Australian Journal of Taxonomy
Open-access, online, rapid taxonomy
https://doi.org/10.54102/ajt

Gehyra woondagoom sp. nov. (Squamata; Gekkonidae), a new gecko from the Yampi Peninsula and Buccaneer Archipelago of Western Australia

Wesley J. Read[1]*, Rebecca J. Laver[1] & Stephen M. Zozaya[1]

[1]Research School of Biology, Australian National University, Canberra, ACT, 2600, Australia.
*Corresponding author: Wesley.Read@anu.edu.au

Wesley J. Read https://orcid.org/0009-0003-8505-6395; Rebecca J. Laver https://orcid.org/0000-0002-6319-7213; Stephen M. Zozaya https://orcid.org/0000-0003-3451-3552

Abstract

Here we describe a new gekkonid lizard, *Gehyra woondagoom* sp. nov., from the Yampi Peninsula and surrounding islands of the Kimberley region, Western Australia. Genomic data indicate that *Gehyra woondagoom* sp. nov. is a deeply divergent species sister to the clade containing *Gehyra multiporosa* and *Gehyra occidentalis*. The new species can be distinguished from *G. multiporosa* by a lower average pore count (21–34 *versus* 45–49) and larger maximum snout-vent length (62 mm *versus* 50 mm), and from the morphologically similar *G. occidentalis* by 19 nucleotide sites in the *ND2* mitochondrial gene. The new species is likely more widespread than currently known given large sampling gaps on the Yampi Peninsula. This is the 13th recognised *Gehyra* species endemic to the Kimberley region of north-western Australia.

Key words: *Gehyra occidentalis; Gehyra multiporosa;* Kimberley; genealogical divergence index; single nucleotide polymorphism.

Cite this paper as: Read WJ et al. (2026). *Gehyra woondagoom* sp. nov. (Squamata; Gekkonidae), a new gecko from the Yampi Peninsula and Buccaneer Archipelago of Western Australia. *Australian Journal of Taxonomy* 135: 1–13. doi: https://doi.org/10.54102/ajt.berkw

https://zoobank.org/NomenclaturalActs/8B7961C3-2C7A-4408-A06E-2381BC566AE0

Introduction

Gehyra Gray, 1834 is the most species-rich genus of gekkotan lizard in Australia, currently totalling 50 recognised species (Wilson & Swan 2025; ASH 2025; Uetz 2025), many of which occur in sympatry and are difficult to distinguish morphologically. Nearly half of these have been described since 2018, and in many cases from morphologically cryptic species complexes (e.g., Oliver et al. 2016a; Doughty et al. 2018a; Doughty et al. 2018b; Kealley et al. 2018; Oliver at al. 2020). However, several recalcitrant species complexes remain unresolved. One such is the *Gehyra occidentalis* King, 1984 group, which includes *G. occidentalis* and *Gehyra multiporosa* Doughty,

This paper was submitted on 5 March 2026 and published on 28 September 2026 (2026-09-27T22:48:32.906Z). It was reviewed by Paul Doughty and an anonymous reviewer, and edited by Subject Editor Mark Harvey under the guidance of Associate Editor Kenny Travouillon. Stephen Zozaya is an Editor of the Australian Journal of Taxonomy. He did not at any stage have access to the manuscript while in peer review, and had no influence on its acceptance or handling, as is standard practice for manuscripts submitted by editors. Australian Journal of Taxonomy. ISSN: 2653-4649 (Online).

Palmer, Sistrom, Bauer & Donnellan, 2012, hereafter referred to as the *occidentalis* complex. Previous phylogenetic studies using dense geographic sampling and mtDNA and nuDNA sequencing have highlighted three divergent lineages within what is currently recognised as *G. occidentalis*: these are referred to here as *occidentalis*-KL ('true' *occidentalis*), *occidentalis*-YI (Yampi Peninsula and islands), and *occidentalis*-OR (Oscar Range) (Doughty et al. 2012; Oliver et al. 2016b; Lau et al. 2025; Read et al. 2025). Members of the *occidentalis* complex are morphologically similar and replace each other parapatrically within the Kimberley region of northwestern Australia, an area known for its high species richness of rock-dwelling geckos (Oliver et al. 2016a; Doughty et al. 2018; Zozaya et al. 2023). Analyses in Read et al. (2025) indicated no historical introgression between *occidentalis*-YI and the geographically adjacent *occidentalis*-KL; importantly, these analyses included samples of *occidentalis*-KL from the Yampi Peninsula's offshore islands, suggesting long-term genetic isolation rather than underestimation due to sparse sampling. Combined with the deep phylogenetic placement of *occidentalis*-YI, this strongly suggests that this lineage represents a distinct species. However, that study was not focused on species delimitation and found limited morphological divergence among members of the *occidentalis* complex, and modest genetic divergence between *occidentalis*-KL and *occidentalis*-OR.

Here, we explicitly test species boundaries in the *G. occidentalis* complex. We recognise and delimit species in the spirit of the Biological Species Concept (BSC), under which species are conceptualised as groups of interbreeding natural populations that are reproductively isolated from other such groups (Dobzhansky 1937; Mayr 1963, 1996). Because all candidate species considered herein are allopatric — at least as far as our sampling indicates — inferring reproductive isolation by, for example, assessing admixture at contact zones is not feasible. Consequently, we use an integrative taxonomic framework that draws on multiple lines of evidence (Padial et al. 2010), with a focus on genomic data. We did this by complementing previously published analyses of phylogenomic relationships, historical introgression, and morphometric divergence (see Read et al. 2025) with new analyses using genome-wide single nucleotide polymorphism (SNP) data. We use these SNP data to test the robustness of phylogenetic relationships, assess genetic clustering, and quantify fixed allelic differences among candidate species. We also used previously published data to perform heuristic species delimitation using the genealogical divergence index (*gdi*), and to assess diagnostic nucleotide differences in the *ND2* mitochondrial gene. Finally, meristic morphological characters were examined to complement existing morphometric data for the *G. occidentalis* complex with the aim of identifying diagnostic characters. For clarity and ease of interpretation in text and figures, we hereafter refer to *occidentalis*-YI as *Gehyra woondagoom* sp. nov.

Methods

SNP filtering and analyses

We used single-nucleotide polymorphism (SNP) data from previous studies (Fenker et al. 2021; Lau et al. 2025; Read et al. 2025), generated by Diversity Arrays Technology (DArT; Canberra, Australia) using the DArTseq platform, a restriction-enzyme-based genotyping-by-sequencing method (Sansaloni et al. 2010; Kilian et al. 2012). All sequences are available via the Zenodo repository. The dataset was restricted to samples representing the four candidate species within the *occidentalis* complex. Four samples of *G. nana* Storr, 1978 (nana4 lineage; see Read et al. 2025) were retained as an outgroup for phylogenetic analyses. Filtering was conducted in dartR v.2.9.7 (Gruber et al. 2018) using a sequential protocol: minimum read depth ≥ 6; maximum read depth ≤ 80; locus reproducibility ≥ 0.99; locus call rate ≥ 0.8; individual call rate ≥ 0.5; minor allele count ≥ 3; and removal of monomorphic loci. To minimise linkage, a single SNP per locus was retained using the "best" method, which selects the site with the highest information content. The final SNP dataset comprised 2,488 variant sites. For phylogenetic inference, heterozygous sites were resolved by randomly assigning one of the two alleles.

Phylogenetic relationships were inferred from the concatenated SNP dataset to assess congruence with previously published nuclear exon-capture phylogenies. Maximum-likelihood inference was performed in IQ-TREE v.2.1.3 (Minh et al. 2020), with the substitution model selected using ModelFinder (Kalyaanamoorthy et al. 2017). An ascertainment bias correction was applied to account for using only variant sites and associated inflation of branch lengths. Statistical support was evaluated using 1,000 ultrafast bootstrap replicates implemented via ufboot2 (Hoang et al. 2018) and 1,000 SH-aLRT replicates (Guindon et al. 2010; Hoang et al. 2018). We then visualised genetic structure using a principal coordinates analysis (PCoA) implemented in dartR. Fixed allelic differences among candidate species were assessed using the *gl.fixed.diff* function with threshold = 0, meaning only absolute fixed differences (loci at which the two populations shared no alleles) were counted.

Genealogical divergence index

We further assessed the evolutionary independence of candidate species using the genealogical divergence index (*gdi*; Jackson et al. 2017), a metric for heuristic species delimitation under the multispecies coalescent (Leaché et al. 2019). The *gdi* represents the probability that two gene copies sampled from the same population/species coalesce more recently with each other than with a gene copy from a second population. Values range from 0 to 1, with higher values indicating greater genealogical independence. A frequently used heuristic

interprets values > 0.7 as strong evidence for species-level divergence, values < 0.2 as intraspecific differentiation, and intermediate values (0.2–0.7) as equivocal (Jackson et al. 2017). Values were calculated using posterior estimates of node height and effective population size obtained from a multispecies coalescent analysis of 1,000 exonic loci using BPP v.4.4.0 (Flouri et al. 2020) by Read et al. (2025); data are available via the Zenodo repository. That analysis included four samples for each of the focal candidate species, except *G. multiporosa*, which was represented by three samples. Although that analysis also included lineages of the *G. nana* complex, only posterior draws corresponding to the *occidentalis* complex were used here to calculate *gdi*.

Molecular diagnosis

Given pervasive morphological conservatism among *Gehyra* species, we identified diagnostic nucleotide differences among species within the mitochondrial *NADH dehydrogenase subunit 2* (*ND2*) gene. This served as a post hoc tool for species diagnosis, rather than being used for species delimitation itself. As such, we combined *occidentalis*-KL and *occidentalis*-OR under a single taxon given that our analyses do not support these as distinct species. We used the *ND2* alignment from Read et al. (2025), which was subset to include only the *occidentalis* complex. The final alignment was 1,041 bp long and contained 274 samples, including 23 for *G. woondagoom* sp. nov., 173 for *G. occidentalis*-KL, 39 for *G. occidentalis*-OR, and 39 for *G. multiporosa*. To provide a consistent reference for nucleotide positions, we aligned sequences to an annotated mitochondrial genome of *Gehyra marginata* (GenBank accession AB661662) and then manually inspected the alignment in Geneious v2025.0.3 to ensure all sequences were in the correct reading frame. Diagnostic nucleotide differences were then identified using a custom R script, alignments and script are available via the Zenodo repository.

Morphology

Morphological measurements and scalation were assessed for 14 adult *G. woondagoom* sp. nov., 42 *occidentalis*-KL, 17 *multiporosa*, and 5 *occidentalis*-OR specimens lodged at the Western Australian Museum (WAM). Specimens were assigned to lineages based on previously published mtDNA and nuDNA sequencing data. All data are available via the Zenodo repository.

The following measurements from Read et al. (2025) were taken using digital calipers to the nearest 0.01 mm: snout-to-vent length (SVL), tip of snout to anterior margin of cloaca; head length (HL), tip of snout to mid anterior margin of ear; snout length (SL), tip of snout to anterior margin of orbit; head width (HW), widest point across head (between orbitals and ears); head depth (HD), deepest point of the head (just posterior to orbitals); orbit width (OR), anterior to posterior margin of orbital; width-between-eyes (WBE), smallest distance between orbitals across the top of head; inter-limb length (ILL), distance between posterior insertion of the forelimb and anterior insertion of the hindlimb; hindlimb length (HLL), heel to knee (ankle and knee bent at 90°); and forelimb length (FLL), palm to elbow (palm and elbow bent at 90°).

The following meristic characters were recorded: subdigital lamellae (Lam) on digit IV of hindlimb, from tip of digit to end of enlarged lamellae row, excluding apical wedge (illustrated in Zozaya et al. 2019); supralabial (SupLab) and infralabial (InfLab) scale rows, starting at the posterior margins of the rostral and mental scales, respectively, with counts terminating where labials cease to be twice the size of the adjacent head scales that do not border the mouth; internarial scales (IntNsc), the number of scales between the supranasal scales bordering the upper margin of the rostral; supranasal scales (SupNas), the number of scales bordering the narial, excluding the first supralabial and rostral; the number of pre-cloacal pores in males (PCP). Sex was determined by the presence of PCPs, which occur only in male *Gehyra*. A subset of the same measurements (SVL and all meristic data) were collected from a further nine adult specimens of *G. woondagoom* sp. nov. during field surveys at Kimbolton, WA. These data are included in the ranges and means reported in the 'Morphology', 'Diagnosis', and 'Comparisons with sympatric and related species' sections below.

Results

SNP-based analyses

Gehyra woondagoom sp. nov. was recovered as a strongly supported, monophyletic lineage by IQ-TREE (SH-aLRT = 100; UFB = 100) that is sister to a clade containing *occidentalis*-KL, *occidentalis*-OR and *G. multiporosa* (SH-aLRT = 99.8; UFB = 100) (Fig. 1A). Together, *occidentalis*-KL and *occidentalis*-OR were recovered as a closely related sister pair with full support. While concatenation methods can overestimate statistical support, these results are concordant with the multispecies coalescent analyses in Read et al. (2025) that were based on exonic sequence data (Fig. 1E). Despite their geographic proximity, no samples of *G. woondagoom* sp. nov. nor *occidentalis*-KL were intermediate between these two lineages, suggesting a lack of recent introgression in line with previous study (Read et al. 2025).

All lineages formed discrete clusters according to the PCoA (Fig. 1C), with axis 1 accounting for 44.5% of the overall SNP variation and separating *G. multiporosa* and *G. woondagoom* sp. nov. from the remaining two candidate species, while axis 2 accounted for 14.3% of variation and separated *G. woondagoom* sp. nov. from the other three candidate species. Of note, *occidentalis*-OR forms a cluster that is only narrowly separated from the remainder of *occidentalis*-KL, especially when compared to within-species diversity seen in *G. multiporosa*.

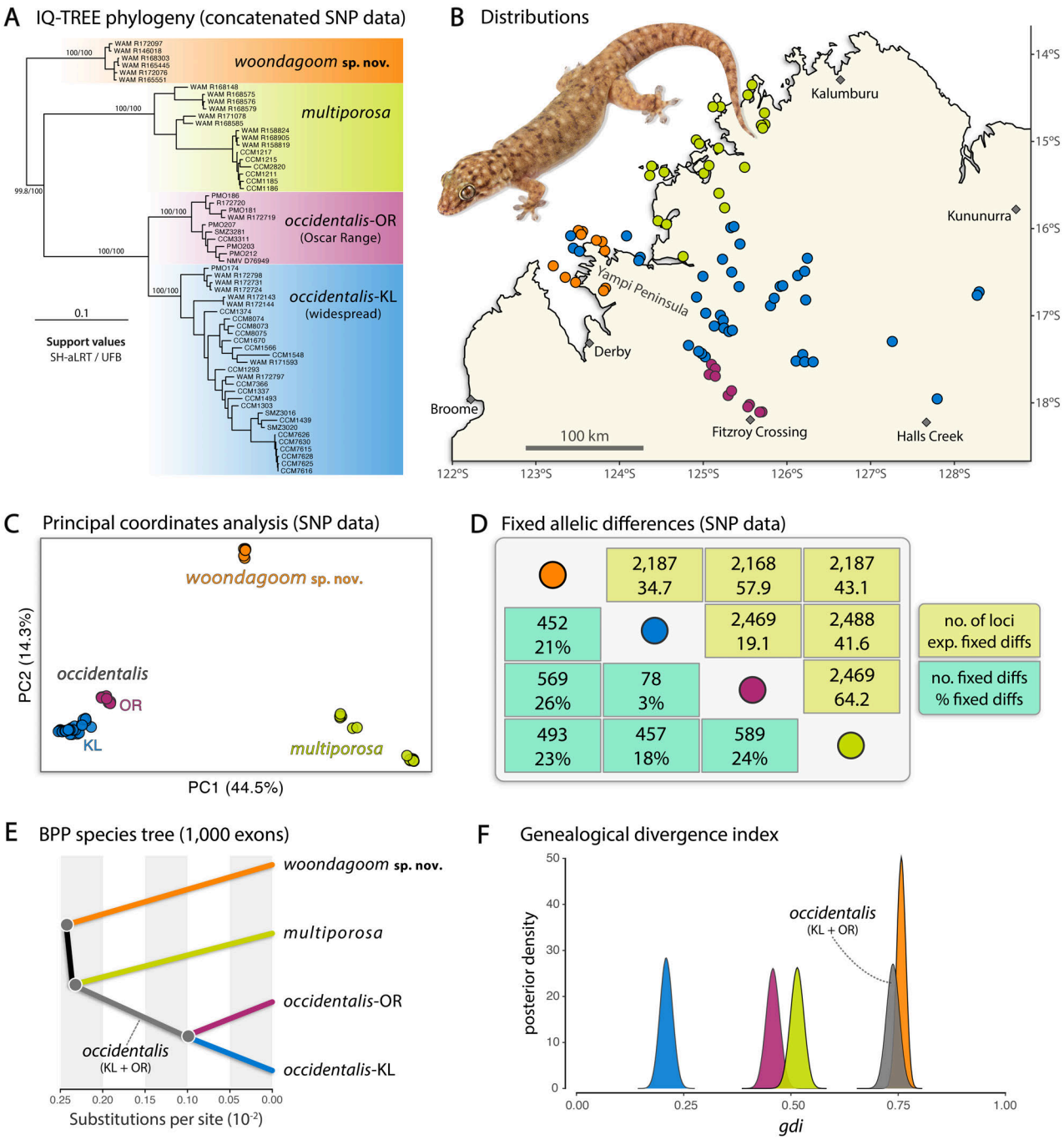

Figure 1. Phylogenomics, species delimitation, and occurrence records of the *Gehyra occidentalis* complex. (A) Maximum likelihood phylogenetic relationships among the *occidentalis* complex inferred using IQ-TREE from 2,806 variant sites. Shimodaira–Hasegawa-like approximate likelihood ratio test (SH-aLRT) and ultrafast bootstrap (UFB) support values are provided for major branches. The tree was rooted using *Gehyra nana* (nana4 lineage), which was excluded here for graphical clarity. (B) Occurrence records of the *G. occidentalis* complex in the Kimberley region of north-western Australia. (C) Ordination plot of the first and second dimension from principal coordinates analyses (PCoA) of genome-wide SNP data. (D) Results of fixed differences analysis using the genome-wide SNP dataset. The upper triangle shows the number of loci for each respective comparison and the number of expected fixed allelic differences given sample sizes (i.e., expected number of false positives). The lower triangle shows the actual number of fixed allelic differences and proportion of sites with fixed differences. (E) Relationships estimated using the MSC species tree analysis in BPP with 1,000 exons, taken from the analytical output of Read et al. (2025). All relationships were fully supported (pp = 1.0). The scale shows expected number of substitutions per site. (F) Genealogical divergence index (*gdi*) estimated from the phylogeny appearing in (E); values > 0.7 are typically regarded as strong evidence for species status (Jackson et al. 2017; Leaché et al. 2019). Photo credit: Stephen Zozaya.

The percentage of fixed allelic differences between lineages was high (≥ 18%) except between *occidentalis*-KL and *occidentalis*-OR (3%; Fig. 1D). The proportion of fixed differences between *G. woondagoom* sp. nov. and *occi-*

dentalis-KL was 21%, which is similar to values observed between the morphologically distinct *G. multiporosa* and *occidentalis*-KL (18%) and *occidentalis*-OR (24%). Given that we only counted sites where zero alleles were shared between populations, this suggests a lack of recent or ongoing gene flow between *G. woondagoom* sp. nov. and *occidentalis*-KL as even a single admixed individual would have resulted in far fewer fixed differences compared to lineage pairs of similar divergence. Importantly, for all pairwise comparisons the observed number of fixed differences far exceeded the number of false positives expected from sampling error alone ($P < 0.001$ for all comparisons).

Genealogical divergence index

The multispecies coalescent phylogeny inferred by Read et al. (2025) using 1,000 exonic loci with BPP, which was used to calculate *gdi* values, is shown in Figure 1E. Estimated *gdi* values were high for *G. woondagoom* sp. nov. [*gdi* = 0.757, 95% Highest Posterior Density (HPD): 0.737–0.778], *occidentalis*-KL + *occidentalis*-OR (*gdi*= 0.738: 0.708–0.768) and *G. multiporosa* (*gdi* = 0.514: 0.483–0.545), but low for *occidentalis*-KL (*gdi* = 0.209: 0.181–0.239) and *occidentalis*-OR (*gdi* = 0.458: 0.427–0.489) (Fig. 1F). If the commonly used *gdi* thresholds of > 0.7 are interpreted as support of species status, then *G. woondagoom* sp. nov. is the most strongly supported species (*gdi* = 0.757), with only the lineage that includes both *occidentalis*-KL and *occidentalis*-OR being recovered with similarly high values (*gdi* = 0.738).

Molecular diagnosis

We identified 19 diagnostic nucleotide sites that unambiguously distinguish *G. woondagoom* sp. nov. from both *G. occidentalis* and *G. multiporosa* across the 1,041 bp ND2 gene (Table 1).

Morphology

To avoid repetition, complete morphometric and scale count data for the eight type specimens of *G. woondagoom* sp. nov. are presented in Table 2; these data, alongside data from a further 14 individuals, are summarised in the species description below with further information on colour-pattern, scale characters, and comparisons with other *Gehyra* spp. Briefly, the new species is a medium-to-large *Gehyra* (mean SVL 60 mm), typically with a singular internarial, three supranasals, 7–10 supralabials; 7–9 infralabials, 8–10 divided subdigital lamellae, and cream-brown to dark yellow-brown background colouration with scattered, often faded or irregular, pale yellow to cream spots and dark blotches along the dorsum. It most closely resembles *G. occidentalis sensu stricto*, differing only in having a higher mean PCP count but with broadly overlapping ranges, and is best differentiated based on genetic data and locality. Pairwise comparisons of multidimensional morphometric variation by Read et al. (2025) revealed significant differences between *multiporosa* + *occidentalis*-KL and *multiporosa* + *G. woondagoom* sp. nov., but no differences among other pairwise comparisons within the *occidentalis* complex. Thus, all populations currently assigned to *G. occidentalis* — including *G. woondagoom* sp. nov. — resemble each other closely in morphology but differ from *G. multiporosa* in having larger body sizes and lower PCP counts.

Taxonomic decisions

Here, we recognise and describe *Gehyra woondagoom* sp. nov. as a new and distinct species based on the following: 1) phylogenomic evidence from both exonic sequence data (Read et al. 2025; Fig. 2C) and genome-wide SNP data (Fig. 1A) that the lineage is sister to the rest of the *occidentalis* complex, thus rendering *G. occidentalis* as currently recognised paraphyletic with respect to *G. multiporosa*; 2) no evidence of historical genomic introgression between the new species and the geographically adjacent *occidentalis*-KL (see Read et al. 2025), suggesting a long history of genomic isolation; 3) evidence from genome-wide SNP data that the new species forms a distinct genetic cluster (Fig. 1C) with a high proportion of fixed allelic differences compared to other members of the *occidentalis* complex (Fig. 1D); 4) *gdi* values exceeding 0.75 (Fig. 1F), higher than any other lineage in the complex and above the commonly used threshold of 0.7 taken as strong support for species status. We consider this genomic evidence as strong support for recognising *G. woondagoom* sp. nov. as a distinct species. Furthermore, *G. woondagoom* sp. nov. is morphologically divergent from *G. multiporosa*, having a distinctly larger body size and lower and non-overlapping precloacal pore counts (see 'Comparisons with sympatric and related species' below). The new species

Table 1. Nineteen diagnostic nucleotide sites in the *ND2* protein-coding mitochondrial gene (1,041 bp) that distinguish *Gehyra woondagoom* sp. nov. from both *G. occidentalis* and *G. multiporosa*. Note that the *occidentalis*-KL and *occidentalis*-OR lineages are here treated together as G*. occidentalis sensu stricto*. Sample sizes for *ND2* sequences were 23 for *G. woondagoom* sp. nov., 173 for *occidentalis*-KL, 39 for *occidentalis*-OR, and 39 for *G. multiporosa*.

	ND2 nucleotide site position																		
	44	64	81	82	186	267	288	309	423	564	588	603	735	789	795	964	976	978	1017
G. woondagoom sp. nov.	**T**	**T**	**A**	**T**	**T**	**C**	**T**	**G**	**G**	**A**	**T**	**T**	**A**	**G**	**T**	**G**	**G**	**C**	**A**
G. occidentalis	C	G	G	C	C	A/G	C	A	A/C	C	A/G	C	C/T	A	C	A/C	A	A/T	C
G. multiporosa	C	G	G	C	C	A	C	A	C/T	C	A	C	C/T	A	C	C	A	A	C/T

Table 2. Morphometric and meristic data for the type series of *Gehyra woondagoom* sp. nov. All mensural traits are reported in millimetres (mm) while meristic characters represent counts. Mensural characters are: SVL–snout-to-vent length; HL–head length; HD–head depth; HW–head width; SL–snout length; OR–orbit width; WBE–width-between-eyes; ILL–inter-limb-length; HLL–hindlimb-length; FLL–forelimb-length. Meristic characters are: PCP–pre-cloacal pores; IntNsc–internarial scales; SupNas–supranasal scales; PosNas–postnasal scales; Lam–lamellae; SupLab–supralabial scales; InfLab–infralabial scales.

WAM reg.	**R172708**	**R172097**	**R172078**	**R114453**	**R158009**	**R172086**	**R172104**	**R172076**
Type status	holotype	paratype	paratype	paratype	paratype	paratype	paratype	paratype
Latitude °S	16.0617	16.6225	16.6164	16.15	16.1194	16.5575	16.4247	16.2542
Longitude °E	123.5525	123.4714	123.4764	123.75	123.7275	123.3553	123.175	123.8244
Sex	male	female	male	female	female	female	male	male
SVL	69.0	55.7	60.3	57.7	59.1	60.1	54.7	63.22
Tail state	regrown	regrown	regrown	regrown	regrown	regrown	regrown	original
HL	16.3	14.0	14.6	14.7	14.0	15.0	13.3	15.6
HD	6.6	6.0	6.9	6.1	6.9	6.5	5.7	7.1
HW	13.1	10.6	11.6	10.9	10.9	12.3	10.1	13.0
SL	7.0	5.9	6.0	6.1	6.0	6.3	5.7	6.5
OR	5.1	4.3	4.8	4.3	4.3	5.1	4.2	4.7
WBE	4.9	4.2	4.5	4.2	4.4	4.5	4.0	4.6
ILL	28.2	25.4	26.4	24.2	26.6	27.6	25.2	28.5
HLL	9.3	7.9	8.4	8.0	8.3	8.7	7.8	8.7
FLL	8.2	7.0	7.6	7.1	7.4	7.9	7.0	7.8
PCP	21	–	33	–	–	–	34	27
IntNsc	1	1	1	2	0	1	1	1
SupNas	3	3	3	3	3	3	3	3
Lam	9	9	9	8	9	9	9	8
SupLab	7	8	9	9	10	9	10	10
InfLab	7	7	9	8	9	9	8	8

does not differ significantly from *G. occidentalis sensu stricto* in multivariate morphometric space (Read et al. 2025), with substantial overlap in trait space between the two taxa. Given this, we also include a molecular diagnosis using mitochondrial sequence data for the *ND2* gene.

In contrast, we consider the evidence presented here and elsewhere (Read et al. 2025) insufficient to recognise the *occidentalis*-OR lineage as a distinct species from *occidentalis*-KL for the following reasons: 1) levels of phylogenomic divergence are similar to those observed among sites within *G. multiporosa* (Fig. 1A); 2) narrow separation in genomic clustering analysis (Fig. 1C) with a low proportion of fixed allelic differences in the SNP dataset (3%; Fig. 1D); 3) *gdi* values that were modest (*occidentalis*-OR = 0.458) to low (*occidentalis*-KL = 0.209), but with a high *gdi* when the two lineages were treated as a single taxon (*gdi* = 0.738; Fig. 1F); and 4) no diagnostic morphological differences. Accordingly, we treat both lineages as *G. occidentalis sensu stricto*.

Discussion

Gehyra woondagoom sp. nov. brings the total number of recognised *Gehyra* in Australia to 51. It is also the 13th recognised *Gehyra* species endemic to the Kimberley region. Eleven of these endemic species are saxicoline, highlighting the remarkable species richness of rock inhabiting Kimberley gekkonids. Similar to other recent *Gehyra* species descriptions (e.g. Oliver et al. 2016a; Doughty et al. 2018a; 2018b; Oliver et al. 2020), we relied heavily on genomic data to delimit species within the *G. occidentalis* complex. Several more gekkonid species complexes are currently known from the Kimberley, such as the *G. nana* complex (Moritz et al. 2018; Read et al. 2025) and the *Heteronotia binoei* and *H. planiceps* complexes (Pepper et al. 2011; Zozaya et al. 2023; Zozaya et al. 2025). Resolving such complexes will continue to require genomic data along with careful consideration of the biological meaning of different divergence metrics, rather than taking diagnosability alone as evidence of species boundaries.

We consider the results presented here — namely the deep genetic divergence, a high proportion of fixed site differences, and published analyses demonstrating a lack of historical introgression (see Fig. 2C, Read et al. 2025) — to provide strong evidence for recognising *G. woondagoom* sp. nov. as a distinct species. Furthermore, chromosomal changes have been identified among other closely related *Gehyra* species (King 1979; Moritz 1986), and it may be that *G. woondagoom* sp. nov. also has distinctive chromosomal arrangements. We acknowledge that denser geographic sampling, particularly from areas of close parapatry with *G. occidentalis*, would be informative for assessing gene flow and more rigorously testing species hypotheses. Were further geographic sampling and new genomic data to suggest recent and ongoing gene flow between *G. woondagoom* sp. nov. and *G. occidentalis*, we would consider the two lineages to be conspecific. Finally, the absence of diagnostic morphological characters is likely to complicate field identification of individuals found between the

known ranges of *G. woondagoom* sp. nov. and *G. occidentalis*.

Taxonomy

Gehyra woondagoom sp. nov.

Figures 2, 3, 4A

https://zoobank.org/NomenclaturalActs/BCD33D20-C6A3-4FD2-B295-455A29F1622E

Holotype (Fig. 2). WAM R172708, adult male collected from Kathleen Island, WA (16.0617°S, 123.5525°E), collected by R. A. How, R. J. Teale, and M. A. Cowan, 4 April 2012.

Paratypes (N = 7). WAM R172097, Lachlan Island, WA (16.6225°S, 123.4714°E); WAM R 172078, Lachlan Island, WA (16.6164°S, 123.4764°E); WAM R114453, Koolan Island, WA (16.15°S, 123.75°E); WAM R158009, Koolan Island, WA (16.1194°S, 123.7275°E); WAM R172086, Long Island, WA (16.5575°S, 123.3553°E); WAM R172104, Sunday Island, WA (16.4247°S, 123.175°E); WAM R172076, North-west Molema Island, WA (16.2542°S, 123.8244°E).

Diagnosis. A relatively large (54–69 mm, mean 60 mm SVL) *Gehyra*; no webbing of skin between toes III and IV; no skin-fold along posterior of hindlimb; rostral scale with a deep medial groove on the dorsal half of the scale; single internarial scale usually present (range 0–2); three supranasals, first (bordering rostrum) largest, followed by third, second smallest; mental scale wedge-shaped posteriorly; 2–3 pairs of postmental scales, inner pair largest; 7–10 supralabials; 7–9 infralabials; snout straight to slightly convex in lateral view; 8–10 divided subdigital lamellae on the expanded portion of the fourth toe, excluding the apical wedge; sometimes with singular granules separating proximal lamellae; adult males with 21–34 pre-cloacal pores arranged in a shallow wedge that points anteriorly; background colouration cream-brown to dark yellow-brown; dorsal pattern variable with indistinct pale yellow to cream spots and dark blotches, arranged in alternating transverse rows along the dorsum. *Gehyra woondagoom* sp. nov. further differs from *G. occidentalis* and *G. multiporosa* in at least 19 putatively fixed nucleotide differences in the 1,041 bp *ND2* mitochondrial gene (Table 1).

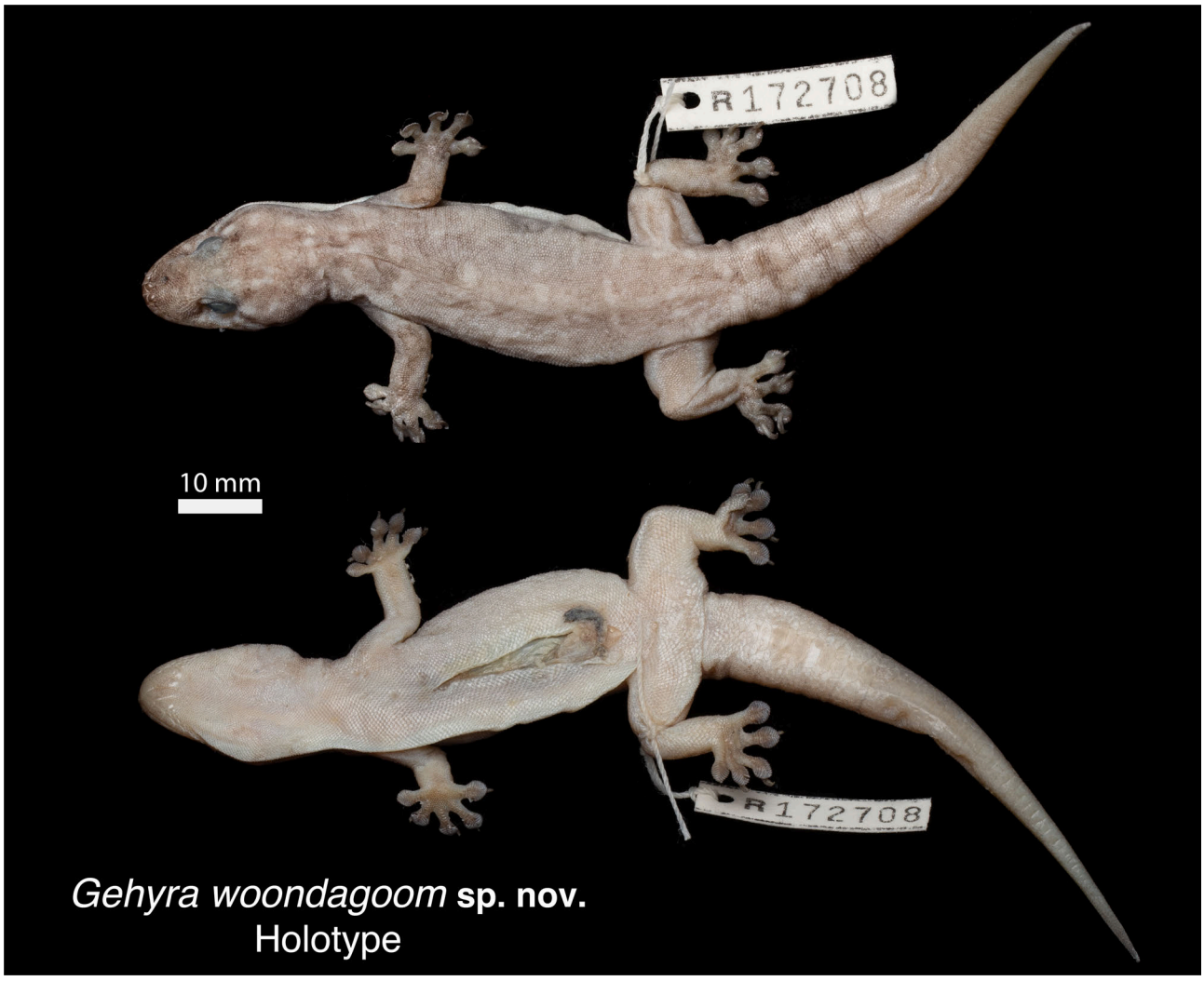

Figure 2. *Gehyra woondagoom* **sp. nov.** holotype WAM R172708 (Kathleen Island, WA) in preservative.

Figure 3. Photos of *Gehyra woondagoom* sp. nov. in life from Kimbolton, Yampi Sound Training Area, Western Australia. Colouration and patterning of *G. woondagoom* sp. nov. varies according to substrate; individuals from dolerite boulder fields are darker and less boldly patterned (A, D), while individuals from Yampi Formation sandstone habitats are lighter and more boldly patterned (B, C). Note individual (C) has a regenerated tail. (A) SMZ3664, (B) SMZ3666, (C) SMZ3667, and (D) an unsampled juvenile. Photos: (A, D) W. Read; (B-C) S. Zozaya.

Description of type series. Individual measurements and scale counts for the type series are given in Table 2. The following data are presented as a range (min–max) followed by mean ($\bar{x}$) for linear measurements or mode for counts. Sample sizes are eight unless otherwise noted. Measurements are rounded to the nearest 0.1 mm.

Measurements. SVL 54.7–69.0 mm ($\bar{x}$ = 60.0 mm). HL 13.3–16.3 mm ($\bar{x}$ = 14.7 mm). HD 5.7–7.1 mm ($\bar{x}$ = 6.5 mm). HW 10.1–13.1 mm ($\bar{x}$ = 11.6 mm). Snout length (SL) 5.7–7.0 mm ($\bar{x}$ = 6.2 mm). OR 4.2–5.1 mm ($\bar{x}$ = 4.6 mm). WBE 4.0–4.9 mm ($\bar{x}$ = 4.4 mm). ILL 24.2–28.5 mm ($\bar{x}$ = 26.5 mm). HLL 7.8–9.3 mm ($\bar{x}$ = 8.4 mm). FLL 7.0–8.2 mm ($\bar{x}$ = 7.5 mm).

Scale Characters. PCP 21–34 (*n* = 4; all values unique), forming a shallow chevron anterior to the cloaca with central pores anteriormost; PCPs absent in females. IntNsc 0–2 (mode = 1). SupNas three, first (contacting rostral) largest, then third (contacting first supralabial), middle smallest. SupLab 7–10 (mode = 9,10). InfLab 7–9 (mode = 9). Lam 8–9 (mode = 9).

Colouration in life (Figs. 3, 4A, 4B). Background colouration varies from cream-brown to dark yellow-brown depending on substrate background. Patterning consists of scattered, often faded or irregular, pale-yellow to cream spots and dark brown to purple-brown blotches and bars; often arranged in alternating transverse rows along the dorsum. In darker individuals, patterning is most obvious along the vertebral region (Fig. 3A). Ventral surfaces off-white and unpatterned. Pattern on dorsum of original tails consists of alternating, often indistinct pale-yellow to cream blotches and dark blotches, occasionally forming transverse bars; regenerated tails largely patternless or with indistinct brown or grey mottling (Fig. 3C).

Colouration in preservative (Fig. 2). Background colouration faded to pale grey. The pale spots and darker blotches are indistinct and almost entirely absent in some specimens. It should be noted that all preserved specimens examined were collected prior to 2013.

Etymology. In the Woddordda language (also spelt Worrorra), the word woondagoom (also spelt wundukum or wundugum) can mean either "night" or "gecko" depending on context. The name was first suggested to us by Dambimangari Rangers during fieldwork at Kimbolton and was kindly approved for use through consultation with the Dambimangari Aboriginal Corporation. The epithet is treated as an indeclinable noun in apposition.

Figure 4. *Gehyra woondagoom* sp. nov. (A) from Kimbolton compared to the closely related *Gehyra occidentalis* (B) from Bell Gorge and *Gehyra multiporosa* (C) from Mitchell Plateau, as well as five sympatric congeners: *Gehyra kimberleyi* (D) from Dampier Peninsula; *Gehyra nana* (E) from Gogo Station; *Gehyra granulum* (F) from Mornington Wildlife Sanctuary; *Gehyra gemina* (G) from Broome; and *Gehyra chimera* (H) from Theda Station. Photos: Wesley Read (A, B, E, G); Stephen Zozaya (C, D, F, H).

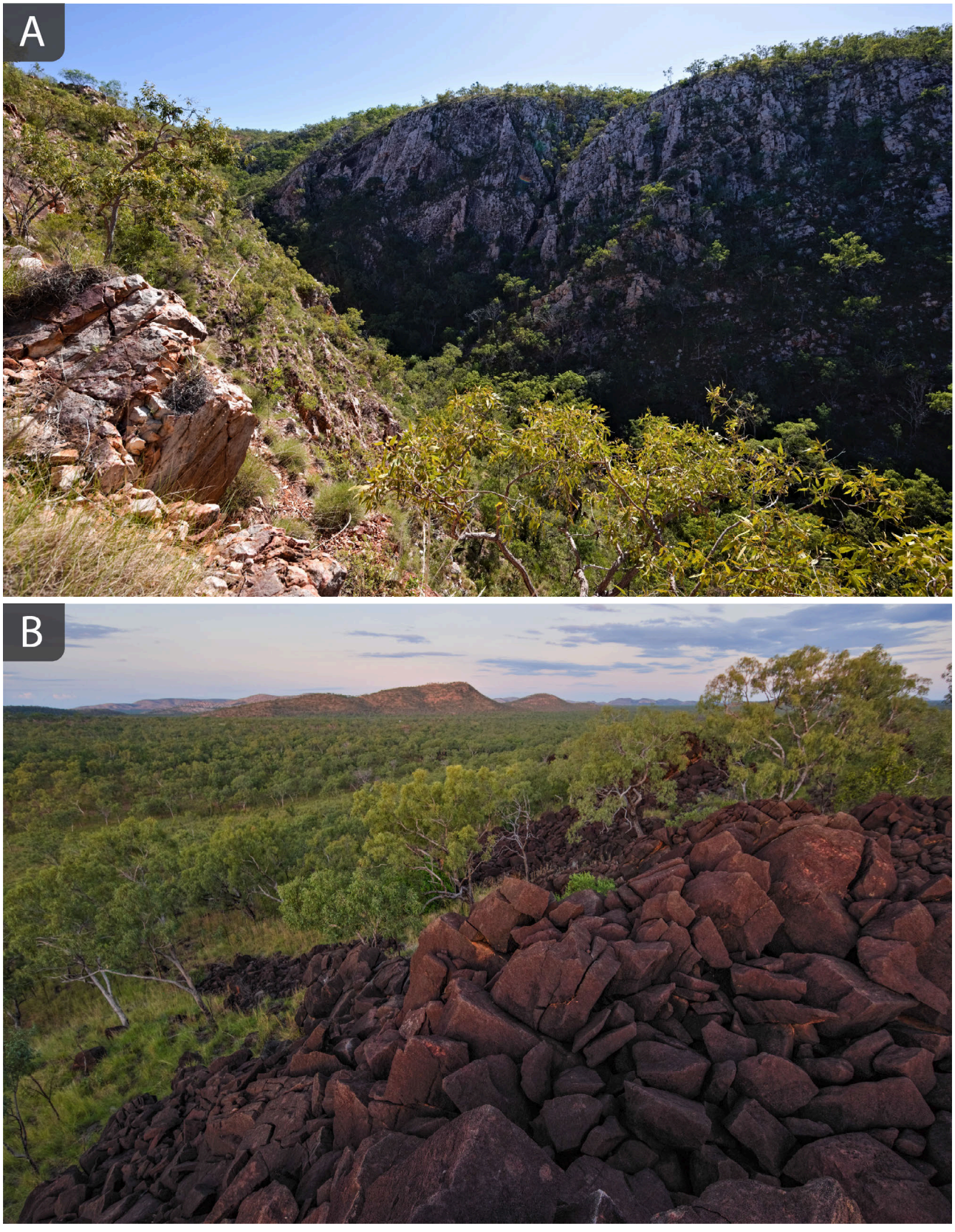

Figure 5. Habitat of *Gehyra woondagoom* sp. nov. at Yampi Sound Training Area: (a) Yampi Formation sandstone outcrops; (B) Hart Dolerite boulder fields. Photos: Ian Bool.

Proposed common name. Yampi Rock Gehyra. We propose this common name given that the species is only known from the Yampi Peninsula and surrounding islands.

Comparisons with sympatric and related species. *Gehyra woondagoom* sp. nov. is known to be sympatric with, or occur near to, *G. occidentalis, G. multiporosa, G. kimberleyi* Börner & Schüttler, 1982, *G. nana*, *G. granu-*

lum Doughty, Palmer, Bourke, Tedeschi, Oliver & Moritz, 2018, *G. gemina* Oliver, Prasetya, Tedeschi, Fenker, Ellis, Doughty & Moritz, 2020, and *G. chimera* Oliver, Prasetya, Tedeschi, Fenker, Ellis, Doughty & Moritz, 2020 (Fig. 4). *Gehyra woondagoom* sp. nov. is difficult to distinguish from *G. occidentalis* (Fig. 4B) but sometimes has a higher PCP count (21–34 *versus* 21–30); however, the degree of overlap means this is unlikely to be a useful character for field identification, and the two species are best differentiated using genetic data and locality. The new species is distinguished from *G. multiporosa* (Fig. 4C) by its larger size (SVL 55–69 mm *versus* 43–55 mm) and lower PCP count (21–34 *versus* 45–49). *Gehyra woondagoom* sp. nov. can be distinguished from *G. kimberleyi* (Fig. 4D) by the former's larger size (SVL 55–69 mm *versus* 42–61 mm,) and higher PCP count (21–34 *versus* 12–17). *Gehyra woondagoom* sp. nov. can be distinguished from *G. nana* (Fig. 4E) and *G. granulum* (Fig. 4F) by its larger size (SVL 55–69 mm *versus* 35–56 mm in *G. nana* and 35–46 mm in *G. granulum*), light yellow-brown to dark yellow-brown background colouration (*versus* orange to light pinkish-grey for both *G. nana* and *G. granulum*), and higher PCP count (21–34 *versus* 10–22 in *G. nana* and 10–19 in *G. granulum*). *Gehyra woondagoom* sp. nov. can be distinguished from *G. gemina* (Fig. 4G) and *G. chimera* (Fig. 4H) by the former's divided lamellae (*versus* undivided in *G. gemina* and *G. chimera*), light yellow-brown to dark yellow-brown background colouration (*versus* grey), higher PCP count (21–34 *versus* 10–16 in *G. gemina* and 9–11 in *G. chimera*), and the presence of small, irregular light and dark patches across the dorsal surface (*versus* only small, obscure dark dorsal patches and/or fine vermiculations in *G. gemina* and *G. chimera*).

Distribution & habitat. Gehyra woondagoom sp. nov. is currently known from Kimbolton, Yampi Sound Training Area, on the Yampi Peninsula and from eight islands surrounding the peninsula, many of which form part of the Buccaneer Archipelago: Bathurst Island, Irvine Island, Molema Island, Kathleen Island, Koolan Island, Sunday Island, Lachlan Island, and Long Island. The Yampi Peninsula remains poorly surveyed and difficult to access, and it is likely that this species is more widespread in rocky areas across the peninsula. We note here that the record in Oliver et al. (2016b) of *G. occidentalis* (*occidentalis*-KL) from Kimbolton is in error and that the sample corresponds to *G. woondagoom* sp. nov. The new species is associated with areas of exposed rock among savanna woodland (Fig. 5). This includes the sandstone ridges and outcrops that dominate the geology of the Yampi region and the boulder fields formed by Hart Dolerite intrusions (Tyler & Griffin 1992). At present, *G. woondagoom* sp. nov. and *G. occidentalis* are not known to occur in sympatry, but further field surveys will likely close the apparent distribution gap between the two species.

Most specimens observed during field surveys on 21 June 2024 were found on rocks, or *Ficus* sp. trees growing among rocks. No other *Gehyra* species were recorded in immediate sympatry with *G. woondagoom* sp. nov. during these field surveys, although it should be noted that this search effort was conducted over a single night.

Conservation status. Gehyra woondagoom sp. nov. is currently known from nine sites, with an estimated extent of occurrence (EOO; the minimum convex polygon that encompasses all known occurrence points) of 3,365 km^2 and an area of occupancy (AOO; the total area of 4 km^2 grid cells the species is known from) of 64 km^2 following IUCN guidelines (IUCN 2024). Despite this limited number of sites, the species is likely widespread across the extensive rock formations of the Yampi Peninsula and surrounding islands. Much of this region is remote and inaccessible and the Yampi Sound Training Area is co-managed for conservation by the Australian Wildlife Conservancy. Considering these points, there is no evidence of plausible threats or population declines in this species; therefore, we recommend *G. woondagoom* sp. nov. be listed as *Least Concern.*

Acknowledgments

We thank the Dambimangari Aboriginal Corporation for approving the name *woondagoom*, Tom Gill for facilitating this, and the Dambimangari Rangers who first told us of this name during our visit to Kimbolton. We are indebted to Pippa Kern (Australian Wildlife Conservancy) for her advice, encouragement, and facilitating access to Kimbolton and its facilities so that we could photograph the new species in life. We thank the Australian Defence Force for kindly approving our visit to Yampi Sound Training Area, and Steve Eager for guidance and support during our visit. We thank Craig Moritz for his support during this project. Finally, we thank Ian Bool for discussions and providing photographs, Brian La Rance for enthusiastic assistance during field surveys at Kimbolton, Ian Brennan for assistance with analyses, and Paul Oliver for comments that improved the manuscript. This work was funded by an Australian Research Council Discovery Project (DP210102267) and a post-doctoral fellowship to SMZ from the Australian Biological Resources Study (ABRS) National Taxonomy Research Grant Program (NTRGP).

Supplementary Data

All data and analysis input and output files are available from the Zenodo repository: https://doi.org/10.5281/zenodo.22240287

References

ASH (2023) Australian Society of Herpetologists Official List of Australian Species. https://www.australiansocietyofherpetologists.org/ash-official-list-of-australian-species.

Dobzhansky T (1937) Genetic nature of species differences. *The American Naturalist* 71: 404–420. https://doi.org/10.1086/280726

Doughty P, Palmer R, Sistrom MJ, Bauer AM, & Donnellan SC (2012) Two new species of *Gehyra* (Squamata: Gekkonidae) geckos from the north-west Kimberley region of Western Australia. *Records of the Western Australian Museum* 27; 117–134. https://doi.org/10.18195/ISSN.0312-3162.27(2).2012.117-134

Doughty P, Bauer AM, Pepper M, & Keogh JS (2018a) Spots before the eyes: revision of the saxicoline geckos of the *Gehyra punctata* (Squamata: Gekkonidae) species complex in the Pilbara region of Western Australia. *Records of the Western Australian Museum* 33: 1–50. https://doi.org/10.18195/issn.0312-3162.33(1).2018.001-050

Doughty P, Bourke G, Tedeschi LG, Pratt RC, Oliver PM, Palmer RA, & Moritz CC (2018b) Species delimitation in the *Gehyra nana* (Squamata: Gekkonidae) complex: cryptic and divergent morphological evolution in the Australian Monsoonal Tropics, with the description of four new species. *Zootaxa* 4403: 201–244. https://doi.org/10.11646/zootaxa.4403.2.1

Fenker J, Tedeschi LG, Melville J, & Moritz CC (2021) Predictors of phylogeographic structure among codistributed taxa across the complex Australian monsoonal tropics. *Molecular Ecology* 30: 4276–4291. https://doi.org/10.1111/mec.16057

Flouri T, Jiao X, Rannala B, & Yang Z (2018) Species tree inference with BPP using genomic sequences and the multispecies coalescent. *Molecular Biology and Evolution* 35: 2585–2593. https://doi.org/10.1093/molbev/msy147

Guindon S, Dufayard J-F, Lefort V, Anisimova M, Hordijk W, & Gascuel O (2010) New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. *Systematic Biology* 59: 307–321. https://doi.org/10.1093/sysbio/syq010

Gruber B, Unmack PJ, Berry OF, & Georges A (2018) Dartr: An r Package to Facilitate Analysis of SNP Data Generated From Reduced Representation Genome Sequencing. *Molecular Ecology Resources* 18: 691–699. https://doi.org/10.1111/1755-0998.12745

Hoang DT, Chernomor O, von Haeseler A, Minh BQ, & Vinh LS (2018) UFBoot2: Improving the Ultrafast Bootstrap Approximation. *Molecular Biology and Evolution* 35: 518–522. https://doi.org/10.1093/molbev/msx281

IUCN (2024) Guidelines for using the IUCN Red List categories and criteria. https://www.iucnredlist.org/resources/redlistguidelines

Jackson ND, Carstens BC, Morales AE, & O'Meara BC (2017) Species delimitation with gene flow. *Systematic Biology* 66: 799–812. https://doi.org/10.1093/sysbio/syw117

Kalyaanamoorthy S, Minh BQ, Wong TKF, von Haeseler A, & Jermiin LS (2017) ModelFinder: Fast Model Selection for Accurate Phylogenetic Estimates. *Nature Methods* 14: 587–589. https://doi.org/10.1038/nmeth.4285

Kealley L, Doughty P, Pepper M, Keogh JS, Hillyer M, & Huey J (2018) Conspicuously concealed: revision of the arid clade of the *Gehyra variegata* (Gekkonidae) group in Western Australia using an integrative molecular and morphological approach, with the description of five cryptic species. *PeerJ* e5334. https://doi.org/10.7717/peerj.5334

Kilian A, Wenzl P, Huttner E, Carling J, Xia L, Blois H, Caig V, Heller-Uszynska K, Jaccoud D, Hopper C, Aschenbrenner-Kilian M, Evers M, Peng K, Cayla C, Hok P, & Uszynski G (2012) Diversity arrays technology: a generic genome profiling technology on open platforms. *Methods in Molecular Biology* 888: 67–89. https://doi.org/10.1007/978-1-61779-870-2_5

King M (1979) Karyotypic evolution in *Gehyra* (Gekkonidae: Reptilia) I. The *Gehyra variegata-punctata* Complex. *Australian Journal of Zoology* 27: 373–393. https://doi.org/10.1071/ZO9790373

Lau CC, Christian K, Fenker J, Laver RJ, O'Hara K, Zozaya SM, Moritz CC, & Roycroft E (2025) Range size variably predicts genetic diversity in *Gehyra* geckos. *Evolution* 79: 1086–1095. https://doi.org/10.1093/evolut/qpaf057

Leaché AD, Zhu T, Rannala B, & Yang Z (2019) The spectre of too many species. *Systematic Biology* 68: 168–181. https://doi.org/10.1093/sysbio/syy051

Mayr E (1963) *Animal Species and Evolution.* Harvard University Press.

Mayr E (1996) What is a species, and what is not? *Philosophy of Science* 63: 262–277. https://doi.org/10.1086/289912

Minh BQ, Schmidt HA, Chernomor O, Schrempf D, Woodhams MD, von Haeseler A, & Lanfear R (2020) IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. *Molecular Biology and Evolution* 37: 1530–1534. https://doi.org/10.1093/molbev/msaa015

Moritz CC (1986) The population biology of *Gehyra* (Gekkonidae): chromosome change and Speciation. *Systematic Biology* 35: 46–67. https://doi.org/10.1093/sysbio/35.1.46

Moritz CC, Pratt RC, Bank S, Bourke G, Bragg JG, Doughty P, Keogh JS, Laver RJ, Potter S, Teasdale LC, Tedeschi LG, & Oliver PM (2018) Cryptic lineage diversity, body size divergence, and sympatry in a species complex of Australian lizards (*Gehyra*). *Evolution* 72: 54–66. https://doi.org/10.1111/evo.13380

Oliver PM, Bourke G, Pratt RC, Doughty P, & Moritz CC (2016a) Systematics of small *Gehyra* (Squamata: Gekkonidae) of the southern Kimberley, Western Australia: redescription of *G. kimberleyi* Börner & Schüttler, 1983 and description of a new restricted range species. *Zootaxa* 4107: 49–64. https://doi.org/10.11646/zootaxa.4107.1.2

Oliver PM, Laver RJ, Martins FDM, Pratt RC, Hunjan S, & Moritz C (2016b) A novel hotspot of vertebrate endemism and an evolutionary refugium in tropical Australia. *Diversity and Distributions* 23: 53–66. https://doi.org/10.1111/ddi.12506

Oliver PM, Prasetya AM, Tedeschi LG, Fener J, Ellis RJ, Doughty P, & Moritz CC (2020) Crypsis and convergence: integrative taxonomic revision of the *Gehyra australis* group (Squamata: Gekkonidae) from northern Australia. *PeerJ* e7971. https://doi.org/10.7717/peerj.7971

Padial JM, Miralles A, De la Riva I, & Vences M (2010) The integrative future of taxonomy. *Frontiers in Zoology* 7: 16. https://doi.org/10.1186/1742-9994-7-16

Pepper M, Fujita MK, Moritz C, & Keogh JS (2011) Palaeoclimate change drove diversification among isolated mountain refugia in the Australian arid zone. *Molecular Ecology* 20: 1529-1545. https://doi.org/10.1111/j.1365-294X.2011.05036.x

Read WJ, Laver RJ, Lau CC, Moritz M, & Zozaya SM (2025) Repeated Mitochondrial Capture with Limited Genomic Introgression in a Lizard Group. *Molecular Ecology* 34: e17766. https://doi.org/10.1111/mec.17766

Sansaloni CP, Petroli CD, Carling J, Hudson CJ, Steane DA, Myburg AA, Grattapaglia D, Vaillancourt RE, & Kilian A (2010) A high-density Diversity Arrays Technology (DArT) microarray for genome-wide genotyping in *Eucalyptus*. *Plant Methods* 6: 16. https://doi.org/10.1186/1746-4811-6-16

Tyler IM, & Griffin TJ (1992) *Explanatory Notes on the Yampi 1:250000 Geological Sheet, Western Australian (2nd ed.).* Western Australia Geological Survey, Record 1992/8.

Uetz P, Freed P, Aguilar R, Reyes F, Kudera J, & Hošek J (2025) The Reptile Database. http://www.reptile-database.org.

Wilson SK & Swan G (2025) *A Complete Guide to Reptiles of Australia*. *7th Edition.* Reed New Holland, Sydney.

Zozaya SM, Fenker J, MacDonald SL (2019) A new species of rock-dwelling gecko (Gekkonidae: *Gehyra*) from the Mt Surprise region of northern Queensland, Australia. *Zootaxa* 4688: 503–518. https://doi.org/10.11646/zootaxa.4688.4.3

Zozaya SM, Macor SA, Schembri R, Higgie M, Hoskin CJ, O'Hara K, Lau CC, Read WJ, Moritz CC (2025) Contact zones reveal restricted introgression despite frequent hybridization across a recent lizard radiation. *Evolution* 79: 411–422. https://doi.org/10.1093/evolut/qpae174

Zozaya SM, Teasdale LC, Tedeschi LG, Higgie M, Hoskin CJ, & Moritz CC (2023) Initiation of speciation across multiple dimensions in a rock-restricted, tropical lizard. *Molecular Ecology* 32: 680–690. https://doi.org/10.1111/mec.16787