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Monitoring the birds and the bees: Environmental DNA metabarcoding of flowers detects plant–animal interactions

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Original Article

Abstract
Animal pollinators are vital for the reproduction of ~90% of flowering plants. However, many of these pollinating species are experiencing declines globally, making effective pollinator monitoring methods more important than ever before. Pollinators can leave DNA on the flowers they visit, and metabarcoding of these environmental DNA (eDNA) traces provides an opportunity to detect the presence of flower visitors. Our study, collecting flowers from seven plant species with diverse floral morphologies, for eDNA metabarcoding analysis, illustrated the value of this novel survey tool. eDNA metabarcoding using three assays, including one developed in this study to target common bush birds, recorded more animal species visiting flowers than visual surveys conducted concurrently, including birds, bees, and other species. We also recorded the presence of a flower visit from a western pygmy possum; to our knowledge this is the first eDNA metabarcoding study to simultaneously identify the interaction of insect, mammal, and bird species with flowers. The highest diversity of taxa was detected on large inflorescence flower types found on Banksia arborea and Grevillea georgeana. The study demonstrates that the ease of sample collection and the robustness of the metabarcoding methodology has profound implications for future management of biodiversity, allowing us to monitor both plants and their attendant cohort of potential pollinators. This opens avenues for rapid and efficient comparison of biodiversity and ecosystem health between different sites and may provide insights into surrogate pollinators in the event of pollinator declines.

Key Words
avian metabarcoding assay, insect eDNA, plant–animal interactions, pollination, vertebrate eDNA

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INTRODUCTION

Close to 90% of all 400,000 flowering plant species are dependent on animals for pollination (Ollerton et al., 2011). The taxonomic identities and ecology for many of these pollinators remains, however, an area of ongoing discovery (Forister et al., 2019; Knight et al., 2018). Concerningly, many of these potential pollinating species (scientifically described and undescribed) are experiencing rapid declines around the world (Rafferty, 2017; Regan et al., 2015; Sánchez-Bayo & Wyckhuys, 2019). For example, wild pollinator diversity has more than halved in some areas in Europe (see Biesmeijer et al., 2006) and some pollinator species in North America have fallen in relative abundance by over 95% (Jacobson et al., 2018). Concurrently, native plant communities globally are showing community shifts that are altering the availability of foraging and nesting resources for wild pollinating species (Scheper et al., 2014). For instance, native plant species in America have shown range declines between 3 and 50% (see MacKenzie et al., 2019), while some areas in Europe have seen over 125 plant species lost (see Finderup Nielsen et al., 2019). The decline in native foraging resources threatens the resilience of remaining native pollinators, especially those with specialized plant relationships (Mola et al., 2021; although see Simanonok et al., 2021). These declines in wild insects and other animals, as well as the plants they interact with are driven by a combination of environmental and anthropogenic stressors (i.e., habitat loss, invasive species, and climate change; Potts et al., 2010). Consequently, there is an ever-growing need to increase our understanding of plant–animal interactions to ensure informed management decisions are made for species conservation and habitat restoration.

Insects have historically been the most frequently studied pollinators, with a bias toward managed insects such as the European honey bee (Apis mellifera). Out of nearly 4000 studies relating to pollination ecology, 65% cited insects (Millard et al., 2020). Many other vertebrate taxa, including birds (Krauss et al., 2018; Whelan et al., 2008), mammals (bats, primates, rodents, and marsupials; Carthew & Goldingay, 1997; Kunz et al., 2011), and reptiles (lizards; Olesen & Valido, 2003) are recognized as having important pollination impacts and effects on plant mating systems. Such diversity is especially pronounced for the South-Western Australia’s Floristic Region (SWAFR), a globally recognized biodiversity hotspot with over 8379 vascular plant species and high levels of endangerment (Gioia & Hopper, 2017). Here, approximately 15% of all plant species are pollinated by vertebrates (Brown et al., 1997; Keighery, 1980) with insects also providing key pollination services (i.e., Lunau et al., 2021; Menz et al., 2013). As with elsewhere in the world, pollinators of native species in the SWAFR are experiencing declines in abundance, geographic range, and genetic connectivity due to habitat loss and fragmentation, climate change and associated increase in fire frequency (Bezemer et al., 2019; Campbell et al., 2022; Phillips et al., 2010; Prendergast, 2022). Due to the pace of decline in pollinators (Potts et al., 2010) there is a need to develop fast and accurate methods to detect animal visitors to flowers which, until now, relied on time-intensive field observation by specialists.

Conventional approaches for the identification of insect visitors and pollinators have relied on morphological identification after capture/observation, including pan, vane and camera traps, targeted netting, trap-nests, and observational records (O’Connor et al., 2019; Saunders et al., 2013). However, the accuracy of each method can vary between animal taxa and may miss certain groups, creating sampling bias (Prendergast et al., 2020; Prendergast & Hogendoorn, 2021). For instance, there are limitations in the ability of visual surveys to detect reclusive pollinators (Krauss et al., 2017). While camera traps can overcome this limitation and can provide valuable behavioral data (Droissart et al., 2021), they require a substantial time commitment not only in the field but also through the screening process as a result of technological complications such as false triggers (Krauss et al., 2017). In addition, the reliance on taxonomic expertise for morphological identification of species, a field that is in decline globally (Pearson et al., 2011), represents a substantial bottleneck when insects are involved in pollination (Stork, 2018). Direct observational approaches are also limited as the field time commitment may not capture all insect visitors/pollinators (Blüthgen, 2010). Therefore, to determine plant–animal interactions and to construct pollinator networks on multiple plant species within a highly biodiverse landscape, using conventional methods would be challenging. Instead, a variety of techniques and expertise are required to obtain reliable classifications and accurate information.

Environmental DNA (eDNA) metabarcoding is a recently developed molecular approach that may provide an opportunity to rapidly detect the presence of all floral visitors and pollinators. During plant–animal interactions, DNA can be deposited on flowers in detectable amounts (Evans & Kitson, 2020). eDNA metabarcoding involves the extraction of this DNA and high-throughput sequencing of taxonomically informative genome regions, known as “barcode regions,” that have been amplified using polymerase chain reaction (PCR) technology (Taberlet et al., 2012). These approaches have successfully been tested as a means to detect flower-visiting insects (Thomsen & Sigsgaard, 2019). Similarly, eDNA has been used to detect a variety of vertebrates including birds (Ushio et al., 2018), mammals (Ishige et al., 2017) and reptiles (Kucherenko et al., 2018), from substrates such as soil (Andersen et al., 2012; Ryan et al., 2022), water (Ushio et al., 2018), scat (Van Der Heyde et al., 2021), and saliva deposited on plant material by browsing animals (Nichols et al., 2012). Thus, eDNA metabarcoding offers an exciting opportunity to rapidly detect both insect and vertebrate visits from multiple flowering plant species simultaneously.

While the ability to detect insect visits to flowers using eDNA shows promise (Evans & Kitson, 2020; Gamonal Gomez et al., 2022; Harper et al., 2022; Thomsen & Sigsgaard, 2019), the technique has only recently been used to identify vertebrate flower visitors (Jensson et al., 2023; Walker et al., 2022). Furthermore, while eDNA metabarcoding surveys have been shown to outperform the use of both visual (Barata et al., 2020) and camera trap (Leempoel et al., 2020) techniques in other contexts, there are limitations of the method, including limited knowledge on the deposition and
persistence of eDNA on floral surfaces (Barnes & Turner, 2016; Harrison et al., 2019; Valentin et al., 2021). To better understand any limitations of this novel approach, we compared eDNA metabarcoding of flowers with conventional plant-animal interaction survey methods. We tested this technique using flowers from seven plant species, with diverse floral morphologies, within a pristine natural environment (Helena and Aurora Range) that is home to more than a dozen rare, short-range endemic, and threatened plant species (Gibson et al., 2012). Three eDNA barcoding assays were used to determine if eDNA metabarcoding can reliably detect plant-animal interactions verified with conventional pollinator visual surveys. Ease of data collection and the robustness of the metabarcoding methodology has profound implications for future management of biodiversity, allowing us to monitor both plants and their attendant cohort of potential pollinators. This opens avenues for us to compare biodiversity and ecosystem service health rapidly and efficiently between different sites.

2 | METHODS

2.1 | Study site

Our site was within the Helena and Aurora Range (Kalamaia name: “Bungalbin”), in the Goldfields-Esperance region of Western Australia (Figure 1). We undertook two visits: one in spring time September 2020, when visual pollinator surveys for insect, bird and mammal pollinators were conducted for six focal flowering species – *Acacia adinophylla*, *Eremophila clarkei*, *Eremophila oppositifolia*, *Grevillea georgeana*, *Leucopogon spectabilis* and *Tetratheca aphylla* subsp. *aphylla*, followed by the collection of flowers for eDNA analysis, and one in autumn May 2021, when the same procedures were repeated for *Banksia arborea*, which was not flowering on the first visit. These plants represented a range of species with different flower morphologies and different assumed pollinators. Furthermore, many of the plant species sampled are of conservation concern, with little information on pollinating taxa currently available (Figure 2; Appendix S5).

2.2 | Flower sample collection

A total of 175 samples were taken from the same individual plants surveyed for bird and insect pollinators and subsequently used in the eDNA metabarcoding study. Based on morphology and size, flowers were assigned to one of three categories: large inflorescence, small inflorescence, or single flower (Figure 2). From the seven plant species, five complete flowers or inflorescences were collected from five individual plants totaling 25 flowers/inflorescences per species. To prevent contamination, single-use sterile nitrile gloves were worn during sampling and all flowers were collected in individual sterile plastic tubes. All samples were then stored on ice in a well-insulated polystyrene ice box (60-mm walls) after sampling and stored below -20°C after returning from the field (within 48h) until DNA extraction.

2.3 | Bird surveys

Bird pollinator surveys were undertaken during peak foraging times for birds: before 1000 and after 1500 (Gilpin et al., 2017). Each plant was surveyed once during each time period, with all visible inflorescences on each focal plant observed simultaneously for 20 min from a distance of approximately 20 m to minimize disturbance (Gilpin et al., 2017). However, where it was not possible to survey from this distance due to vegetation and terrain restrictions, surveys were undertaken from no <10 m and as close to 20 m as possible. The specific plant and observation time for each plant was chosen at random to avoid temporal bias, and the species and number of birds that interacted with flowers recorded. A full list of the taxa observed are listed in Table S1.

2.4 | Insect surveys

Insect pollinators were surveyed on the same individual plants surveyed for bird pollinator surveys during daylight hours when temperatures were warm enough for bee activity (approx. 0900-1600, >16°C) by a single experienced entomologist (K.S.P). Surveys were conducted on each plant for 10 min, approximately 1 m away from the plants, except for flora that were inaccessible (*L. spectabilis*). Visiting insect taxa were classified to the lowest taxonomic level possible via visual observation in the field. For the purposes of analyses, insect taxa observed were collapsed to family level; a full list of the taxa observed are listed in Table S2.

2.5 | Nocturnal surveys

Nocturnal surveys were conducted approximately 40 min after sunset using torches for 60 min throughout the study site on two consecutive nights to detect nocturnal mammal pollinators. No fauna was seen.

2.6 | Bird primer design

Searches for available mitochondrial DNA sequences of 134 common bush birds of south-western Australian (SWWA) were conducted using NCBI’s nucleotide database (Altschul et al., 1990). The mitochondrial gene NADH dehydrogenase subunit 2 (ND2) provided the most extensive number of available sequences (120 species, each ~1040bp length; Appendix S7, Table S10). The identified avian ND2 sequences were downloaded from NCBI (Altschul et al., 1990) and aligned using the MUSCLE plugin (default settings) in Geneious v11.0.12 (Kearse et al., 2012). Based
on the alignments, candidate universal primer sets were designed using Primer3 within Geneious (Koressaar & Remm, 2007; Untergasser et al., 2012). Candidate primers were then visually assessed to determine the best sites for primer pairing and maximum taxonomic resolution within the internal amplified regions. To allow primer annealing to polymorphic sites, both the forward and reverse primers were modified to include degenerate bases, and primer characteristics were analyzed (G/C content, temperature, secondary structures, primer pair compatibility) to further improve the choice of primer using both Primer3 within Geneious (Koressaar & Remm, 2007; Untergasser et al., 2012) and the online bioinformatics tool Sequence Manipulation Suite: PCR Primer Statsn (Stothard, 2000). The following ND2 assay was designed to generate an approximately 229 bp amplicon (excluding primers): BirdND2F 5′ CCATTCCACTTAYTGRRTYCC 3′ and BirdND2R: 5′GGGAGATDGADGARAADGC 3′.

In silico analysis was then performed to test the specificity of the priming sites for target taxa and resolution of internal amplified regions. Specificity of the primer set was tested through in silico PCR using the “search_PCR” command in USEARCH v11.0.667 (Edgar, 2010), targeting both the newly generated target bird species list and custom generated full-length mitochondrial DNA reference databases (Sakata et al., 2022). These DNA reference databases were comprised of 18,283 mammals, 10,594 fish, 4,510 birds, 1,461 reptiles, and 746 amphibian sequences (35,597 vertebrate sequences). In silico PCR was performed under the following parameters: min amplicon size: 100, max amplicon size 1000, mismatch 0, 1, 2, 3. To determine the dissimilarity of internal amplified regions generated from both the custom target taxa database and full-length mitochondrial bird database the “dist.dna” function within the “ape” package (Paradis & Schliep, 2019) was used in R v.4.0.3 (R Core Team, 2013).

To assess PCR amplification, efficiency, sensitivity, and optimal annealing temperature, in vitro testing was conducted using the gDNA of two bird species: Red-tailed black cockatoo (Calyptorhynchus banksii) and rainbow lorikeet (Trichoglossus moluccanus). A temperature gradient from 51 to 61°C, in combination with seven 10-fold gDNA dilutions from 1:10 to 1:10^12, inclusive.
of non-template controls (NTCs), were evaluated. The temperature gradient showed 53°C as the optimal annealing temperature with NTCs undetected and gDNA detected at all levels of dilution from the quantitative PCR (qPCR) assay.

To determine the efficacy of the newly developed assay, in vitro testing was conducted on bird bath water ($n = 8$; 500 mL each) from Perth, Western Australia, and a mixed positive genomic DNA (gDNA) sample containing red-tailed black cockatoo (C. banksii), rock dove (Columba livia), and southern boobook (Ninox novaeseelandiae) gDNA. Bird bath water samples were filtered through a Pall 0.45 μm GN-6 Metricel® mixed cellulose ester membranes using a Pall Sentino® Microbiology pump (Pall Corporation) and frozen at −21°C prior to extraction. For all but A. adinophylla samples, DNA was extracted using a DNeasy Blood and Tissue Kit (Qiagen) with lysis performed by either adding a small flower, small inflorescence, or half filter membrane to a 2-mL plastic tube, adding 60 μL of Proteinase K, 540 μL of ATL lysis buffer and digesting for 17 h at 56°C. For A.

### 2.7 Sample processing and DNA extraction

All laboratory processes were conducted in dedicated laboratories within the Trace and Environmental DNA (TrEnD) Laboratory, Curtin University, Perth, Western Australia. Large inflorescences ($B. arborea$, $G. georgeana$) were individually placed in decontaminated plastic containers and covered with purified distilled water (~500 mL) for 10 min, manually agitated twice for 30 seconds at 5-min intervals. Water samples were then individually filtered across Pall 0.45 μm GN-6 Metricel® mixed cellulose ester membranes using a Pall Sentino® Microbiology pump (Pall Corporation) and frozen at −21°C prior to extraction. For all but A. adinophylla samples, DNA was extracted using a DNeasy Blood and Tissue Kit (Qiagen) with lysis performed by either adding a small flower, small inflorescence, or half filter membrane to a 2-mL plastic tube, adding 60 μL of Proteinase K, 540 μL of ATL lysis buffer and digesting for 17 h at 56°C. For A.
adino"phylla"

teraction parameters remained the same except for 120 μL of Proteinase K and 1080 μL of ATL lysis buffer added due to the absorbent property of the flowers. DNA was then extracted from the digest supernatant using the QIAcube extraction platform (Qiagen). To detect possible cross-contamination during sample filtering, 500 mL of bleach solution, used for rinsing the pump equipment and containers between samples, was filtered and processed in the same way as field samples (n = 2). Similarly, digest (n = 1) and extraction controls (n = 4) were processed with each batch of samples.

2.8 | Assessment of DNA extracts

Two assays were used to amplify eDNA from all flowers (n = 175), fwhF2/fwhR2n (F: 5’-GGAACCGGGTGAAGGTGATGAAGTATC-3’; R: 5’-GTRATWGCHCDDGCTARACWG-3’; Vamos et al., 2017), hereafter referred to as fwh, designed to amplify a 205 bp fragment of the arthropod cytochrome c oxidase I (COI) gene region and birdND2 (229 bp) designed to target local bird species (see above). On all B. arborea (n = 25) and G. georgeana (n = 25) flowers, the 16Smam1/2 assay (F: 5’-CTTGGTTGACCTCGCA-3’; R: 5’-GCTTATCGCTAGGTAAAC-3’; Taylor, 1996), hereafter referred to as 16Smam, designed to amplify a ~130 bp fragment of mammalian 16S ribosomal gene region was also used to detect small mammals known to pollinate these taxa.

To assess the quality and quantity of DNA in each extract, and determine the optimal level of DNA input, qPCR was carried out on three PCR replicates per sample at neat, 1:10, and 1:100 dilutions (Murray et al., 2015). All qPCR reactions were performed on a StepOnePlusTM Real-Time PCR system (Applied Biosystems) with reaction volumes totaling 25 μL. Reactions contained 1× PCR Gold buffer (Applied Biosystems), 2.5 mM MgCl2 (Applied Biosystems), 0.4 mg/mL BSA (Fisher Biotec), 0.25 mM of each dNTPs (Astral Scientific Australia), 0.25 μM forward and reverse primer, 1 U AmpliTaq Gold (Applied Biosystems), 0.6 μL SYBR Green (Life Technologies) and 2 μL of template eDNA. Cycling conditions were initial denaturation at 95°C for 5 min, followed by 55 cycles at 95°C for 30 s, then 30 s at primer specific annealing temperature (50°C for fwh, 53°C for birdND2 and 55°C for 16Smam), and 45 s at 72°C, ending with 10 min elongation at 72°C. To detect possible contamination a non-template control (reagents only) was used, and a positive control with sufficient DNA quantity and quality were assigned a unique combination of MID tag (fusion) primers with the same reagents and cycling conditions described above. Template eDNA volumes varied based on the qPCR amplification ΔRn values, CT values, and melt curves generated, resulting in reaction volumes ranging from 25–35 μL containing 2–12 μL of template eDNA (Table S3). MID tag amplicons were then pooled together with other MID-tag amplicons according to ΔRn values. Pooled samples were then quantified using the QIAxcel Advanced System (Qiagen) and concentrations (ng/μL) used to combine all pools in appropriate equimolar ratios creating a DNA sequence library. Size selection of amplicons (200–400 bp) was then performed using a PippinPrep (Sage Science) before samples were purified using a QIAquick PCR Purification Kit (Qiagen), and re-quantified using a Qubit Fluorometer (Invitrogen). Sequencing was then performed on an Illumina MiSeq platform (Illumina), as per Illumina protocols for single-end sequencing (MiSeq® v2 Reagent Kit 300 Cycles PE), with a final library molarity of 6 pM containing 7% PhiX.

2.10 | Sequence analysis (filtering and taxonomic assignment)

Sequence filtering and taxonomic assignment were conducted using the eDNAFlow bioinformatics pipeline (Mousavi-Derazmahalleh et al., 2021) via the supercomputer Magnus, based at the Pawsey Supercomputing Centre in Kensington, Western Australia. Quality checking of sequence reads was performed using FASTQC (Andrews, 2010), and quality filtered (minimum Phred quality score of 20), including trimming sequences with Ns using AdapterRemoval v2 (Schubert et al., 2016). Demultiplexing was achieved using obitools (ngsfilter; Boyer et al., 2016) and sequences under 60 bp removed (obigrep). Dereplication and the creation of zero-radius operational taxonomic units (ZOTUs; min sequence abundance = 4) and ZOTU tables were then generated using the USEARCH unioise3 algorithm (Edgar, 2016). The ZOTUs were queried using the following parameters: % identity ≥ 97, evalue ≤ 1 e−3, % query cover 100, max target sequences = 10 via a BLASTN search (Altschul et al., 1990) against NCBI’s GenBank nucleotide database (accessed in January 2022). Erroneous ZOTUs were identified and removed using the post clustering curation method LULU with the minimum threshold of sequence similarity at 95% (Frøslev et al., 2017). A custom python script (Mousavi-Derazmahalleh et al., 2021) was then used to taxonomically assign ZOTUs by the lowest common ancestor (LCA) approach, with taxonomic assignment collapsed to the LCA if the percent identity of two hits with 97% query cover and 95% identity, differed by <1%.

Further filtering of the metabarcoding data was performed using the “phyloseq” package (McMurdie & Holmes, 2013) in R v.4.0.3 (R Core Team, 2013). Initially, sequence counts in eDNA samples below the threshold value of 5 were discarded. Following this, ZOTUs present in negative controls, common PCR contaminants (e.g., human and ungulate sequences), and taxonomic assignments higher than family level were removed from the data set. Species likely not present at the sample site were also removed from the data set.
or collapsed to genus or family level based on species distribution data (e.g., *Cymbacha similis* to *Cymbacha sp.* and *Exorista deligata* to *Exorista sp.*). Genera *Colluricinclia* and *Manorina* were then reassigned to *Colluricinclia harmonica* (grey shrike-thrush) and *Manorina flavigula* (yellow-throated miner), respectively, based on existing species distribution data. ZOTUs from all metabarcoding assays were combined for further analysis and individual flower samples agglomerated to plants. The ZOTU table was then transformed to presence-absence data for community comparisons.

### 2.11 | Statistical analysis

Statistical analysis was performed in R v.4.0.3 (R Core Team, 2013). Initially, animal ZOTU richness was calculated for each flowering plant species using the "phyloseq" package (McMurdie & Holmes, 2013). Species accumulation curves were then calculated using the number of observed ZOTUs by the number of flower samples using the “accumcomp” function in the “BiodiversityR” package (Kindt & Coe, 2005) with *A. adinophylla* and *L. spectabilis* removed due to the detection of a taxa on only a single plant. Observed ZOTU richness was then square-root transformed to meet the assumption of normality and homogeneity of variance and an analysis of variance (ANOVA) was used to compare the square-root transformed ZOTU richness detected between plant species (factor = plant species, level 6). A Tukey-HSD post-hoc test was then run to assess the significant differences between plant species. Data were visualized using the package “ggplot2” (Wickham, 2016).

A Kruskal-Wallis rank-sum test was used to compare the observed ZOTU richness between flower types (factor = sample type, levels 3; large inflorescence, small inflorescence, single flower). A pairwise Wilcoxon post-hoc test was then run to assess the significant differences between flower types with a Benjamini-Hochberg correction for multiple comparisons with visual surveys.

Data were then transformed to presence-absence data and a one-way permutational MANOVA (PERMANOVA) was conducted to compare the ZOTU presence/absence composition between the different species using the "vegan" package (Oksanen et al., 2013) with Jaccard similarity and 9999 permutations. Pairwise comparisons were performed using the “PairwiseAdonis” (Arbizu, 2020) package with a Benjamini-Hochberg correction for multiple comparisons. A Sankey plot was created using R package network3D (Allaire et al., 2017) to show the links between plants and all taxa detected within this study.

To make direct comparisons with visual surveys, while bird and mammal species identifications were retained at species level, all arthropods detected using eDNA metabarcoding were collapsed to family level (see insect survey methods outlined above). The similarity between eDNA metabarcoding and conventional visual surveys was then calculated between species presence/absence matrices per plant (matrices of species x plants surveyed) using a Mantel test (Pearson method, 999 permutations) on dissimilarity indices calculated using the Jaccard method, computed with the function “mantel” of the “vegan” package (Oksanen, 2009).

### 3 | RESULTS

#### 3.1 | Evaluation of birdND2 metabarcoding assay

The specificity of each newly developed birdND2 assay was evaluated through in silico PCR, with avian taxa showing the highest amplification levels (Appendix S7, Table S11). A distance matrix (Appendix S7, Table S12) showed the number of bases that differ within internal amplified regions of target taxa varied between 0 and 74bp, with a mean of 49.9 bp (SE = 9.3). Only three closely related species pairs (Anas castanea and Anas gibbonrions gracilis, *Cacatua sanguinea* and *Cacatua pastinator*, *Calyptrorhynchus baudinii*, and *Calyptrorhynchus lateralis*) contained identical amplicon regions and therefore would not be able to be resolved to species level if detected via eDNA metabarcoding.

The newly developed birdND2 avian and existing 12S-V5 general vertebrate metabarcoding assays were evaluated in vitro using both a mock community and filtered water obtained from local bird baths, to infer their ability to detect avian taxa. A total of 899,914 avian sequences were generated from the birdND2 and 12S-V5 assays, yielding 612,188 and 287,726 quality-filtered sequences, respectively. The newly developed birdND2 data set included a total of 17 avian ZOTUs, 14 assigned to species, and three to genus (Figure 3). BirdND2 outperformed the 12S-V5 assay which identified a total of five avian ZOTUs, two assigned to species, three assigned to genus and one assigned to a family. However, the birdND2 assay failed to detect Australian wood duck (*Chenonetta jubata*) and galah (*Eolophus roseicapilla*) successfully detected by the 12S-V5 assay (Figure 3).

#### 3.2 | eDNA metabarcoding of flowers and visual surveys

In total, 8,028,614 metabarcoding reads were generated by the three assays used to detect animal DNA from flower samples, with 3,676,391 sequences remaining after quality filtering. Of these, the birdND2 assay yielded 2,601,729 sequences from 21 samples (mean = 123,892, SD = 21,505), the fwh assay yielded 1,074,431 sequences from 30 samples (mean = 35,814 SD = 14,569), and the 16Smam assay yielded 1,118 sequences from 5 samples (mean = 224, SD = 106). Prior to filtering, over 90% of sequences generated from the 16Smam assay were *Homo sapiens*, with a further six contaminant mammal species identified (Canis sp., Ovis sp., Bos taurus, Sus scrofa, *Pan troglodytes*, Felis sp.), all of which were removed from the data set (Appendix S6, Table 9). Similarly, two arthropod species likely not present at the sample site, *Liposcelis bostrychophila* (book-louse) and *Parastodes fictillaria*, were also removed from the data set. Three non-target plant species (*Lotus japonicus*, *Telopea speciosisima*, and *Bignoniaeaeae sp.*) were also detected using the BirdND2 assay and subsequently removed. In total, across all three assays, eDNA metabarcoding detected 59 unique taxa (Figure 4) from the classes Mammalia (*n* = 5), Aves (*n* = 7), and Arthropoda (*n* = 47), for a total of 41 families detected within 16 orders. Of these taxa, 26 were
assigned to species level (Mammalia = 3, Aves = 7, Arthropoda = 16), 21 to genus (Mammalia = 1, Arthropoda = 20), and 12 to family (Mammalia = 1, Arthropoda = 11).

3.3 | Differences in taxa detected by plant species

eDNA metabarcoding of flowers detected arthropods on all plant species, while vertebrate pollinators were detected solely on B. arborea, E. clarkei, and G. georgeana (Figure 5). An ANOVA test on ZOTU richness found a significant difference in the number of ZOTUs detected between plant species ($F = 7.151, df = 6, p < 0.001$). Total ZOTU richness was highest for B. arborea and G. georgeana, with the Tukey-HSD test indicating a significant difference between B. arborea and all species except G. georgeana (Figure 5). Conversely, no significant difference was found between G. georgeana and all species (Figure 5). No significant difference was seen between all other plant species (Figure 5: Table S5). A Kruskal–Wallis rank-sum test showed a significant difference between flower types ($X^2 = 17.535, df = 2, p < 0.001$) with a greater number of ZOTUs detected on large inflorescences (B. arborea and G. georgeana) than both small inflorescences and single flowers (Table S4). No difference in the number of ZOTUs was seen between small inflorescences and single flower samples (Table S4). The Sankey plot shows that the highest diversity of taxa was also detected on the large inflorescence flower types found on B. arborea and G. georgeana (Figure 6). Conversely, only a single termite genus (Amistermes sp.) was detected on the relatively small A. adinophylla inflorescences. eDNA metabarcoding of the specialized, likely buzz-pollinated T. aphylla subsp. aphylla flowers (see Ladd et al., 2019) only detected feral honey bees (Apidae) and failed to detect Australian bee species known to be present in the area. Of the animal species detected on L. spectabilis only those in the insect order Diptera (Heterotrissocladius sp., Coenosia octopunctata, and Ochlerotatus camptorhynchus) could be considered potential pollinators (Keighery, 1996).

A PERMANOVA detected a significant difference in animal community composition between plant species ($F = 2.702, df = 6, R^2 = 0.283, p < 0.001$) with a pairwise comparison indicating the species composition of B. arborea significantly differed from E. oppositifolia, G. georgeana and T. aphylla subsp. aphylla. Similarly, E. clarkei significantly differed from G. georgeana. (Table S6). NMDS did not show clear segregation between plant species (Figure S1).

Although multiple flowers (n = 5) were taken from each plant surveyed, eDNA metabarcoding did not amplify animal DNA from all the flower samples. eDNA metabarcoding only detected taxa on a single flower for both A. adinophylla and L. spectabilis. In contrast, taxa were detected on 21 B. arborea and 14 G. georgeana inflorescences surveyed. ZOTU richness did not reach an asymptote for any species as the number of flowers sampled increased (Figure 7).

3.4 | Visual survey diversity recorded

Visual surveys resulted in the detection of 14 arthropods and two bird taxa, with no mammal detections, culminating in a total of 13 families across four orders. All bird taxa detected were assigned to species level. Of the arthropod taxa detected, one was assigned to species level, five to genus, seven to family, and one to order.

3.5 | Taxonomic composition differences between visual surveys and eDNA

A Mantel test found no significant correlation between the taxa detected on plants by visual surveys and eDNA metabarcoding of flowers (Mantel statistic = 0.065, $p = 0.902$). Of the 35 individual plants
NEWTON et al. surveyed, eDNA metabarcoding and visual surveys detected taxa on 19 and 23 plants, respectively. However, eDNA metabarcoding of flowers detected a greater number of taxa \( n = 59 \) compared with visual surveys \( n = 16 \); Figure 4). Of the taxa detected by both eDNA and visual surveys, only Apidae sp., Formicidae sp. and the singing honeyeater \((\text{Gavicalis virens})\), were detected on the same plant using both survey methods (Figure 4). While eDNA metabarcoding detected a variety of arthropod species, the most abundant arthropod family detected in visual surveys Apidae (represented solely by the introduced European honey bee; \( \text{Apis mellifera} \)), detected on 13 out of 35 plants surveyed, was only detected on four plants using eDNA metabarcoding. Similarly, eDNA metabarcoding failed to detect the brown honeyeater \((\text{Lichmera indistincta})\), despite this species being recorded in visual surveys. However, an additional assay targeting the 12S-V5 mitochondrial region was run on selected flowers with positive visual sightings (see Appendix S4 for methods) and successfully amplified brown honeyeater’s DNA. Only eDNA surveys detected mammal species including the successful detection of the western pygmy possum \((\text{Cercartetus concinnus})\). Similar to eDNA metabarcoding, visual surveys failed to detect potential buzz pollinators on \( \text{T. aphylla} \) subsp. \( \text{aphylla} \), although visual surveys did successfully detect potential pollinators on \( \text{A. adinophylla} \) (European honey bee and hover fly \([\text{Syrphidae}]\) species; Figure 4). Visual surveys also identified significant native bee fauna diversity (e.g., \( \text{Megachilidae} \), and oligolecic \( \text{Euhesma} \) [\text{Colletidae}] on \( \text{Eremophila} \) species that were undetected using eDNA metabarcoding. While both eDNA and visual surveys detected a variety of potential pollinator species, eDNA metabarcoding of flowers also detected various non-pollinator species including phytophagous insects (e.g., thrips and aphids), gall inducers (e.g., \( \text{Cecidomyiidae} \)), predators (e.g., spiders), and large mammals (e.g., kangaroo and horse families).

**FIGURE 4** Animal diversity identified from visual surveys and eDNA metabarcoding of flowers collected from the Helena and Aurora Range. Arthropods detected using eDNA metabarcoding are collapsed to family level. Graphic made in BioRender.

The metabarcoding of eDNA from flowers detected a wide range of organisms including three mammal species, eight bird species, and 57 arthropod taxa, with different assemblages of animals detected on each plant species. Multiple bird pollinator species, including the singing honeyeater \((\text{Gavicalis virens})\) and the yellow-throated miner \((\text{Manorina flavigula})\) were detected on \( \text{E. clarkei} \), \( \text{B. arborea} \), and \( \text{G. georgeana} \), all of which have related taxa that are known to be bird pollinated (e.g., \( \text{E. glabra} \) ssp. \( \text{glabra} \), Elliott, 2009; \( \text{B. menziesii} \), Krauss et al., 2018; \( \text{G. macleayana} \), Whelan et al., 2009). A cryptic mammal species, the western pygmy possum, was also detected on \( \text{B. arborea} \) flowers—indicating its presence in the area and role as a potential pollinator. Furthermore, many of the arthropod

4 | DISCUSSION

In this study, we successfully detected the DNA of both invertebrates and vertebrates on flowers, including the detection of both bird and mammal flower visitors using eDNA metabarcoding. This suggests that eDNA metabarcoding of flowers can offer a strong complement to conventional plant–animal interaction monitoring techniques, increasing the capacity to identify a more complete set of floral visitors. Furthermore, this study demonstrates the utility of this survey method for understudied and rare plant species that may be difficult to monitor if they grow in remote regions, receive relatively few pollinator visits, or are visited by cryptic/reclusive animal species.

4.1 | eDNA metabarcoding survey

The metabarcoding of eDNA from flowers detected a wide range of organisms including three mammal species, eight bird species, and 57 arthropod taxa, with different assemblages of animals detected on each plant species. Multiple bird pollinator species, including the singing honeyeater \((\text{Gavicalis virens})\) and the yellow-throated miner \((\text{Manorina flavigula})\) were detected on \( \text{E. clarkei} \), \( \text{B. arborea} \), and \( \text{G. georgeana} \), all of which have related taxa that are known to be bird pollinated (e.g., \( \text{E. glabra} \) ssp. \( \text{glabra} \), Elliott, 2009; \( \text{B. menziesii} \), Krauss et al., 2018; \( \text{G. macleayana} \), Whelan et al., 2009). A cryptic mammal species, the western pygmy possum, was also detected on \( \text{B. arborea} \) flowers—indicating its presence in the area and role as a potential pollinator. Furthermore, many of the arthropod
families identified in this study using eDNA metabarcoding have not previously been recorded as flower-visitors. The moth families Oecophoridae, Xyloryctidae, and Tortricidae have not previously been recorded as flower-visitors for the *Banksia* genus, nor have the moth families Noctuidae, Geometridae and Tortricidae been previously recorded as floral-visitors for the *Grevillea* genus (*Table S8*). Until now, no studies have provided community descriptions for the focal flower visitors for many of these study species; here however, using a relatively non-invasive molecular technique, we identified flower-visiting taxa that may provide pollination services to these conservation priority plant species. As such, this study indicates that eDNA metabarcoding of flowers offers a survey method able to detect past interactions and increase the understanding of plant-animal interactions of commonly understudied species.

Supporting Thomsen and Sigsgaard (2019), we found that inflorescence size had the greatest impact on the number of taxa detected using eDNA metabarcoding. Larger inflorescences attracted an array of species, and we detected a significantly greater number...
of animal species on these flower types than we did on small inflorescences and single flowers (Figure 6). Of these smaller specialized flowers, eDNA metabarcoding of flowers was unsuccessful at detecting many expected pollinators. For example, eDNA metabarcoding of flowers from *T. aphylla* subsp. *aphylla* failed to detect Australian bee fauna known to "buzz" pollinate other *Tetratheca* species with similar flower morphology (e.g., *Lasiglossum* species, which pollinate *Tetratheca paynterae* subsp. *paynterae*; Ladd et al., 2019). Similarly, native bee species that are considered major pollinators of *Leucopogon* species were not detected on *L. spectabilis* (Keighery, 1996). While this may in part be due to sample size, some of our study species (e.g., *T. aphylla* subsp. *aphylla* and *A. adinophylla*) where few animal taxa were detected using eDNA metabarcoding, also showed a similar result with visual surveys, suggesting a lack of pollinator activity at the time of sampling. This emphasizes the need to adapt sampling methodologies to the plant species sampled to detect the full range of taxa. For all flower types, but particularly smaller flowers, an increase in sample size (both the number of flowers and the number of plants sampled) may increase the likelihood of detecting pollinator taxa. Similarly, sampling at multiple time points may also increase the likelihood of detecting pollinators absent at the time of sampling.

A limitation of eDNA metabarcoding of flowers to detect pollinators is its inability to distinguish between animals that simply come into contact with flowers versus those that act as pollinators. We detected not only a variety of potential pollinators (bees, birds and butterflies) but also non-pollinator taxa such as phytophagous insects (e.g., thrips and aphids), gall inducers (e.g., Cecidomyiidae), predators (e.g., spiders), and large mammals (e.g., kangaroo and horse). While this suggests opportunities for further applications of eDNA metabarcoding such as the detection of agricultural pests (Kestel et al., 2022), explicitly determining pollinators, requires exclusion experiments with plant-centric sampling that targets floral organs specific to reproductions (i.e., stigmas and anthers), as well as insect-centric sampling to target pollen collected during foraging.

### 4.2 Comparison of eDNA metabarcoding and visual surveys

The ability to detect pollinators through direct visual observations is limited by the time allocated per survey and the capacity to detect cryptic/reclusive species (Petanidou et al., 2008). In this study, some common diurnal pollinators such as the European honey bee and singing honeysinger were detected with both eDNA and visual surveys; however, other common pollinators such as the Red Wattlebird were not observed during visual surveys. eDNA metabarcoding also detected nocturnal species such as the western pygmy possum and a range of arthropod pollinators including moth species. Nocturnal species such as moths are commonly underrepresented in visual surveys (see Macgregor et al., 2019), especially for plant species that lack the characteristics typically associated with moth pollination (i.e., white floral morphology and/or crepuscular scent production; Pellmyr, 2002). Various alternative survey techniques could be used to detect potential pollinators such as autonomous sound recording devices (birds; e.g., Darras et al., 2019), a camera trap array (mammals; e.g., Ortmann & Johnson, 2021) or a pitfall/trap grid (mammals; e.g., Waudby et al., 2019), and can offer advantages over eDNA metabarcoding, mostly in regards to abundance metrics. However, all require considerable field effort and have ethical requirements. As such, eDNA metabarcoding of flowers represents a major advance, providing a valuable complement to conventional monitoring surveys, able to detect common visitor/pollinator species and, perhaps most importantly, difficult-to-observe species that are often missed with traditional trapping and monitoring techniques.

The inability of eDNA metabarcoding of flowers to detect some species observed during visual surveys highlights common limitations present in eDNA studies. For example, there is a highly diverse fauna of *Euhesma* bees that are oligolectic on *Eremophila* (Exley, 1998) that were observed in the visual surveys, but not detected with eDNA metabarcoding. While eDNA metabarcoding is a powerful monitoring tool, its ability to accurately reflect total biodiversity is commonly
affected by the ability of primers to amplify all taxa present (Alberdi et al., 2018). For example, in our study, eDNA metabarcoding using the birdND2 assay failed to detect Brown Honeyeater observed on G. georgeana plants sampled despite sequences present on NCBI’s nucleotide database. While future development and validation of the birdND2 assay may alleviate this issue, it highlights the difficulty in designing an assay not only broad enough to target a variety of taxa but also specific enough to differentiate between closely related taxa such as those of the Honeyeater family (Meliphagidae). However, the subsequent detection of this species through the use of a second assay further highlights the benefits of including additional assays and targeting different gene regions to increase the detection and/or specificity of eDNA metabarcoding surveys (Alberdi et al., 2018; Newton et al., 2022).

Incomplete reference databases also commonly reduce the resolution of taxonomic identifications in eDNA metabarcoding studies (Margaryan et al., 2021). With reference barcode sequences currently not available for all species, this not only affects the ability to detect potential pollinator species but also prevents identification of all taxa to species level, which would be vital if appropriate plant-pollinator associations are to be made. This low taxonomic resolution, particularly for insect taxa, then hinders our ability to properly understand and conserve plant-pollinator interactions (Prendergast & Hogendoorn, 2021). However, as more reference sequences are generated and made publicly available, this problem should be alleviated. In addition, by complementing eDNA detections with visual surveys, there is an opportunity to identify which species are missed by eDNA metabarcoding and target them for locally relevant DNA sequence reference database generations.

While eDNA metabarcoding also detected a greater number of taxa compared with visual surveys, the two methods did not perfectly overlap. eDNA metabarcoding detected 84% of the total species detected and visual surveys 27%, with eDNA metabarcoding failing to observe confirmed interactions with plants surveyed such as native bee species (Megachile species). This finding is similar to those of previous studies comparing eDNA metabarcoding with conventional survey methods, (e.g., camera traps) which show each to detect unique, but not all visiting taxa (Gogarten et al., 2020; Leempoel et al., 2020; Ryan et al., 2022). Therefore, eDNA metabarcoding used in conjunction with conventional survey methods is recommended to yield the highest species diversity.

4.3 | Conservation implications

Surveying animal assemblages in remote locations and identifying the species associated with rare or infrequently visited plants can be challenging (Gilpin et al., 2014; Ladd et al., 2019; Smith & Gross, 2002). For example, remote locations present a logistical challenge to thoroughly survey in a relatively short timeframe (i.e., Ladd et al., 2019), and it is difficult to capture the full flower-visitor cohorts for rarely visited flowering plants with short visual surveys (i.e., 15 min; see Whelan et al., 2008). Here, eDNA collected from flowering material provided a complementary tool to help survey and monitor plant-animal interactions (Figure 4). Although not all of these organisms detected are likely to affect pollination, these data do provide a general overview of the flower-visitor community (and potential pests) for plant species of interest (see Thomsen & Sigsgaard, 2019), and may provide information that would otherwise not be available. We do note, however, that eDNA does not universally deliver more complete community descriptions than visual observations. For example, eDNA detections accounted for only 21% of all animals visiting E. oppositifolia (Figure 4).

4.4 | Future directions

Further baseline studies are necessary to establish eDNA metabarcoding of flowers as a robust tool for assessing flower-visiting animals. To date, few studies have examined the relevant factors (i.e., temperature, UV, and rainfall) that may influence DNA degradation on plant material (although see Valentin et al., 2021), with no studies, to the best of our knowledge, examining the factors that influence deposition of eDNA on flowers. Therefore, it is currently impossible to determine if relatively low flower-visiting animal diversity is a result of few visitations (as suggested by visual surveys in our study) or DNA degradation due to environmental factors (Evans & Kitson, 2020; Goldberg et al., 2018).

We also caution that a baseline understanding is necessary of the organisms likely to affect pollination for the plant species under study. As mentioned above, not all of the species detected using eDNA metabarcoding are likely to affect pollination, as any organism that moves across a flower surface (or potentially secretes DNA into plant tissue, that is, sap-sucking organisms; see Thomsen & Sigsgaard, 2019) could be detected. Therefore, a species or genus understanding of the animal visitors likely to affect pollination in the plant species of interest is a necessary starting point before interpreting flower-visiting communities derived from eDNA metabarcoding. With these caveats, we predict that eDNA could provide rapid and reliable community-level descriptions for a wide range of flowering plant species.

AUTHOR CONTRIBUTIONS

JN conducted the study and wrote the initial manuscript. JN, PB, PN, NW, JK, and MH were involved in the experimental design; Primers were designed and tested by JN, NW, and MH; Samples were collected by JN, PB, PN, and KP and processed by JN and MH; bioinformatics work was performed by JN; JN analyzed data with assistance from JK; the manuscript was edited by all authors.

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CONFLICT OF INTEREST STATEMENT
The authors declare that they have no conflict of interest.

DATA AVAILABILITY STATEMENT
Sequencing data are available at the Dryad Digital Repository https://doi.org/10.5061/dryad.pg4f4qv5.

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