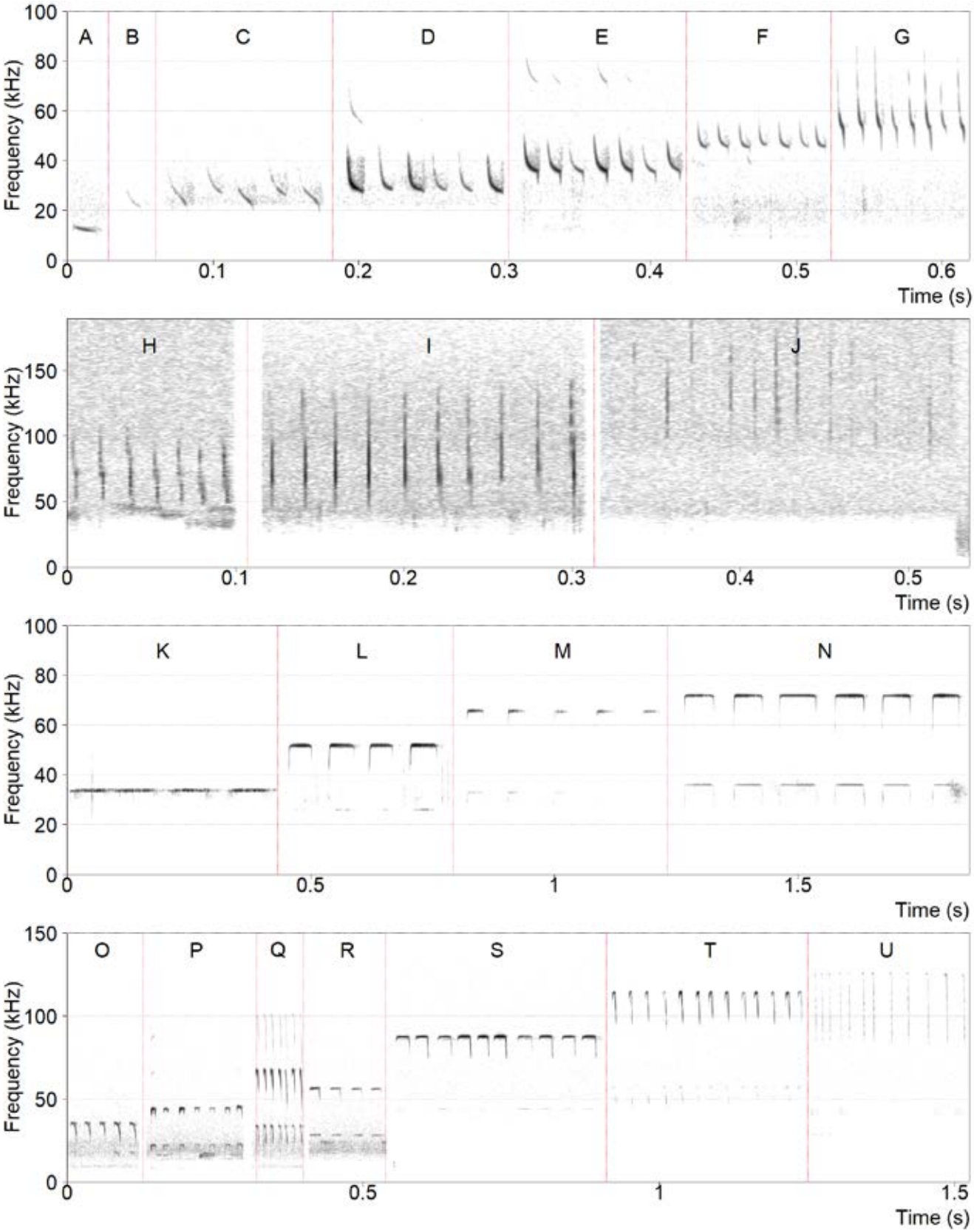


Figure 4.1. Representative sequence portions of the 20 call types recognised from the acoustic recordings in 2019, grouped by main body type of the call (time between pulses is compressed; scale of x and y axes vary).

A: *13 cFM Austronomus kuboriensis*;
B: *20 cFM Chaerephon jobensis*;
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,J: *80 bFM Kerivoula muscina / Murina florium*;
K: *33 lCF Rhinolophus* sp. cf. *robertsi*;
L: *52 lCF Rhinolophus euryotis*;
M: *65 lCF Rhinolophus megaphyllus*;
N: *70 lCF Rhinolophus mcintyrei*;
O: *35 i.fFM.d Emballonura dianae*;
P: *45 i.fFM.d Emballonura raffrayana*;
Q: *65 i.fFM.d Mosia nigrescens*;
R: *58 mCF Hipposideros diadema*;
S: *88 mCF Hipposideros wollastoni*;
T: *120 sCF Aselliscus tricuspidatus*;
U: *125 sCF Hipposideros maggietaylorae*.

Species Richness

Species Richness was compared among different distances from the ROW, different elevations, and among the three survey years. A significant difference was observed among treatment levels for distance and elevation but not for survey year; and there were no significant interaction terms between the three factors (Table 4.4). Thus, there was no evidence of a change in the use of the forest edge habitats by bats in the period 2015–2019.

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). However, while Species Richness was lower inside the forest canopy it was similar along the remainder of each transect (20–220 m). Species Richness was also significantly greater at lower elevations, particularly at Arakubi Quarry (1,000 m asl), and to a lesser extent at KP107 (1,400 m asl), than in BAA 1. Although the overall patterns in Species Richness show a trend of increasing number of species with decreasing elevation, and an increase at the forest edge (Figure 4.2), decomposing the overall plots by both distance and elevation reveals that the number of species detected at forest edges was higher only at the two lowest elevations (Figure 4.3). On Hides Ridge, the number of species along the transects was relatively similar. The basis for this pattern is revealed with other metrics.

Given that the start of transects at the edge of the ROW had significantly greater Species Richness in BAA 2, 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', as well as a greater prevalence of these species at lower elevation sites (GLMM; Table 4.5).

When the proportion of Edge species relative to that of Open and Clutter species was plotted for increasing distance from the ROW and elevation, it was clear that there was greater representation of Edge species at the forest edge. However, the pattern varied over the length of the transect, with Edge species representation being almost as high at the end of the transect furthest into the forest (Figure 4.4). There was also a clear pattern of increasing Edge species representation with increasing elevation.

To explore the patterns in Species Richness even further to have a better appreciation of what elements of the bat assemblage were contributing most to 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 (GLMM; Table 4.4), with the greatest number of *cFM* bat species recorded at distance '0 m' (Table 4.5).

Table 4.4. 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; the model fit used was: glmer(total_richness.t ~ dist + elev + year + dist*elev + elev*year + dist*year + dist*elev*year + (1 | transect), data = y, family=gaussian(link="log"), nAGQ = 25, control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=2e5))). Total Species Richness was replaced with the number of Edge species, *cFM* species and Phylogenetic Diversity in the successive analyses.

Species Richness	**Chi-square**	**df**	**P**	**Pairwise**
Distance	65.2	5	<0.001***	0 > 20*** 20 > 70*** 0 > 70*** 20 > 120*** 0 > 120*** 20 > 170*** 0 > 170*** 20 > 220*** 0 > 220*** 70 > 170*
Elevation	47.1	3	<0.001***	1,000 > 2,200*** 1,000 > 2,200*** 1,000 > 2,700*** 1,400 > 2,700**
Year	4.6	2	0.10 NS	—
Distance*Elevation	21.8	15	0.11 NS	—
Distance*Year	12.1	10	0.27 NS	—
Elevation*Year	11.6	6	0.07 NS	—
Distance*Elevation*Year	25.3	30	0.71 NS	—
Species Richness—Edge species	**Chi-square**	**df**	**P**	**Pairwise**
Distance	48.9	5	<0.001***	0 > 20*** 0 > 170*** 0 > 70*** 0 > 220*** 0 > 120*** 20 > 120*
Elevation	42.9	3	<0.001***	1,000 > 2,200*** 1,000 > 2,200*** 1,000 > 2,700***
Year	3.4	2	0.18 NS	—
Species Richness—*cFM* species	**Chi-square**	**df**	**P**	**Pairwise**
Distance	24.4	5	<0.001***	0 > 20*** 0 > 170*** 0 > 70*** 0 > 220*** 0 > 120*** 20 > 120*
Elevation	3.1	3	0.37 NS	—
Year	0.64	2	0.72 NS	—
Phylogenetic Diversity	**Chi-square**	**df**	**P**	**Pairwise**
Distance	1.8	5	0.50 NS	—
Elevation	2.6	3	0.87 NS	1,000 > 2,700*
Year	0.08	2	0.46 NS	—
Distance*Elevation	69.4	15	<0.001***	—
Distance*Year	1.2	10	0.99 NS	—
Elevation*Year	2.6	6	0.85 NS	—
Distance*Elevation*Year	103.6	29	<0.001***	—

Table 4.5. 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 4.2 and 4.3; Appendix 4.1) 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 4.4).

Distance (m)	Species Richness	Edge species	*cFM* species	Phylogenetic Diversity	Functional Diversity
0	**4.2 ± 3.2**	**3.2 ± 1.8**	**2.4 ± 1.0**	0.32 ± 0.21	1.26
20	2.6 ± 3.2	1.3 ± 1.3	1.0 ± 1.0	0.26 ± 0.26	1.19
70	2.2 ± 1.8	1.0 ± 0.7	0.8 ± 0.6	0.27 ± 0.16	1.17
120	1.6 ± 1.5	0.5 ± 0.7	0.4 ± 0.6	0.17 ± 0.15	0.72
170	1.4 ± 1.3	0.6 ± 0.6	0.6 ± 0.6	0.16 ± 0.16	0.81
220	1.8 ± 1.7	1.1 ± 0.9	0.9 ± 0.7	0.23 ± 0.21	0.54
Elevation (m)					
1,000	**5.3 ± 3.4**	**2.2 ± 2.2**	1.1 ± 1.3	0.41 ± 0.22	1.16
1,400	2.2 ± 2.1	1.2 ± 1.6	0.9 ± 1.2	0.21 ± 0.19	1.06
2,200	1.5 ± 1.2	1.0 ± 0.8	1.0 ± 0.8	0.20 ± 0.17	0.79
2,700	1.3 ± 0.7	1.1 ± 0.6	1.1 ± 0.6	0.15 ± 0.12	0.83
Year					
2015	2.3 ± 2.3	1.3 ± 1.3	0.9 ± 0.9	0.23 ± 0.18	—
2017	2.8 ± 2.9	1.6 ± 1.6	1.2 ± 1.2	0.28 ± 0.23	—
2019	1.9 ± 2.0	1.0 ± 1.2	0.9 ± 1.0	0.22 ± 0.19	—

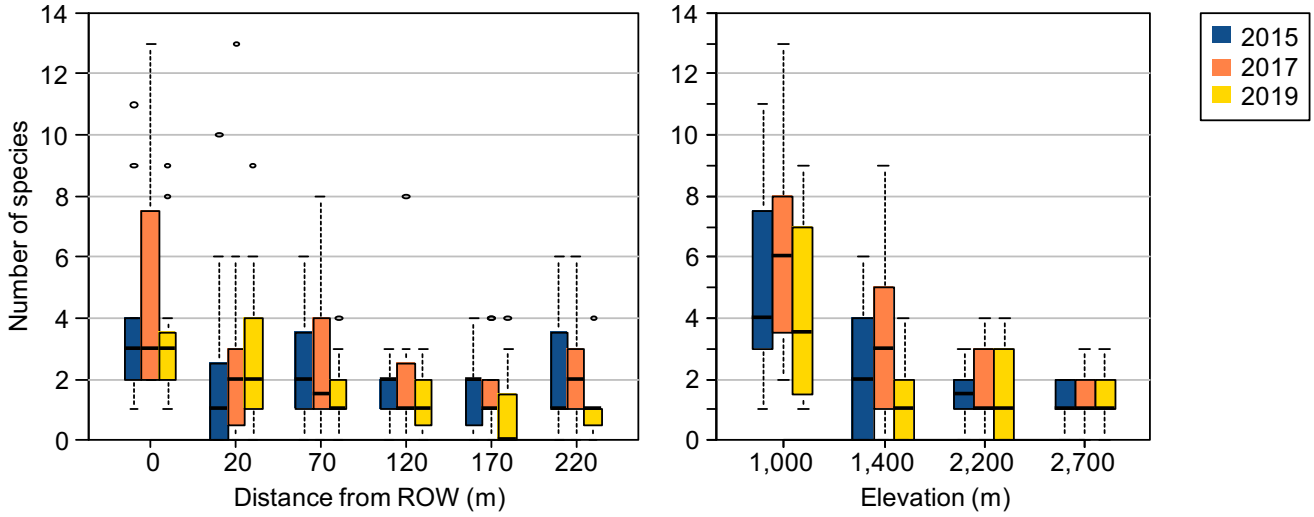


Figure 4.2. Summary of the patterns of Species Richness with increasing distance from the ROW, and with increasing elevation. All sites have been combined for each of the two factors, but segregated by year. [Boxplot components: central bar—median; boxes—inter-quartile range, with second quartile group below median, third quartile group above median; bars—minimum and maximum values; circles—statistical outliers]

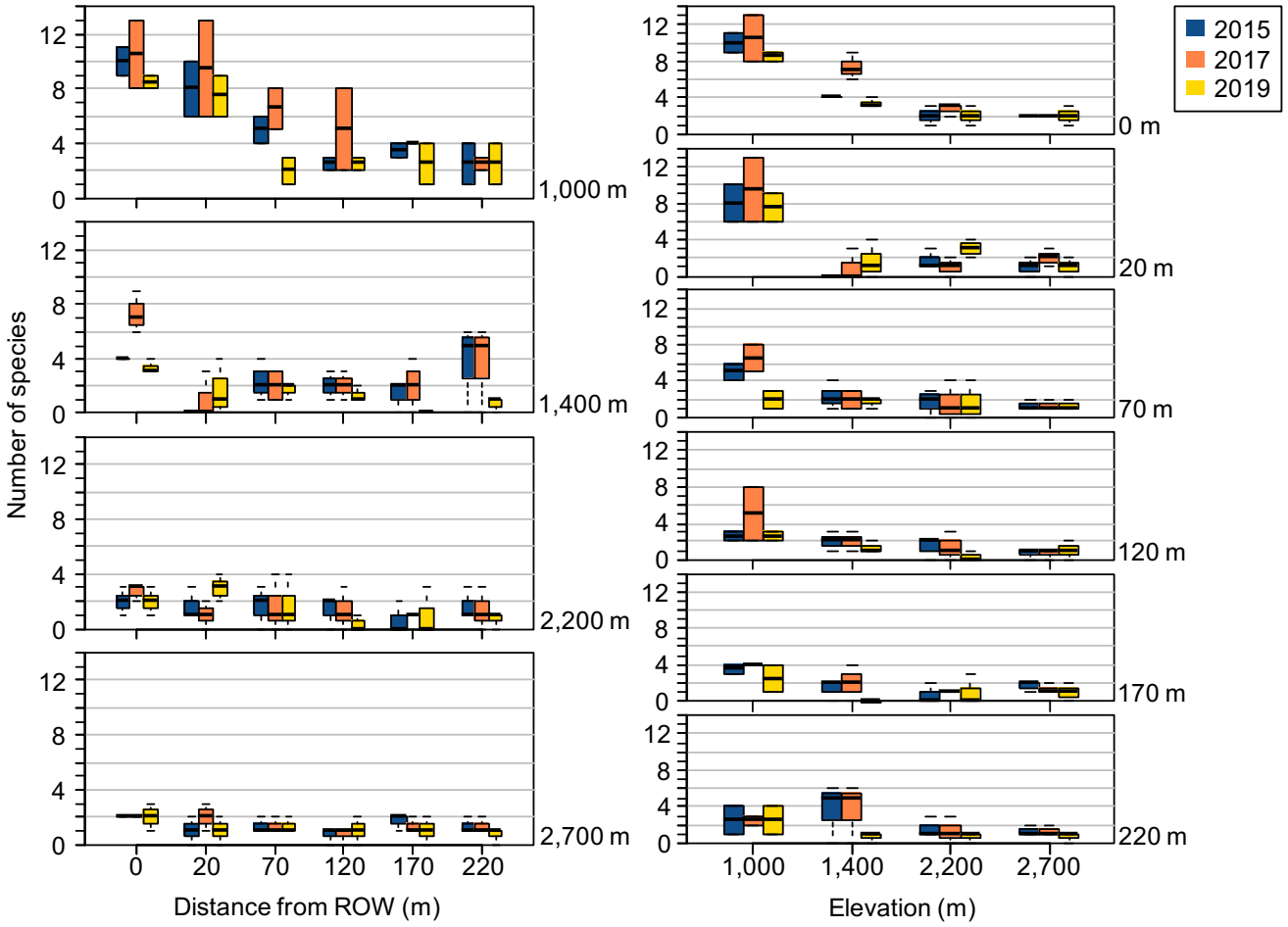


Figure 4.3. Summary of the patterns of Species Richness with increasing distance from the ROW at each elevation, and with different elevation levels for each distance from the ROW.

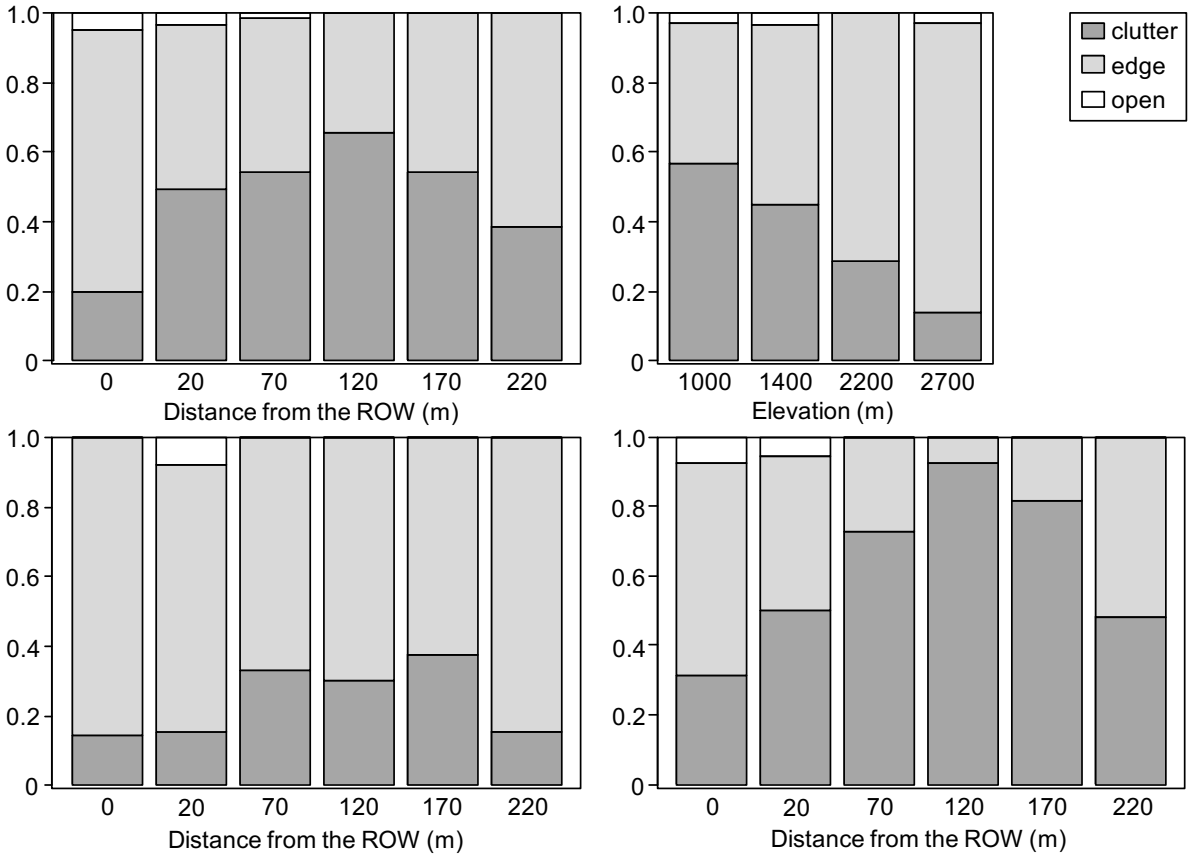


Figure 4.4. Summary plots of the proportion of bats occupying three different flight spaces at increasing distance from the ROW, and at increasing elevation for all sites combined (top); and with increasing distance from the ROW in BAA 1 (bottom left) and BAA 2 (bottom right).

Phylogenetic Diversity

When plotted against total Species Richness, Faith's (1992) Phylogenetic Diversity increased in an approximately 1:1 relationship (data not shown), suggesting that there was no over- or under-representation of bat families generally across the entire study area. An additional statistical test (GLMM) was undertaken to compare Phylogenetic Diversity among different distances from the ROW, different elevations, and across the three survey years to understand if there were any biases in terms of bat genera or even families that were associated with the factor levels. While there was an indication that Phylogenetic Diversity might be slightly greater at 1,000 m asl (Figure 4.5), there was no statistically significant difference in the evolutionary diversity within any factor (Table 4.4). The interpretation is that there is no environmental factor operating at recording sites that favours one particular family of bats.

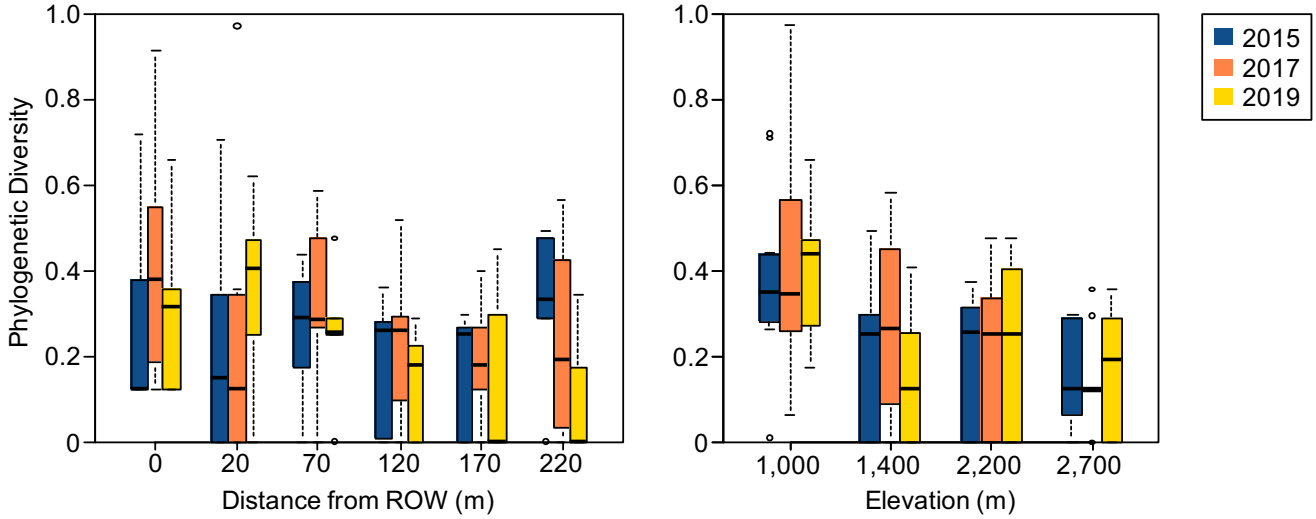


Figure 4.5. Summary plots of the pattern of Phylogenetic Diversity at increasing distance from the ROW and at increasing elevation.

Functional Diversity

Values of Petchey and Gaston's (2002) Functional Diversity, or diversity of bat ecological niches, showed a similar trend across survey years (Figure 4.6). The metric decreased overall with increasing distance from the ROW, and decreased with increasing elevation. These patterns are consistent with the patterns from Species Richness and Phylogenetic Diversity, illustrating that bat diversity is greatest at lower elevations, and that more species can be found at the forest edge.

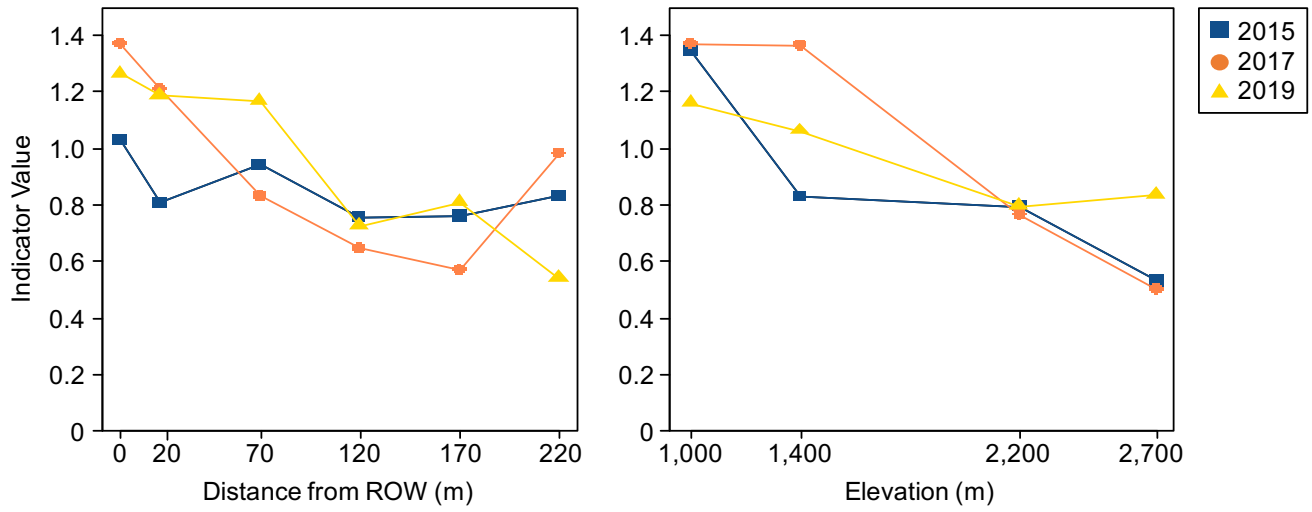


Figure 4.6. Summary plots of Functional Diversity at increasing distance from the ROW, and at increasing elevation.

Species composition

Analyses thus far have shown clearly that Species Richness is greatest at the edges of transects in BAA 2, and at lower elevations. This greater richness is attributable to species that can exploit forest edges and open habitats, as well as other species that prefer to forage in the forest interior. 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 are subsets of the larger assemblages, or whether there is species replacement. This is relevant to ask because forest interior species tend to be specialists, and thus more dependent on closed habitats than bat species common in a more dissected forest landscape.

Non-metric Multidimensional Scaling (NMDS) ordination plots showed that the higher elevations differed slightly in species representation (Figure 4.7). However, there is substantial overlap in species composition at different distances from the ROW, although the recording sites at '0 m' were clustered more tightly. The pattern overall is suggestive of a subsetting of the broader assemblage at higher elevations, and at different distances along sampling transects. Some families were absent from Hides Ridge in all survey years (Hipposideridae; all Rhinolophidae except McIntyre's Horseshoe Bat *Rhinolophus mcintyrei*), and other families are only represented by low frequency encounters of one particular species in a particular year (Molossidae: New Guinea Free-tailed Bat *Austronomus kuboriensis* in 2019; Emballonuridae: *Mosia nigrescens* in 2015; see Tables 4.2 and 4.3; Armstrong 2017; Armstrong et al. 2019).

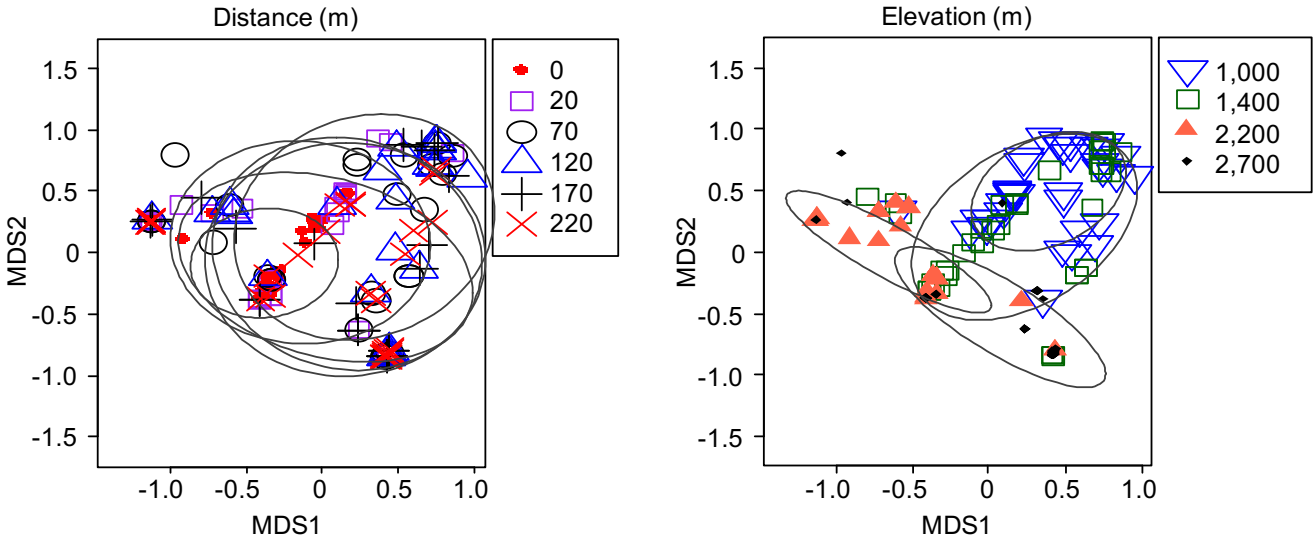


Figure 4.7. Non-metric Multidimensional Scaling (NMDS) ordinations summarising patterns of species composition (as derived from species lists at each recording site) at increasing distance from the ROW, and at different elevations, for all survey years combined.

Species-level patterns

Overall patterns can change when component species sensitive to changes in their habitat 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 ecological generalists or more specialised.

Compiling Relative Abundance shows how frequently each species was detected amongst the recording sites. This highlights 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 4.8; Appendices 4.3 and 4.4). Both this species and the unidentified bent-winged bat *Miniopterus* sp. 1 'large' (call type *38 st.cFM*) occurred at a higher Relative Abundance at higher elevations in BAA 1, relative to other species. The long-eared bat *Nyctophilus* sp. also had a higher relative abundance on Hides Ridge.

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 (distance values of 0 m) 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 unidentified species of free-tailed bat *Otomops* sp. (call type *30 sFM*) (Figure 4.8). Species with higher Indicator Species values within the forest were Maggie Taylor's Leaf-nosed Bat *Hipposideros maggitaylorae* (call type *125 sCF*), the long-eared bat *Nyctophilus* sp. (call type *50 bFM*) and *Kerivoula muscina* / *Murina florium* (call type *80 bFM*). All of these associations are consistent with what be expected given their echolocation call types.

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

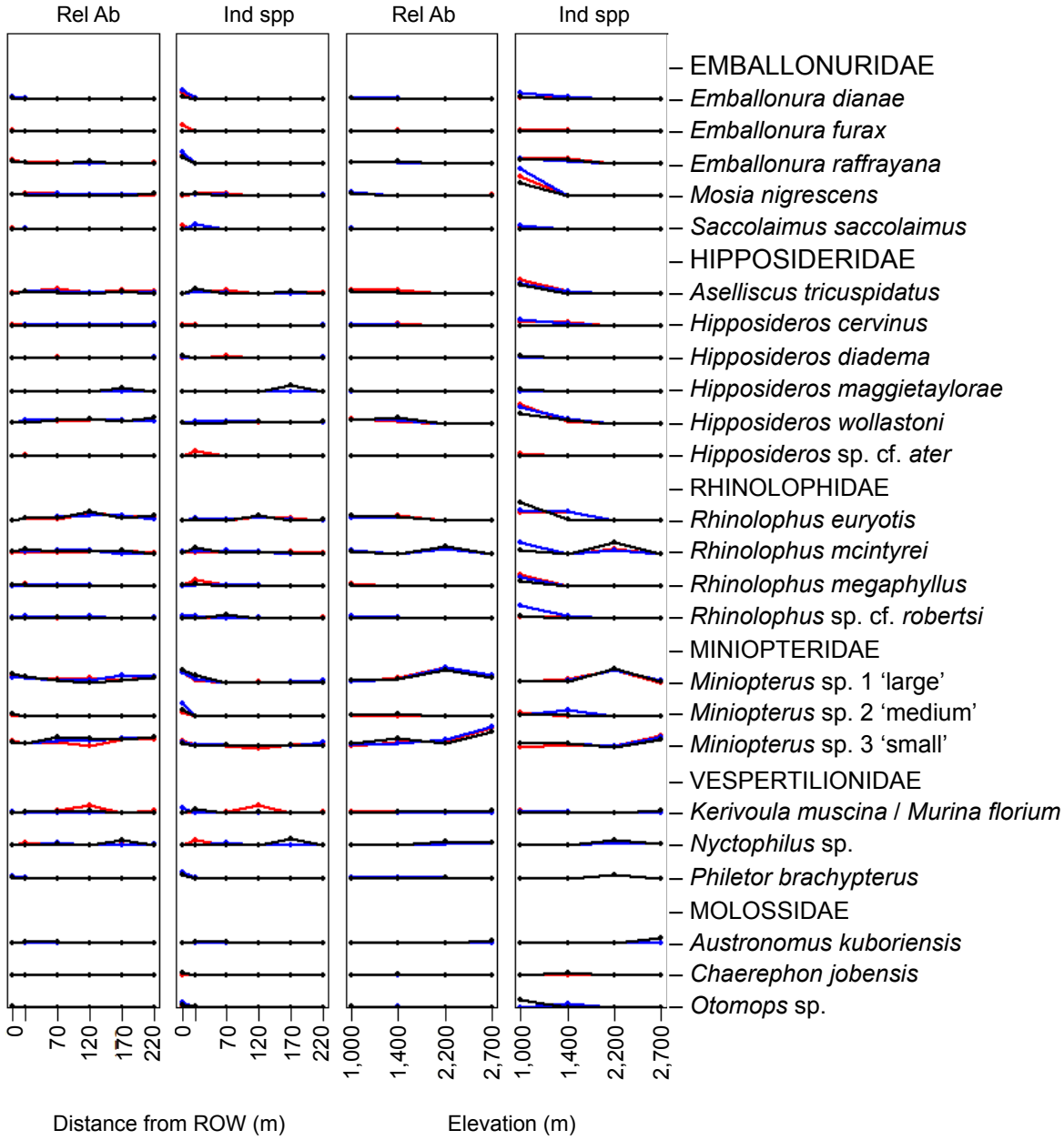


Figure 4.8. Summary of trends in Relative Abundance and Indicator Species indices with increasing distance from the ROW, and by elevation (red: 2015; blue: 2017; black 2019).

Discussion

Long-term trends

This component of the PMA3 monitoring study seeks to determine whether there are ongoing impacts from linear infrastructure construction on adjacent forest habitats that is reflected in changes to bat communities. The total number of bat species detections from all sites combined (i.e., the number of species detected at each site, added together in one survey year) varied across years (154 in 2015, 177 in 2017, and 124 in 2019), but there was no statistical difference in Species Richness or Phylogenetic Diversity across the three surveys (Tables 4.4 and 4.5). A comparison of the similarity of bat species composition amongst recording sites using NMDS ordination did not reveal any trend or clustering associated with particular survey years that would suggest a change in the combination of species present (Figure 4.7). Likewise, the diversity of ecological niches, as measured by the Functional Diversity metric, varied somewhat over the three years, but there was no clear difference (Figure 4.6). A slight increase of Functional Diversity in 2019 at 2,700 m is probably related to the detection of one species from the Molossidae for the first time at this elevation (New Guinea Free-tailed Bat *Austronomus kuboriensis*). Thus, the diversity and composition of bat communities in both BAAs appears to have remained stable since 2015.

The design of the PMA3 monitoring program does not incorporate a long-term quantitative assessment of the vegetation community at the sampling sites, so it is not possible to directly correlate bat diversity with specific habitat features or condition. However, field observations over the three surveys (K. Armstrong, personal observation) suggest that there have been few changes to forest structure at sampling locations since 2015. For example, the forest edge has not shifted at the start of most transects, the trees with transect markings were present, and the canopy coverage appeared unchanged. Exceptions include the removal of one tree from the beginning of transects H2 and M2, and of one tree within the middle of transect M4 between 2015 and 2017 (Richards et al. 2019). The treefalls at H2 and M2 moved the edge of the forest back around five metres, and opened a clearing around 20 metres in diameter on M4. Treefalls resulting from the major earthquake of March 2018 also opened the tree canopy on H4. The relatively small spatial scale of such tree loss is not expected to have a significant effect on bat activity. Thus, in the absence of an obvious and developing environmental gradient along transects, it is not surprising that bat diversity remains at similar levels since 2015.

A long-term perspective of changes in bat communities adjacent to the ROW must also include consideration of the original community of bats in relatively undisturbed forest. This is difficult to assess for Arakubi where linear infrastructure has been in place for an extended period, and there was probably some degree of change in the foraging habits of the bat community within the approximately four years following the the development of the ROW on Hides Ridge, and before the beginning of the PMA3 study in 2015. The original bat survey conducted for the PNG LNG environmental impact assessment by G. Richards (2005, 2008) represents the only available pre-construction baseline information for comparison. A re-analysis of the data collected from sites 'Hides 3' and Benaria was able to provide an updated perspective on the identification of call types, because of more recent progress in an understanding of their species attribution (Specialised Zoological 2017). Direct comparisons with this earlier work are constrained because the baseline sampling sites are different from the PMA3 long-term study sites, but it was possible to assess whether the same species were present in both studies.

A simple comparison of the bat species inventory between pre-construction and the combined PMA3 surveys shows that significantly more species have been identified in the three most recent surveys (24 species versus at least 13 species; Appendix 4.5). There are still two or more species detected in 2005 that have not yet been encountered on the PMA3 surveys. The Maluku Myotis *Myotis moluccarum* is not expected to occur in the PMA3 study sites because specific habitats are not present (streams with flowing water). Up to three species of *Pipistrellus* might be present, but their calls are similar to those of *Miniopterus* spp., and observations made to date suggest that only the latter is present. Other species recorded by Richards (2005) but not by Armstrong (2017) such as an unidentified free-tailed bat *Otomops* sp.,

and the Greater Northern Free-tailed Bat *Chaerephon jobensis*, were eventually detected in 2017 (Armstrong et al. 2019); and the New Guinea Free-tailed Bat *Austronomus kuboriensis* was eventually detected in 2019 (the present study). Thus, the surveys of PMA3 have recorded a much greater diversity of bats than the baseline studies, and there is no evidence to suggest that bat diversity has declined since construction of the ROW, nor evidence that certain species have appeared (or disappeared) because of this opening of habitat.

Edge effects

This study has to date not detected any gradual changes in the bat community with increasing distance from the forest edge. However, it has identified that the forest edge (0 – 20 m) has a significantly different level of usage compared to the remainder of the transect (20 – 220 m)—but only at the two lowest elevations (Tables 4.4 and 4.5; Figure 4.3). The number of species detected foraging at the forest edge is higher at elevations of 1,000 m asl and 1,400 m asl (but not at transects on Hides Ridge BAA 1; Figure 4.3). This pattern is also reflected in higher levels of Functional Diversity at the start of transects (Figure 4.6), though the slightly higher level of Phylogenetic Diversity observed at the start of the transects was not statistically significant (Table 4.4, Figure 4.5). Therefore, in BAA 2 there is a significant difference in how a resident bat community uses the open area of the ROW (and access roads and Arakubi Quarry) and the forest interior, and other analyses have helped to identify the species that drive these patterns.

In terms of flight space preference for foraging in BAA 2, there is a high proportion of species that forage in Edge habitats at a distance of 0 m, with the proportion of species that forage in Clutter greater at all distances within the forest interior (Figure 4.4; see flight space designations for each species in Appendix 4.1). The Indicator Species index (Figure 4.8) helped to highlight which species might be responsible for the pattern of higher diversity at the forest edge. There is a clear association of several Edge species with the transect distance of 0 m, specifically the three species of small sheath-tailed bats *Emballonura*, the three species of *Miniopterus*, and the Short-winged Pipistrelle *Philetor brachypterus*. These species may also use 'Edge habitat' at the top of the canopy, so they are not confined to the ROW. There was also a significantly higher number of detections of bats that produce *cFM*-type calls (mostly *Miniopterus* spp., but also *P. brachypterus* and *C. jobensis*) at the forest boundary (Table 4.4).

The larger proportion of Clutter species that is seen at the lower elevations (Figure 4.4) is mostly attributable to the presence of species in the two families Hipposideridae and Rhinolophidae. While they were sometimes recorded at the forest edge, they had higher encounter rates within the forest (Table 4.3; Figure 4.8). These species contributed to the higher proportions of Clutter species detected within the forest interior (distances of 20 m and greater) and at lower elevations (BAA 2) (Figure 4.4). Thus, the higher species diversity at lower elevations included both Clutter species that forage preferentially in the forest interior, and also Edge species that forage preferentially in the open space of the ROW, access roads and Arakubi Quarry.

By contrast, most species in BAA 1 were classified as Edge species (Figure 4.4). While these species can be detected using the ROW (especially *Miniopterus* sp. 1 'large'), an examination of Table 4.3 shows that they can also be detected using the forest (the canopy, or the interior, or both). The two Clutter species, *Kerivoula muscina / Murina florium* and *Nyctophilus* sp., were almost always recorded inside the forest (Table 4.3).

Patterns with changing elevation

The most obvious pattern in the distribution of bat species detected during the PMA3 surveys is the association of many species with certain elevations. This is most evident when comparing Species Richness between BAA 1 and BAA 2. Over the past three surveys, the greatest number of species have been recorded in BAA 2 (22 species from elevations 1,000 m asl and 1,400 m asl combined, compared with eight species from 2,000 m asl and 2,700 m asl combined; Appendix 4.5). However, the NMDS ordinations (Figure 4.7) did not detect much difference between the two BAAs in terms of species composition because the species present in BAA 1 are mostly a subset of those present in BAA 2 (six out of eight spcies

in BAA 1 are present in BAA 2). The exception is two species, each with a relatively low encounter rate, that have only ever been recorded at higher elevations (Appendix 4.4): the unidentified long-eared bat *Nyctophilus* sp. (probably the Small-toothed Long-eared Bat *N. microdon* that was captured at transect H3 in 2017, and is known from moderate elevations of between 1,900 m asl and 2,200 m asl; Bonaccorso 1998); and *A. kuboriensis* (also known from relatively high elevations of between 1,900 and 2,800 m asl; Bonaccorso 1998; at 2,900 m asl by Armstrong and Aplin 2001; detected at transects H5 and H6 at 2,700 m asl in the present survey). These two species are thought to be adapted to high elevation habitats.

Within each of the BAAs, there was relatively little difference between each of the two elevations. The horseshoe bat *Rhinolophus mcintyrei* has been detected in all survey years at transects in the BAA 1 lower elevation category, but not higher than this (it is also present in BAA 2), and *A. kuboriensis* only at transects in the BAA higher elevation category. In BAA 2, the Eastern Horseshoe Bat *Rhinolophus megaphyllus* and the unidentified leaf-nosed bat *Hipposideros* sp. cf. *ater* (call type *172 sCF*) have only been encountered in the lowest elevation category, however their distributions may be more closely associated with the proximity of a cave roost than any factor related to elevation.

The possible reasons for reduced bat diversity at higher elevations were discussed by Armstrong et al. (2019). In summary, higher elevations are associated with lower mean temperatures that affect both the abundance and activity of insect prey, and the energy budgets of small-sized bats that are reliant on certain levels of prey capture for their survival, and physiological mechanisms to conserve heat and energy during resting periods. To live in a less productive (in terms of insect biomass), higher elevation environment, bats need to be able to enter torpor to maintain energy reserves when prey biomass is insufficient and tempertaures are colder in the early hours of the morning before dawn. Alternatively, they need to have a different prey capture strategy, extended nightly foraging range, and/or physiology that allows activity in the cooler temperatures (the likely situation with *A. kuboriensis*).

In general, the Emballonuridae, Hipposideridae and Rhinolophidae do not appear to be adapted to environments over 2,000 m asl. The summary accounts in Bonaccorso (1998) for each of the species in these families that has been detected in BAA 2 during the PMA3 study indicate upper elevational distribution limits of below 1,800 m asl, though the distribution of Wollaston's Leaf-nosed Bat *Hipposideros wollastoni* is known to extend up to c. 2,000 m asl. However, the PMA3 study has extended the known upper elevational limits (as stated in the authoritative guide of Bonaccorso (1998)) for several species to: 1,400 m asl for Temminck's Leaf-nosed Bat *Aselliscus tricuspidatus* (previously 600 m); 1,000 m asl for Maggie Taylor's Leaf-nosed Bat *Hipposideros maggietaylorae* (previously 300 m); 2,700 m asl for the Lesser Sheath-tailed Bat *Mosia nigrescens*; (previously 1,600 m); and 2,200 m asl for *Rhinolophus mcintyrei* (previously 1,600 m). The record of *Mosia nigrogriseus* at transect H6 in 2015 (Armstrong 2017) is surprising and the recording has been re-checked and the observation confirmed. The consistent records across survey years of *Rhinolophus mcintyrei* at 2,200 m asl on transects H1 and H2 in BAA 1 are very likely because of nearby rocky roosting habitat, and possibly represents the upper limit of this species. Records such as these serve to illustrate that the elevation limits of bat species in PNG remain incompletely documented.

Bat species of conservation significance

No species of conservation significance (in an IUCN threatened category, or assessed as Data Deficient) have been detected on any of the PMA3 surveys conducted to date.

Progress in resolving bat species identities in the study area

In 2017, several bats were captured in harp traps that were either difficult to identify (large-sized bent-winged bats, *Miniopterus* sp.), or were thought to represent species new to science (a woolly bat *Kerivoula* sp. cf. *muscina* (Figure 4.9); a long-eared bat *Nyctophilus* sp. cf. *microdon* (Figure 4.10). Genetic data has been obtained since the previous report, based on the genome-scale DNA sequencing method used to make consistent identifications of rodents and frogs (see Chapters 1 and 3 in this volume). The genetic data helped to make a species-level identification of the *Miniopterus*,

and provides strong support for the species-level distinctness of the *Kerivoula* sp. cf. *muscina* and *Nyctophilus* sp. cf. *microdon* (Appendix 4.6). These two potentially new species produce echolocation calls that are very similar to closely related species, so they cannot be distinguished yet in the acoustic analysis. Their formal taxonomic description will be completed in the future after morphological comparisons are made.

- ***Bent-winged bats***. In 2017, three bent-winged bats *Miniopterus* sp. were captured at 2,700 m asl in a harp trap at Transect H6 on Hides Ridge. The identity of these three individuals was resolved as part of a larger study of the taxonomy of Indo-Australasian *Miniopterus* (S. Wiantoro and K. Armstrong unpublished). All three individuals are the same species, and are referred to a taxon currently known as '*Miniopterus tristis grandis*'.

- ***Woolly bats***. A small bat captured at 2,700 m asl in a harp trap at Transect H6 on Hides Ridge resembles the Fly River Woolly Bat *Kerivoula muscina*, but differs from that species in having relatively darker fur. There are no previous records of *K. muscina* above 1,600 m asl and genetic analysis has confirmed that, while the specimen from BAA 1 is a member of the genus *Kerivoula* it is significantly divergent from *Kerivoula muscina* specimens collected across a relatively large proportion of western PNG (Appendix 4.6). The Hides Ridge *Kerivoula* specimen probably represents a high elevation species that is new to science.

- ***Long-eared bats***. A long-eared bat captured in a harp trap on Transect H6 at an elevation of 2,700 m asl on Hides Ridge resembles the mid-montane-adapted Small-toothed Long-eared Bat *Nyctophilus microdon*, but features of the noseleaf and ear appear to be different. The individual does not resemble the IUCN Critically Endangered Thomas' Big-eared Bat *Pharotis imogene* (photographs of this rare species in Hughes et al. 2014). True *N. microdon* was also captured in 2017, at an elevation of 2,200 m asl at Transect H3 on Hides Ridge, and there are no records of this species occurring above 2,200 m asl (Bonaccorso 1998). Genetic analysis revealed significant divergence between the specimen collected at 2,700 m asl on Hides Ridge and other *N. microdon* from lower elevations, as well as clear genetic separation from another common species, *N. microtis*, collected across a broad area of PNG (Appendix 4.6). The Hides Ridge *Nyctophilus* sp. cf. *microdon* specimen probably represents a high elevation species that is new to science.

- ***Leaf-nosed bats***. In 2015, an echolocation call type (*172 sCF*) never encountered previously in PNG was recorded on Transect M5 in BAA 2 (Armstrong 2017), and it was detected again in 2017 adjacent to Lake Kutubu at KP 87 (Kale et al. 2018c). If this bat can be captured on a future survey, genetic and morphological analysis can be used to confirm its identity and determine whether it is indeed a species new to science.

Conclusions

1. The combined results from the 2015, 2017 and 2019 surveys suggest that the forest adjacent to the ROW has so far retained its value for a diverse community of bats.

2. There have been no detectable changes in the diversity of bat communities within BAA 1 and BAA 2 since 2015.

3. The most obvious pattern detected in the distribution of bat species is the large elevational difference in Species Richness between BAA 2 (22 species in total over three surveys) and BAA 1 (8 species). There are many (16) species in BAA 2 that are not found in BAA 1 (6 spp. are shared), but there are also two species detected acoustically only in BAA 1, which might be specifically adapted to high elevations (Small-toothed Long-eared Bat *Nyctophilus microdon*; New Guinea Free-tailed Bat *Austronomus kuboriensis*).

4. This study has not detected any gradual changes in the bat community with increasing distance from the forest edge, suggesting minimal impacts of edge effects. However, it has identified that the forest edge (0–20 m) has a significantly higher level of usage compared to the remainder of the transect (20–220 m). The forest edge has a significantly higher overall level of Species Richness, a higher proportion of Edge species, and a higher number of species with *cFM* call types. Therefore, some species of bat have responded positively to the opening of canopy in the ROW and access roads (*Emballonura* spp. *Miniopterus* spp., Short-winged Pipistrelle *Philetor brachypterus*).

5. While there is a significantly larger number of Clutter species in BAA 2 (mostly bat species of the families Hipposideridae and Rhinolophidae), these appear to be confined mostly to the forest interior, and there is no clear trend of increasing proportion of forest species as the transect extends from 20 m to 220 m.

6. Two bats captured on Transect H6 in BAA 1 in 2017 (a woolly bat *Kerivoula* sp. cf. *muscina*, and a long-eared bat *Nyctophilus* sp. cf. *microdon*) were thought to possibly represent species new to science, and recent genetic analyses provide support for their distinctness. These results add to the known bat diversity in the study area, but their echolocation calls cannot currently be distinguished from other closely related species. Taxonomic descriptions of these two bat species will be prepared in the future.

Recommendations

1. The acoustic bat monitoring component should be continued in future surveys because of a demonstrated ability for detecting bat responses to open areas and the forest edge.

2. Further effort should be given on future surveys to capture the putative 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 KP 87 adjacent to Lake Kutubu.

3. Future trapping effort should also target species of *Pipistrellus* that are expected to occur, but have not yet been detected acoustically, because of the similarity of their calls with those of medium- and small-sized *Miniopterus*.

4. While abundance data is not available from bat detector recordings, relative levels of activity might reveal more detail about changes in forest usage over time than presence/absence data can suggest. Further consideration could be given to quantifying activity levels of particular species identified in the Indicator Species analysis as Edge and Clutter species, including from past recordings.

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Plate 1

Figure 4.9. *Kerivoula* sp. cf. *muscina*, a putative new bat species captured on Hides Ridge in 2017.

Figure 4.10. *Nyctophilus* sp. cf. *microdon*, a putative new bat species captured on Hides Ridge in 2017.

Appendix 4.1. Summary of bat detections by bat detector and captures in all survey years, (C: captured; E: detected from echolocation calls.

Scientific name	Call type	Main Call type	Flight space	2015	2017	2019
PTEROPODIDAE—2	—	—	—			
Syconycteris australis	—	—	—	C	C	
Syconycteris sp. cf. *australis*	—	—	—	C	C	
EMBALLONURIDAE—5						
Emballonura dianae	*35 i.fFM.d*	*fFM*	Edge	E	E	E
Emballonura furax	*52 i.fFM.d*	*fFM*	Edge	E		
Emballonura raffrayana	*45 i.fFM.d*	*fFM*	Edge	E	E	E
Mosia nigrescens	*65 i.fFM.d*	*fFM*	Edge	E	E	E
Saccolaimus saccolaimus	*25 sFM*	*sFM*	Open	E	E	
HIPPOSIDERIDAE—6						
Aselliscus tricuspidatus	*120 sCF*	*sCF*	Clutter	CE	CE	E
Hipposideros cervinus	*140 sCF*	*sCF*	Clutter	CE	CE	
Hipposideros diadema	*58 mCF*	*mCF*	Edge	E	E	E
Hipposideros maggietaylorae	*125 sCF*	*sCF*	Clutter			E
Hipposideros wollastoni	*88 mCF*	*mCF*	Clutter	E	E	E
Hipposideros sp. cf. *ater*	*172 sCF*	*sCF*	Clutter	E		
RHINOLOPHIDAE—4						
Rhinolophus euryotis	*52 lCF*	*lCF*	Clutter	E	CE	E
Rhinolophus mcintyrei	*70 lCF*	*lCF*	Clutter	E	CE	E
Rhinolophus megaphyllus	*65 lCF*	*lCF*	Clutter	CE	E	E
Rhinolophus sp. cf. *robertsi*	*33 lCF*	*lCF*	Clutter	E	E	E
MINIOPTERIDAE—3						
Miniopterus sp. 1 'large'	*38 st.cFM*	*cFM*	Edge	CE	CE	E
Miniopterus sp. 2 'medium'	*45 st.cFM*	*cFM*	Edge	E	E	E
Miniopterus sp. 3 'small'	*53 st.cFM*	*cFM*	Edge	E	CE	E
VESPERTILIONIDAE—5						
Kerivoula muscina / Murina florium	*80 bFM*	*bFM*	Clutter	E	CE	E
Nyctophilus microdon	*30 bFM*	*bFM*	Clutter		C	
Nyctophilus sp.	*50 bFM*	*bFM*	Clutter	E	E	E
Philetor brachypterus	*30 cFM*	*cFM*	Edge	E	E	E
MOLOSSIDAE—3						
Austronomus kuboriensis	*13 cFM*	*cFM*	Open			E
Chaerephon jobensis	*20 cFM*	*cFM*	Open		E	E
Otomops sp.	*30 sFM*	*sFM*	Open		E	E
Total 27 species				**22**	**23**	**20**

Appendix 4.2. Summary of species detections at each nightly recording site in 2019 (to allow future verification; filled black circle indicate a detection of that species.).

BAA_transect_elevation	Distance from road (m)	Recording unit serial	Recording night in August 2019	*E. dianae*	*E. furax*	*E. raffrayana*	*M. nigrescens*	*S. saccolaimus*	*A. tricuspidatus*	*H. cervinus*	*H. maggietaylorae*	*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'	*K. muscina / M. florium*	*Nyctophilus* sp.	*P. brachypterus*	*A. kuboriensis*	*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*	*125 sCF*	*88 mCF*	*172 sCF*	*52 lCF*	*70 lCF*	*65 lCF*	*33 lCF*	*38 st.cFM*	*45 st.cFM*	*53 st.cFM*	*80 bFM*	*50 bFM*	*30 cFM*	*13 cFM*	*20 cFM*	*30 sFM*
Hides_H1_2200	0	953	15																●								
	20	953	16													●			●								
	70	957	16													●			●		●		●				
	120	536887	16																								
	170	953	17													●			●				●				
	220	954	17																●								
Hides_H2_2200	0	954	13													●			●		●						
	20	954	14													●			●		●		●				
	70	497962	14																								
	120	955	15																								
	170	954	15																								
	220	497962	15																●								
Hides_H3_2200	0	953	12																●					●			
	20	536887	11													●			●			●					
	70	536887	12																●								
	120	953	13																		●						
	170	536887	13																								
	220	536887	14																								
Hides_H4_2700	0	957	15																●		●		●				
	20	954	16																		●						
	70	955	16																		●	●					
	120	955	17																		●						
	170	497462	16																		●						
	220	497962	17																								
Hides_H5_2700	0	953	11																●								
	20	953	10																●						●		
	70	957	12																		●						
	120	957	11																								
	170	957	13																								
	220	957	14																		●						
Hides_H6_2700	0	955	11																●		●						
	20	955	10																								
	70	954	10																						●		
	120	954	11																		●	●					
	170	955	12																		●		●				
	220	955	13																		●						

Appendix 4.2. Species detections at each nightly recording site in 2019—*continued*.

BAA_transect_elevation	Distance from road (m)	Recording unit serial	Recording night in August 2019	*E. dianae*	*E. furax*	*E. raffrayana*	*M. nigrescens*	*S. saccolaimus*	*A. tricuspidatus*	*H. cervinus*	*H. maggietaylorae*	*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'	*K. muscina / M. florium*	*Nyctophilus* sp.	*P. brachypterus*	*A. kuboriensis*	*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*	*125 sCF*	*88 mCF*	*172 sCF*	*52 lCF*	*70 lCF*	*65 lCF*	*33 lCF*	*38 st.cFM*	*45 st.cFM*	*53 st.cFM*	*80 bFM*	*50 bFM*	*30 cFM*	*13 cFM*	*20 cFM*	*30 sFM*
Moro_M1_1400	0	957	23		●														●		●						
	20	957	22																								
	70	957	24										●								●						
	120	957	25		●																						
	170	957	26																								
	220	957	27										●														
Moro_M2_1400	0	955	26																●	●	●					●	
	20	955	25						●						●				●		●						
	70	955	23										●									●					
	120	955	24										●		●												
	170	955	28																								
	220	955	29																		●						
Moro_M3_1400	0	536887	28		●														●		●						
	20	536887	27																			●					
	70	536887	26																		●						
	120	536887	25												●												
	170	536887	23																								
	220	536887	24																								
Moro_M4_1000	0	953	28	●	●		●						●						●	●	●						●
	20	954	29				●		●						●		●		●		●						
	70	953	27						●						●			●									
	120	953	23												●	●					●						
	170	953	22						●		●				●						●						
	220	953	24												●												
Moro_M5_1000	0	954	25		●		●					●	●			●	●		●		●						●
	20	954	24		●		●		●				●		●	●			●		●						●
	70	953	25												●												
	120	954	26										●		●												
	170	953	26										●														
	220	954	27				●						●		●						●						

Appendix 4.3. Summary of Relative Abundance and Indicator Species index for each species at increasing distance (m) from the ROW for 2019 (grey shading indicates the magnitude of the value, with zero as white and 1.0 as black).

	Relative Abundance						Indicator Species Index					
Distance from ROW	**0**	**20**	**70**	**120**	**170**	**220**	**0**	**20**	**70**	**120**	**170**	**220**
EMBALLONURIDAE												
Emballonura dianae							0.1					
Emballonura furax												
Emballonura raffrayana	0.1			0.1			0.2					
Mosia nigrescens	0.1	0.1				0.1	0.1	0.1				
Saccolaimus saccolaimus												
HIPPOSIDERIDAE												
Aselliscus tricuspidatus		0.1	0.1		0.1			0.2			0.1	
Hipposideros cervinus												
Hipposideros diadema							0.1					
Hipposideros maggietaylorae					0.1						0.2	
Hipposideros wollastoni	0.1		0.1	0.2	0.1	0.2				0.1		0.1
Hipposideros sp. cf. *ater*												
RHINOLOPHIDAE												
Rhinolophus euryotis		0.1	0.1	0.3	0.1	0.2		0.1		0.2		
Rhinolophus mcintyrei	0.1	0.1	0.1	0.1	0.1			0.2				
Rhinolophus megaphyllus								0.1				
Rhinolophus sp. cf. *robertsi*			0.1						0.1			
MINIOPTERIDAE												
Miniopterus sp. 1 ‘large’	0.3	0.2	0.1		0.1	0.2	0.4	0.2				
Miniopterus sp. 2 ‘medium’	0.1						0.2					
Miniopterus sp. 3 ‘small’	0.2	0.2	0.3	0.3	0.3	0.4	0.2	0.1	0.1	0.1	0.1	0.1
VESPERTILIONIDAE												
Kerivoula muscina / Murina florium		0.1	0.1	0.1				0.1				
Nyctophilus sp.			0.1		0.2						0.2	
Philetor brachypterus							0.1					
MOLOSSIDAE												
Austronomus kuboriensis			0.1					0.1				
Chaerephon jobensis							0.1					
Otomops sp.	0.1						0.1					

Appendix 4.4. Summary of Relative Abundance and Indicator Species index for each species at each elevation (m) for 2019 (grey shading indicates the magnitude of the value, with zero as white and 1.0 as black).

	Relative Abundance				Indicator Species Index			
Elevation	**1,000**	**1,400**	**2,200**	**2,700**	**1,000**	**1,400**	**2,200**	**2,700**
EMBALLONURIDAE								
Emballonura dianae					0.1			
Emballonura furax								
Emballonura raffrayana	0.1	0.1			0.1	0.1		
Mosia nigrescens	0.1				0.4			
Saccolaimus saccolaimus								
HIPPOSIDERIDAE								
Aselliscus tricuspidatus	0.1				0.3			
Hipposideros cervinus								
Hipposideros diadema					0.1			
Hipposideros maggietaylorae					0.1			
Hipposideros wollastoni	0.1	0.2			0.3	0.1		
Hipposideros sp. cf. *ater*								
RHINOLOPHIDAE								
Rhinolophus euryotis	0.2	0.1			0.6	0.1		
Rhinolophus mcintyrei	0.1		0.2		0.1		0.3	
Rhinolophus megaphyllus					0.2			
Rhinolophus sp. cf. *robertsi*					0.1			
MINIOPTERIDAE								
Miniopterus sp. 1 ‘large’	0.1	0.1	0.4	0.2	0.1	0.1	0.5	
Miniopterus sp. 2 ‘medium’								
Miniopterus sp. 3 ‘small’	0.1	0.3	0.2	0.5	0.1	0.2		0.3
VESPERTILIONIDAE								
Kerivoula muscina / Murina florium				0.1				0.1
Nyctophilus sp.			0.1	0.1			0.2	0.1
Philetor brachypterus							0.1	
MOLOSSIDAE								
Austronomus kuboriensis				0.1				0.1
Chaerephon jobensis						0.1		
Otomops sp.	0.1				0.3			

Appendix 4.5. Comparison between the species identified by Richards (2005; as revised by Specialised Zoological 2017; marked by 'X'), and the three PMA3 surveys combined (● indicates present, o indicates not detected, with the order of the symbols by survey year from left to right: Armstrong 2017; Armstrong et al. 2019; the present study; '? indicates that calls of this type/species might have been present, but they could not be distinguished reliably from another similar species; grey highlight denotes species that have been encountered only on the 2005 survey).

Species	Call type	Benaria 2005	BAA 2	Hides 3 2005	BAA 1
EMBALLONURIDAE					
Emballonura dianae	*35 i.fFM.d*	X	●●●		ooo
Emballonura furax	*52 i.fFM.d*	X	●oo		ooo
Emballonura raffrayana	*45 i.fFM.d*	X	●●●	X	ooo
Mosia nigrescens	*65 i.fFM.d*		●●●		●oo
Saccolaimus saccolaimus	*25 sFM*		●●o		ooo
HIPPOSIDERIDAE					
Aselliscus tricuspidatus	*120 sCF*	X	●●●		ooo
Hipposideros cervinus	*140 sCF*		●●o		ooo
Hipposideros diadema	*58 mCF*		●●●		ooo
Hipposideros maggietaylorae	*125 sCF*		oo●		ooo
Hipposideros wollastoni	*88 mCF*		●●●		ooo
Hipposideros sp. cf. *ater*	*172 sCF*		●oo		ooo
RHINOLOPHIDAE					
Rhinolophus euryotis	*52 lCF*	X	●●●		ooo
Rhinolophus mcintyrei	*70 lCF*	X	●●●	X	●●●
Rhinolophus megaphyllus	*65 lCF*		●●●		ooo
Rhinolophus sp. cf. *robertsi*	*33 lCF*	?	●●●		ooo
MINIOPTERIDAE					
Miniopterus sp. 1 'large'	*38 st.cFM*	X	●●●	X	●●●
Miniopterus sp. 2 'medium'	*45 st.cFM*	?	●●●	?	ooo
Miniopterus sp. 3 'small'	*53 st.cFM*	X	●●●	X	●●●
VESPERTILIONIDAE					
Murina sp. cf. *florium*	*80 bFM*		●●●		●o●
Myotis moluccarum	*40 bFM*	X	ooo		ooo
Nyctophilus sp.	*50 bFM*		ooo	?	●●●
Philetor brachypterus	*30 cFM*	X	o●o	X	●●●
Pipistrellus sp.	*42 st.cFM*	X	ooo		ooo
MOLOSSIDAE					
Austronomus kuboriensis	*13 cFM*		ooo	X	oo●
Chaerephon jobensis	*20 cFM*	X	o●●	X	ooo
Otomops sp.	*18 sFM*		o●●		ooo
Total		**12+**	**22**	**7+**	**8**

Appendix 4.6. Preliminary outcomes of SNP-based genetic analysis of two putative new bat species captured by harp trap on Transect H6 at 2,700 m asl on Hides Ridge in 2017, based on Principal Coordinates Analysis. Left: Separation of the Hides Ridge *Kerivoula* sp. cf. *muscina* individual from *Kerivoula muscina* collected from various locations in the western part of Papua New Guinea; Right: Separation of the Hides Ridge *Nyctophilus* sp. cf. *microdon* individual from *N. microdon* captured relatively close by at an elevation of 2,200 m asl at Transect H3, as well as another closely-related species, *N. microtis*, captured from both north and south of the central cordillera. For further details of the genetic sequencing method, see Chapters 1 and 3, this volume. Comparative material from other localities in PNG is from tissues in the Australian Biological Tissue Collection at the South Australian Museum.