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Taxonomic revision of the Australian arid zone lizards *Gehyra variegata* and *G. montium* (Squamata, Gekkonidae) with description of three new species

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Abstract

The taxonomy of central Australian populations of geckos of the genus *Gehyra* has been uncertain since chromosomal studies carried out in the 1970s and 1980s revealed considerable heterogeneity and apparently independent patterns of morphological and karyotypic diversity. Following detailed molecular genetic studies, species boundaries in this complex have become clearer and we here re-set the boundaries of the three named species involved, *G. variegata* (Duméril & Bibron, 1836), *G. montium* Storr, 1982, and *G. nana* King, 1982, and describe three new species. Two of the new species, *G. moritzi* and *G. pulingka*, include populations formerly assigned to either *G. montium* or *G. nana* Storr, 1982, while the third, *G. versicolor*, includes all of the eastern Australian populations formerly assigned to *G. variegata.*

Key words: Reptilia, Gekkota, systematics, karyotype, cryptic species

Introduction

Species boundaries among the gekkotan lizards of Australia have been subject to considerable scrutiny in recent years as molecular genetic tools have come into wider use and allowed workers to re-open investigations that had stalled decades before. In particular, several studies have revealed relictual patterns of differentiation in rainforest and upland refugia among the carphodactylid leaf-tailed geckos of tropical Queensland (Couper *et al.* 1993, 1997; Hoskin *et al.* 2003), while other studies have revealed exceptional amounts of cryptic diversity in the primarily arid-zone diplodactylids (Oliver *et al.* 2007a, 2007b, 2009; Pepper *et al.* 2008, 2011).

In the case of the arid zone diplodactylids the presence of cryptic diversity in at least some taxa was not unexpected as the studies of these animals were initiated specifically to address chromosomal studies begun by King (e.g., King 1977) that had revealed that several widespread species within *Diplodactylus* comprised two or sometimes more karyotypically different populations In similar studies, King (1979, 1982) found that the gekkonid genus *Gehyra* was another gekkotan lineage in which single morphospecies harboured multiple karyotypic 'races', of uncertain significance in terms of speciation. King's work was continued and expanded by Moritz (1986)

The present work follows directly from our recent work on these lizards (Sistrom *et al.* 2013). We provided a variety of data sets that pointed to the existence and genetic independence of all three of the nominal species that represent the *G. variegata* complex in central Australia, *G. variegata* (Duméril & Bibron, 1836), *G. minuta* King, 1982 and *G. montium* Storr, 1982. In addition we found as many as five clades that could be new species. Three of these latter clades (Clades 1, 2 and 5 of Sistrom *et al*. 2013) have been well-enough sampled to be described below as new. Their description requires re-definition of both *G. variegata* and *G. montium*, which is also formalized here.

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Material and methods

All descriptions are based directly on specimens that have been genotyped using DNA sequences or in a few cases on specimens collected adjacent to such typed specimens. Selection of specimens to be examined for morphological characters was, as much as possible, from individuals for which we had, or could infer, reliable data on life colouring, had been typed for mtDNA and, in some cases, for which we had karyotypic data. Primary molecular genetic data for the existence of the clades described here are presented in Sistrom *et al.* (2013), and that study also showed that multivariate statistical analysis of morphology (scalation and proportions) supported the existence of the same groups. Two lineages identified by Sistrom *et al.* (2013), Clade 3 and Clade 4, are not formally described here as we are not yet willing to affirm that they are species; we lack important data such as karyotype data and information on life colour pattern variation, and for both, sampling is currently inadequate to assess the degree to which they are genetically consistent across their range. We intend to make further collections and analyses to fill these gaps in knowledge to clarify the taxonomic status of these clades.

Morphological data gathered comprised colour and pattern, body size (SVL), head and limb proportions, head scalation features (rostral, narial, labial, mental and postmental scalation, interorbital scale size), numbers of precloacal pores in males, and numbers of adhesive lamellae (scansors) under the expanded portion of the fourth toe. These species of *Gehyra* have a terminal undivided scansor, while all the remainder are divided by a median gap, so that, for example, a count of eight would mean seven divided pairs and a terminal undivided eighth. Measurements were conducted using a ruler to the nearest millimetre (SVL and tail length), digital calipers to the nearest 0.1mm (other measurements) and counts carried out by eye under a dissecting microscope. Bilaterally distributed counts (e.g., labial scales, lamellae) were gathered unilaterally, the side selected being random and driven by accidents of preservation among specimens. The accessory row of enlarged scales that borders the infralabials was referred to as the 'sublabial' row by Sistrom *et al.* (2013), but in the descriptions below we use the term parinfralabials as suggested by King (1982).

Material examined in the course of this study included specimens from the South Australian Museum, Adelaide (SAMA), the Western Australian Museum, Perth (WAM), the Museum and Art Gallery of the Northern Territory (MAGNT), and the Muséum Nationale d'Histoire Naturelle, Paris (MNHN, lectotype and paralectotypes of *Hemidactylus variegatus*).

Chromosomal data were obtained from tissue cultures of reproductive tract epithelia (oviducts in females, efferent ducts in males). Tissues were cultured at 32°C using AmnioMAX-11 (Gibco) complete media. Standard methods were used to establish cultures, harvest and stain metaphase spreads for karyotypic analysis (Freshney 2005). In describing morphological variation we have relied on specimens that have been genetically identified from DNA sequences (Sistrom *et al.* 2013; M. Sistrom unpublished; M. Pepper, pers. com.) or from karyotype. Specimens examined that were karyotyped are indicated by a K superscript after the registration number.

Taxonomic descriptions

The genus *Gehyra* is recognised here in the sense of Bauer & Henle (1994) and Heinicke *et al*. (2011). All of the following species are members of the *variegata-punctata* group (Heinicke *et al*. 2011) first identified by King (1979) as a subgroup within the Australian radiation of the genus. Geckos of this group are relatively small species, differing from other members of the genus in having all but the terminal scansor divided, lacking skin folds and fragile skin and bearing the typical geckkotan clutch size of two sequentially so that gravid females carry only one fertilized egg at a time (Bustard 1965).

Some of the distinguishing external morphological characteristics of the species discussed below are summarized in Table 1.

Gehyra variegata (Duméril & Bibron, 1836)

Figs. 1, 2A, 3, 4A, 5, 6.

Hemidactylus variegatus Duméril & Bibron, 1836: p. 353. Lectotype: MNHN 2295 from Shark Bay, Western Australia. Lectotype designation Wells & Wellington (1983)

TABLE 1. Summary of morphological characters that can be used to help identify members of the *variegata-montium* complex in the field. All species show more variation than the common conditions outlined here.

Character	*variegata*	*montium*	*minuta*	*versicolor*	*moritzi*	*pulingka*
Dorsal background colour	grey to brown	rusty to brown	rusty	grey to brown	rusty	rusty to brown
White dorsal markings - position	adjoin posterior margins of dark markings	independent of dark markings	independent of dark markings	adjoin posterior margins of dark markings	independent of dark markings	independent of dark markings
White dorsal markings - form	short lines or small spots; faint to prominent	small circular dots, often faint	obvious pale spots, or absent	short lines or small spots; faint to prominent	obvious pale spots	obvious pale spots
Form of dark dorsal markings	continuous longitudinal lines or network	continuous longitudinal lines or network	discontinuous short irregular lines	continuous longitudinal lines or network	irregular black spots	discontinuous short irregular lines
Chin shield pairs	usually 2	usually 2	usually 2	usually 2	usually 2	usually 3
Supralabial scales	8–10	8–11	6–9	8–11	8–10	7–10
Max SVL (mm)	61	51	46	57	49	49

Specimens scored for morphology (n=29; all genotyped as "*variegata* clade"): SAMA: R26487–88, 68 km N Colona HS, SA (30º 51'S, 132º 09'E), R31997–98, 5 km S Mitcherie Rockhole, SA (31º 30'S, 132º 50'E), R32175, 8.5 km SW Maralinga, SA (30º 29'S, 131º 31'E), R32281, 42.5 km N Muckera Rockhole, SA (29º 42'S, 130º 07'E), R57176–77, 48.7 km S Vokes Hill Corner, SA (28º 51'S, 130º 29'E), R58995, 47.4 km W Oak Valley, SA (29º 31'S, 130º 15'E), R59074, Mt Gibson camp, WA (29º 45'S, 117º 09'E), R63255–56[K], Eyre Highway at Fraser Range, WA (32º 01'S, 122º 49'E), R63281–83[K], 57 km ENE Balladonia Rock, WA (32º 24'S, 124º 28'E), R65764[K],5.6km ENE Maralinga (30º 08'S, 131º 38'E), R65769[K] , 3.8 km E Maralinga (30º 09'S, 131º 37'E), R65782[K] , 31.8 km NNW Pidinga Tank (30º 36'S, 132º 01'E , R65790[K], 3.9 km E Maralinga (30º 10'S, 136º 11'E). WAM: R100002, Kwolyin, WA (31º 55'S, 117º 46'E), R114039, Peron homestead, WA (25º 50'S, 113º 33'E), R117025, Bush Bay (25°09'S, 113°47'E), R126810, 10km ESE Mardathuna homestead (24°30'S, 114°38'E), R136313, Muggon Station (26°31'S, 115°31' 115°31` E), R141460, R141467, Faure Island, Shark Bay, WA (25º 50'S, 113º 54'E), R141662, Cape Rose, WA (25º 45 S', 113º 39'E), R156674, North-West Coastal Highway, near Billabong Roadhouse (26°49'S, 114°36` E), R165160, 8.5 km WSW Yanyare River mouth (20º 50'S, 116º 22'E). WAM R117025 and 141662 are both sexually immature juveniles (SVL 27 and 28 mm respectively) and were excluded from adult body measurements.

Non-sequenced specimens examined. Paralectotypes: MNHN: 254, 254 A, 254 B, "Van Diemen's Land". Additional topotypic specimens from Peron Peninsula, Shark Bay Western Australia): WAM: R54636, 1 km S Monkey Mia, Shark Bay, WA (25º 48'S, 113º 42'E), R54639–40, Peron Homestead, Peron Peninsula, WA (25º 50'S, 113º 33'E), R54654, Monkey Mia, Shark Bay, WA (25º 48'S, 113º 43'E), R54717, Peron Hills, 28 km NW Denham, WA(25º 43'S, 113º 26'E), R54638, 54806–07, 10 km NE Denham, Shark Bay, WA (25º 52'S, 113º 36'E), R54873, 13 km S Nanga Peron Peninsula, WA (26º 20'S, 113º 54'E), R55003, 55067, 18km SE Nanga, Peron Peninsula, WA (26º 20'S, 113º 58'E), R55069-72, 8 km SE Nanga, Peron Peninsula, WA (26º 17'S, 113º 51'E), R60428, 3 km N Peron Homestead, WA (25º 48'S, 113º 33'E), R123646, 3 km NW Peron Homestead, WA (25º 49 S', 113º 33'E).

Diagnosis. Distinguished from other Australian *Gehyra* (except *G. versicolor*) by a combination of 7 or 8 divided scansors under the expanded portion of the fourth toe, moderate size, generally two pairs of enlarged chin shields, second infralabial notched and a dorsal pattern in which dark lines and white markings coordinate to produce a pattern of dark lines and bars with white trailing edges. Not readily distinguishable by external morphology from *G. versicolor* **sp. nov.** (see below), but distinguished karyotypically by the unique 2n=40b arrangement (King 1979). Otherwise most similar to *G. montium* but distinguished by grey to brown rather than more rufous dorsal colouring, with white markings that form a posterior highlight or margin on the trailing edge of the dark dorsal lines, rather than small poorly contrasting dots that are not coordinated with the dark markings.

This diagnosis applies to populations of *Gehyra* genetically assignable to the "*variegata* clade" of Sistrom *et al*. (2013).

Description (based on the lectotype and recent, genotyped material) Adult snout-vent length 34–49 mm (mean = 44.2 mm, n = 27). Length of original tail 43-48 mm (mean 107% of SVL, n=3). Sarre (1998) recorded that individuals in some Western Australian Wheatbelt populations can reach 60 mm SVL.

Nostril bordered by rostral, first supralabial, supranasal and two subequal post nasals. Most frequently, a single moderate internasal separates the supranasals above the rostral, but supranasals often (f = 0.41) in medial contact . Supralabials 8– 10 (mode 9). Infralabials 7–10 (mode 9). Usually two pairs chin shields (four specimens with 3 pairs), anterior pair in contact with only the first infralabial. Chin shields separated from the third and succeeding infralabials by the interpolation of a series of enlarged scales (parinfralabials, King 1982) that margin the ventral edge of the infralabials. Second infralabial notched where this parinfralabial scale row starts (Fig 4A). Scansors under pad of fourth toe divided, 6–8 (mode 8). Precloacal pores in males 10–15 (mean = 12.5, n = 11) arranged in a chevron with median pore anterior most.

The karyotype shown in Fig. 2A is 2n=40b (King 1979, Moritz 1986).

In life, dorsally light to medium grey or brown, generally with a complex pattern of white-edged black lines (Figs 1B, 5 A-B). These usually include several temporal streaks and often form continuous paravertebral and dorsolateral irregular lines, often with short cross bars that may form a vaguely ladder-like pattern. A trend is for specimens from rock-dwelling populations to have bolder and more contrasting markings, especially the white highlights which are expressed as spots (Fig. 5A), while some animals from arboreal populations may have only weakly contrasting patterns (Fig. 5B). However, colour pattern and intensity is variable both within and between populations, and individual animals can change colour intensity from pale to very dark in the course of a day. In preservative, the colour pattern is often greatly reduced in contrast and can be hard to discern. These patterns of extensive interpopulation, intrapopulation and temporal colour variation are characteristic of most species of Australian *Gehyra.*

Distribution. Widespread through the southern half of Western Australia, from the west coast as far north as the Pilbara, east to the Central Ranges and southeast to the western interior of South Australia (Fig. 3).

Comments. General. The combination *Gehyra variegata* has long been applied Australia-wide to populations of morphologically similar *Gehyra* species with similarly generalist habits. Sistrom *et al*. (2013) clearly distinguished two major genetic clades within these populations, and confirmed that the karyotypic differences between western and eastern populations first noted by King (1979) reflect the existence of at least two distinct species. Indeed, the two are not even sister lineages. The two populations have generally similar colour patterns but are subtly different in proportions. Sistrom et al. (2013) could distinguish samples of the two species using multivariate analysis but extensive overlap of character variation is such that identification of an individual from morphology alone is problematic. Allocation of the name *variegata* to the western species centres on the correct identification of the type locality and evidence that specimens from the vicinity of this locality are conspecific with the more widespread western populations.

Type locality. The syntypes of *Hemidactylus variegatus* in the MNHN collection are from two localities, Shark Bay, Western Australia (one specimen, MNHN 2295) and Tasmania (three specimens, MNHN 254, 254A and 254B). Duméril & Bibron (1836) reported that the collectors of MNHN 2295 were [Jean-René] Quoy and [Joseph Paul] Gaimard, naturalists who travelled with Freycinet's 1817–1820 expedition. The Shark Bay region (specifically the Peron Peninsula and Dirk Hartog Island) was the only location where the expedition spent any time (a week in September 1818) collecting in an area of Australia that would have yielded specimens of *Gehyra* (Arago, 1823). By contrast, the paralectotypes, MNHN 254, 254A and 254B, cannot be associated with a collecting locality. The given locality of Van Diemen's Land (Tasmania) is in error as no *Gehyra* species (in fact, no gekkotans) occur in Tasmania, Hutchinson *et al.* 2001). The three specimens were collected on the Baudin expedition (1800–1803), which visited several localities along the west coast of Western Australia, including Shark Bay, where specimens of *Gehyra* might have been obtained (Bonnemains *et al.* 1988), but there is no more detailed information that would allow the locality to be identified. All four syntypes are in poor condition, very faded, and soft; MNHN 254B is almost macerated. Without seeing any of these specimens, and under the misapprehension that all were from Shark Bay, Wells & Wellington (1983) named "the largest" specimen registered under MNHN 2295 as the lectotype. In fact there is only a single specimen registered under this number.

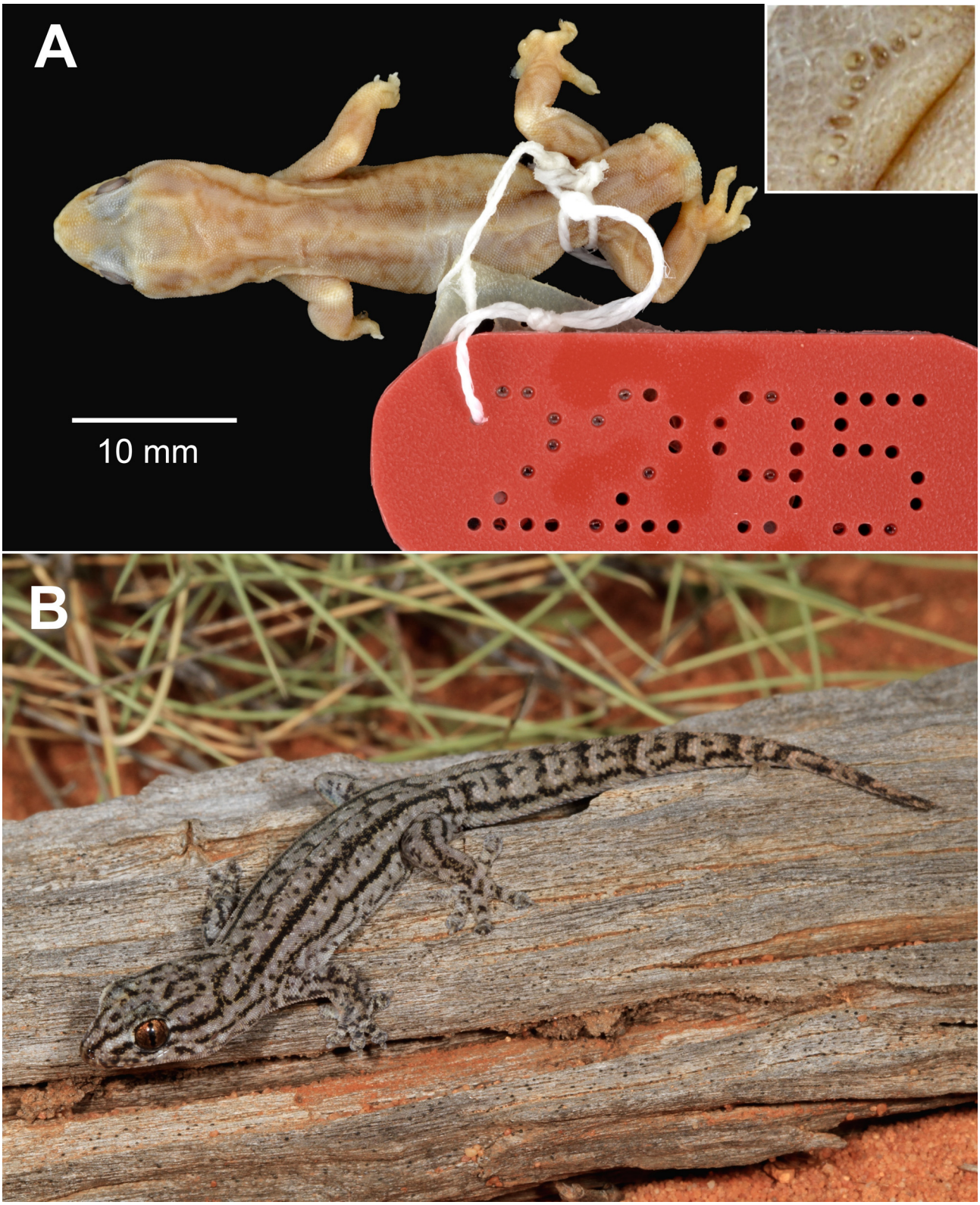

FIGURE 1. A. Lectotype of *Hemidactylus variegatus* Duméril & Bibron, 1836, MNHN 2295, adult male from Shark Bay, Western Australia. Inset shows the active precloacal pores. B. Live male *Gehyra variegata* from 8 km NE of Denham, Peron Peninsula, Western Australia (Photo: Ryan Ellis). This specimen with well-developed dark longitudinal lines; see Fig 5 for some other colour pattern variations.

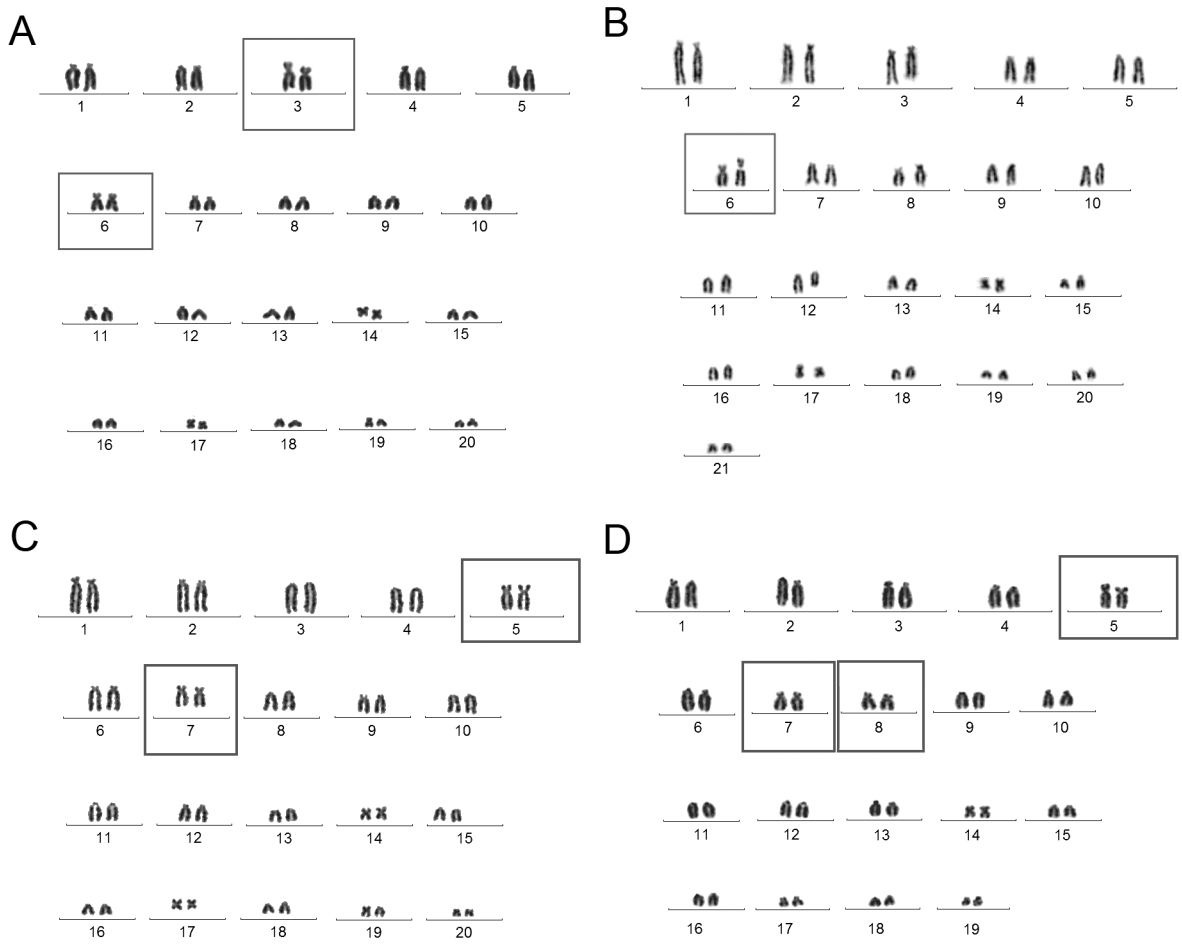

FIGURE 2. Karyotypes which are species-specific. A, 2n=40b, *Gehyra variegata*, SAMA R65764 from the Maralinga area, South Australia. Note submetacentric pairs 3 and 6. B, 2n=42b, *Gehyra pulingka* **sp. nov**, SAMA R51574 from the Amata area, South Australia. The submetacentric pair 6 with a secondary constriction is characteristic. C, 2n=40a, *Gehyra versicolor* **sp. nov**, SAMA R51790 from Yudnamutana Bore, Flinders Ranges, South Australia, with submetacentric pairs 5 and 7. B. 2n=38a karyotype, *G. versicolor* **sp. nov**, SAMA R65948 from Native Gap, SSE of Aileron, NT, with submetacentric pairs 5, 7 and 8.

The lectotype is distinctive in being very small (SVL 35 mm) for an apparently adult male (highly active precloacal pores). A series of 16 Western Australian Museum specimens from the Peron Peninsula was examined and revealed only one *Gehyra* morphotype, similar to the "*variegata* clade" in colour pattern. All specimens are noticeably small in size, the three largest individuals (WAM R54640, 54654 and 55070) being 40 mm SVL. The smallest male with active precloacal pores (WAM R54636) measured 34 mm SVL; the smallest females with an enlarging ovarian follicle or a fully yolked egg measured 38 mm SVL. By comparison, in our random sample of genetically typed specimens from across the species range the smallest male with active pores and smallest ovigerous female both measured 41 mm SVL and the largest animals were 49 mm SVL. Thus the Shark Bay specimen (MNHN 2295) is consistent in its small adult size with recently collected specimens from the same area, and we are confident that the type locality for *Hemidactylus variegatus* is the Peron Peninsula and that MNHN 2295 is correctly designated as lectotype.

Conspecifity of topotypic and "*variegata* clade" populations. Molecular data (Sistrom *et al*. 2013) show that all of the samples that have been DNA sequenced from the vicinity of Shark Bay (specimens from Peron homestead, Cape Rose, Babbage Island, Bush Bay, Faure Island, Baudin Island, and the North-west Highway near 'Billabong' roadhouse) are members of the "*variegata* clade". Our two sequenced Peron Peninsula specimens (Cape Rose and Peron homestead) are closely related, and some other Shark Bay area specimens are relatively close genetically to them (e.g., the Carnarvon area specimens from Babbage Island and Bush Bay), while others are more distant (e.g., the Faure Island specimens). Equally, some geographically remote specimens are close genetic relatives of Shark Bay area specimens; the nearest relative of the Peron Peninsula specimens is a specimen from

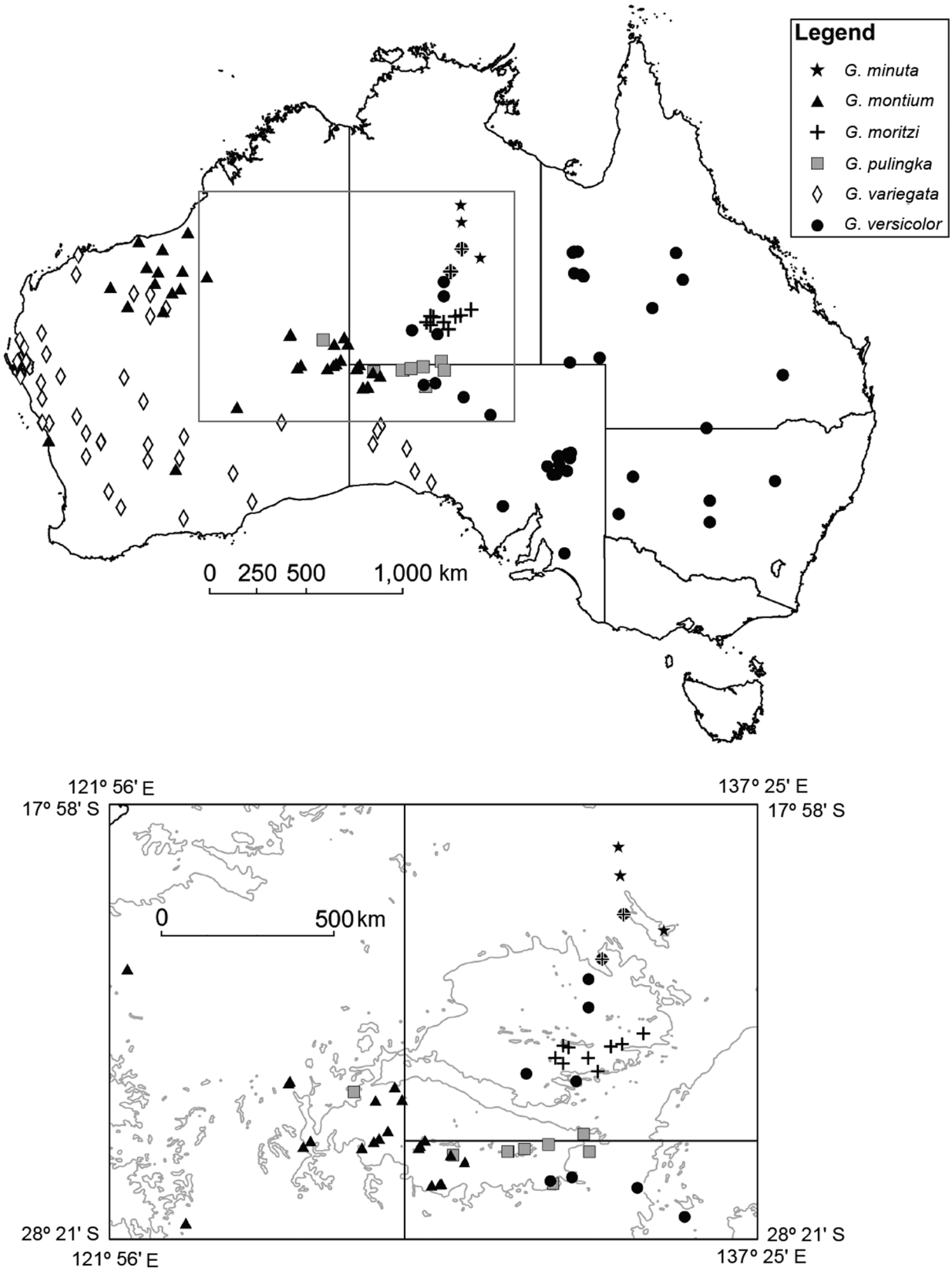

FIGURE 3. Distribution of the species of the *Gehyra montium* - *variegata* complex, based on populations identified from DNA sequences. Inset shows the detailed distributions of species in the Central Ranges area.

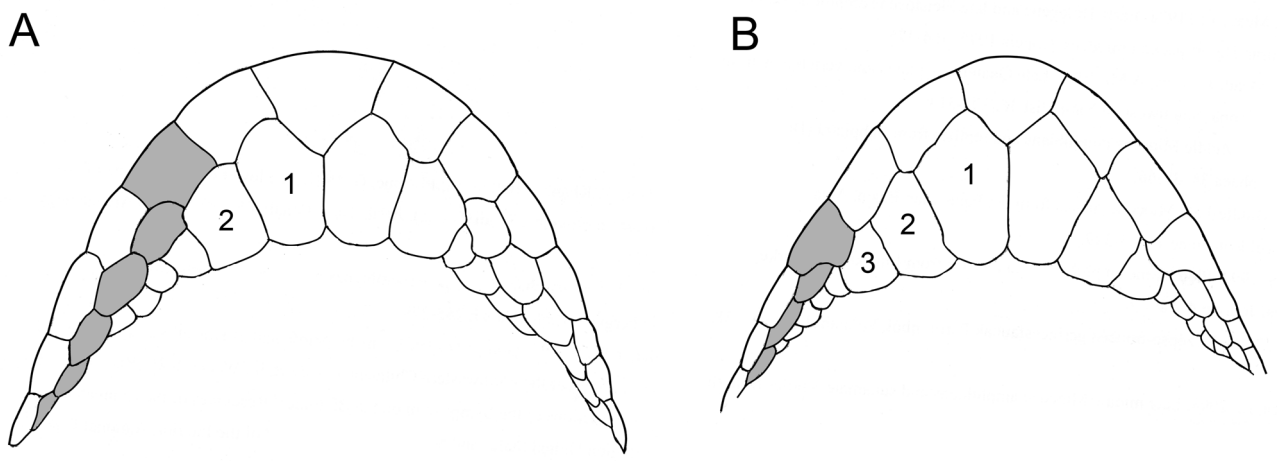

FIGURE 4. Chin shields of *Gehyra* showing features used in species descriptions. Numbers indicate chin shield pairs. Grey shaded scales are the notched infralablial and the parinfralabial scale series. A. *Gehyra variegata* (SAMA R59074), with two pairs of chin shields and the second infralabial notched by the parainfralabials. B. *Gehyra pulingka* **sp. nov** (SAMA R51574), with three pairs of chin shields and the third infralabial notched by the parainfralabials.

FIGURE 5. *Gehyra variegata* Duméril & Bibron, 1836. A. Adult female, SAMA R63256, from a rocky microhabitat from Fraser Range, Western Australia, showing a complex reticulate pattern, with strongly contrasting dark markings strongly margined with white. B. Adult female, SAMA R65740, from an arboreal microhabitat from Maralinga South Australia, showing a less well-developed pattern with weaker pale margins.

near Dampier (mouth of the Yanyare River) more than 600 km to the northwest, while the Carnarvon specimens are even more closely related to Pilbara specimens (Pannawonica, Muggon Station), than to the Peron Peninsula specimens, and one of the Faure Island specimens is closest to one from Neale Junction on the edge of the Great Victoria Desert, over 1200 km distant. These patterns of genetic relatedness are consistent with a single species with subpopulations that have undergone dispersal and introgression subsequent to a period of isolation and differentiation. Genetic studies in the Western Australian wheatbelt have suggested that this species of *Gehyra* can disperse widely over relatively short time scales (Hoehn *et al.* 2007).

However the species varies in body size and this morphological variation may be indicating very recent differentiation not reflected in the initial genetic survey. In contrast to the dwarfish populations on the Peron Peninsula, populations in the Western Australian Wheatbelt, can grow to large body sizes. How *et al.* (1988) and Sarre and coworkers (Sarre *et al.* 1995; Sarre 1996, 1998) who worked on these populations reported the smallest breeding female at 44 mm SVL and the maximum recorded SVL as much as 61mm. As with the Peron Peninsula 'dwarfs' these Wheatbelt 'giants' are nested genetically well within the "*variegata* clade". We note that body size alone need not be an indicator of speciation in *Gehyra*, as our data in this study on *G. moritzi* **sp. nov.** (*q.v.*), as well as striking size variation in *G. lazelli* (Sistrom *et al*. 2012) show that intraspecific selection for local differences in body size has happened more than once in the Australian *Gehyra* radiation. Consequently, we conclude that the observed body size variation alone does not overturn the idea of only a single species across these populations. Further work, integrating additional genetic and morphological data, will be necessary to better understand the variation seen among populations of this species as we have construed it.

Contact between *G. variegata* and *G. versicolor,* sp. nov. The contact between our restricted concept of *G. variegata* and the eastern *G. versicolor* **sp. nov.** (2n=40a/Clade 5 of Sistrom *et al.* 2013) appears to occur at the eastern margins of the Nullarbor Plain (Fig.6). King (1979) mapped 2n=40a individuals as far west as Bates on the transcontinental railway line. Sistrom *et al.* (2013 and unpublished) found only true *G. variegata* (DNA data from nine individuals from the far west of South Australia), and these findings have been supported by seven more individuals that we karyotyped from around Maralinga (40 km NW of Bates) and a site on the northeast Nullarbor Plain (23 km SE of Bates) which all proved to have the 2n=40b karyotype. Thus our data, when combined those of King, appear to show an abrupt changeover in this area from *G. variegata* to the eastern species. It is noteworthy that we have found only *G. variegata* (i.e,. 2n=40b) in this area while King found only *G. versicolor* **sp. nov.** (2n=40a), one from Bates, another five from several localities approximately 160–180 km further east. Further detailed sampling in this area with both karyotypic and DNA sequence data would be very useful in exploring whether there is any gene flow between the two.

Gehyra versicolor sp. nov

Figs 2C–D, 3, 6, 7.

Gehyra 2n=40a "*variegata*", 38a "*variegata-montium*", Moritz, 1986: p. 48.

Holotype: SAMA R51968[K], from 1.9 km SW of Reedy Hole Springs, Flinders Ranges, South Australia (30° 15' 55" S, 138° 49' 30" E), collected by J. Bice, on 19 November, 1998 (Fig. 7A).

Paratypes (n=28; all genotyped as 'Clade 5'): SAMA: R26185, Birdsville, Qld (25° 54'S, 139° 21'E), R28201, 1 km S Mt Dutton, SA (27° 49'S, 135° 43'E), R34249, 7 km E Mount Isa, Qld (20° 43'S, 139° 43'E), R38930, Yudnamatana, SA (30° 10'S, 139° 17'E), R38942, R38945, Lancoona HS, NSW (32° 22'S, 145° 53'E), R50277, 7 km SSE Mt Deception, Beltana Station, SA (30° 46'S, 138° 17'E), R51609[K], 26.1 km ENE of Mimili, SA (26° 54' 43" S, 132° 56' 55" E), R51637[K], 30.3 km WNW Indulkana, SA (26° 52' 09" S, 133° 01' 29" E), R51760[K], 1.75 km W Yudnamutana Bore, SA (30° 10'S, 139° 16'E), R51782[K], 10.4 km SW Yudnamutana Bore, SA (30° 14'S, 139° 11'E), R51912, 0.5 km NW Nudlamutana Well, SA (30° 22'S, 139° 21'E), R51962[K], 2.8 km W Moosha Bore, SA (30° 19'S, 138° 47'E), R52366, 4.7 km W Parachilna Hill, SA (31° 08'S, 138° 33'E), R54530, 4.5 km N Station Creek crossing, Prairie–Muttaburra road, Qld (22° 02'S, 144° 37'E), R54546–47, 14 km NW Longreach on Landsborough Highway, Qld (23° 21'S, 143° 12'E), R55133, 2.7 km E Gluepot HS, SA (33° 45'S, 140° 09'E), R55268, Phosphate Hill mine, 'Snappy Site', Qld (21° 53'S, 139° 59'E), R55695–96, 13.4 km NNE Hughenden on Kennedy Developmental Road, Qld (20° 47'S, 144° 19'E), R55905, 9 km N New South Wales/

Queensland border on Mitchell Highway, Qld (28° 58'S, 145° 44'E), R57970, 30.1 km SSW Memory Bore, SA (28° 53'S, 132° 44'E), R63576, Mutawintja NP, NSW (31° 17'S, 142° 18'E), R64097, Terrapinna Springs, SA (29° 55'S, 139° 40'E), R64443, Mt Fitton HS, SA (28° 59'S, 139° 33'E), R64447, 17 km E Mt Fitton HS, SA (29° 54'S, 139° 25'E), R64549, 1.3 km WNW Nantawarrinna, SA (30° 49'S, 138° 58'E), R64863, 6.9 km WNW Arkaroola HS (30° 18'S, 139° 19'E).

Diagnosis. Morphologically shares the external features of *G. variegata* (see above) but distinguished from that species by karyotype (2n=40a or 2n=38a) (Fig. 2C–D). As with *G. variegata, G. versicolor* is most similar *G. montium* but distinguished by grey to brown rather than more rufous dorsal colouring, with white markings that form a posterior highlight or margin on the trailing edge of the dark dorsal lines, rather than forming discrete circular dots that are not coordinated with the dark markings.

This diagnosis applies to populations of *Gehyra* genetically assignable to "Clade 5" of Sistrom *et al*. (2013).

Description. Adult snout-vent length 37–54 mm (mean = 46.7 mm, n = 29). Length of original tail 40–58 mm (mean = 110% SVL, n = 6).

Nostril bordered by rostral, first supralabial, supranasal and two subequal postnasals. Usually a single internasal scale (occasionally 2 or none) separates the supranasals above the rostral. Supralabials 8–11 (mode 9). Infralabials 7–10 (mode 9). Usually (f = 0.6) two pairs of chin shields; if a third pair is visible it is markedly smaller than the second or asymmetric, anterior pair in contact with only the first infralabial. Chin shields separated from the third and succeeding infralabials by the interpolation of a series of enlarged scales (parinfralabials) that margin the ventral edge of the infralabials. Second infralabial notched where this parinfralabial scale row starts. Scansors under pad of fourth toe divided, 7–8 (mode 8). Precloacal pores in males 10–14 (mean = 11.9, n = 15).

Most populations uniformly have the 2n=40a karyotype first reported by King (1979), but within central Australia, geographically interspersed with 2n=40a individuals, are individuals with 2n=38 karyotypes. These specimens all belong to the same clade on the basis ofsequence data. Moritz (1986) reported two variants of the 2n=38 karyotype that differ only in that the 2n=38a karyotype had pair 8 acrocentric while the 2n=38b karyotype had this pair symmetrically metacentric. Our karyotype (Fig. 2B) from Native Gap (a population scored as 2n=38a by Moritz 1986) has a pair 8 that is submetacentric, neither obviously acrocentric nor symmetrically metacentric, and in fact King (1979) described and illustrated his 2n=38 karyotype (later termed the "a" variant by Moritz) as having submetacentric pairs 7 and 8, as ours does. The discrepancy may be artifactual, given the variation in condensation and clarity that is typical across karyotypic preparations. In case further cryptic species are demonstrated among these populations, we have confined our type series for *G. versicolor* to animals from 2n=40a populations only.

In life, dorsally light to medium grey or grey-brown, generally with a complex pattern based on one or two pairs of more or less continuous dark longitudinal irregular dorsal stripes with numerous cross links and reticulations, the dark markings all coordinated with white highlights that can form irregular spots but are consistently in contact with the darker markings as in *G. variegata*. In general, specimens of *G. versicolor*, even when strongly patterned, tend to have less distinct and contrasting patterns (Fig. 7) than do well marked *G. variegata*. Common variant patterns include one where some of the dark dorsal markings form back-swept angular or crescentic bars, each with a whitish spot contained in the angle of the bar, and another where the body is densely stippled with low contrast darker grey bars and blotches with only weakly apparent paler edges. None of these variations is unvarying and the colour patterns show continuous variation both within and between populations.

Distribution. Widespread from the Murray Valley of northern Victoria north and east through New South Wales west of the Great Dividing Range and similar areas of Queensland north to about the latitude of Hughenden. Extends west into most of South Australia, with the exception of the southern and western Eyre Peninsula and the Great Victoria Desert, and north-west into southern and central Northern Territory. Not currently known to occur in Western Australia. Found in both rocky and arboreal situations, as well as on buildings.

Comments. This species is the only one where we find two karyotypic groups appearing to belong to a single taxon. Moritz (1986) reported both 2n=40a and 2n=38 (a and b) from the MacDonnell Ranges and adjacent central Northern Territory, and at present our data suggests all belong to a single species, *G. versicolor*. As with the variable populations of *G. moritzi*, further detailed study combining the same multiple approaches used here are desirable to clarify the gene flow among these chromosomally different populations.

Similar detailed studies are needed in central and western Queensland to better understand the distribution and variation of *G. versicolor* and Clade 4 where they co-occur (Sistrom *et al.* 2013), and the potential contact or

overlap between *G. variegata* and *G. versicolor* in central western South Australia. However, it is clear that over the great majority of its distribution this is a single species, consistently different from other *Gehyra*. Most of the literature pertaining to the biology of "*Gehyra variegata*" (e.g., Bustard 1965, 1967, 1968, 1969; Henle 1990) actually applies to this species, as does recent population genetic work by Duckett and Stow (2010, 2013). Swan *et al*. (2004) report the maximum SVL for this species (as *G. variegata*) as 57 mm.

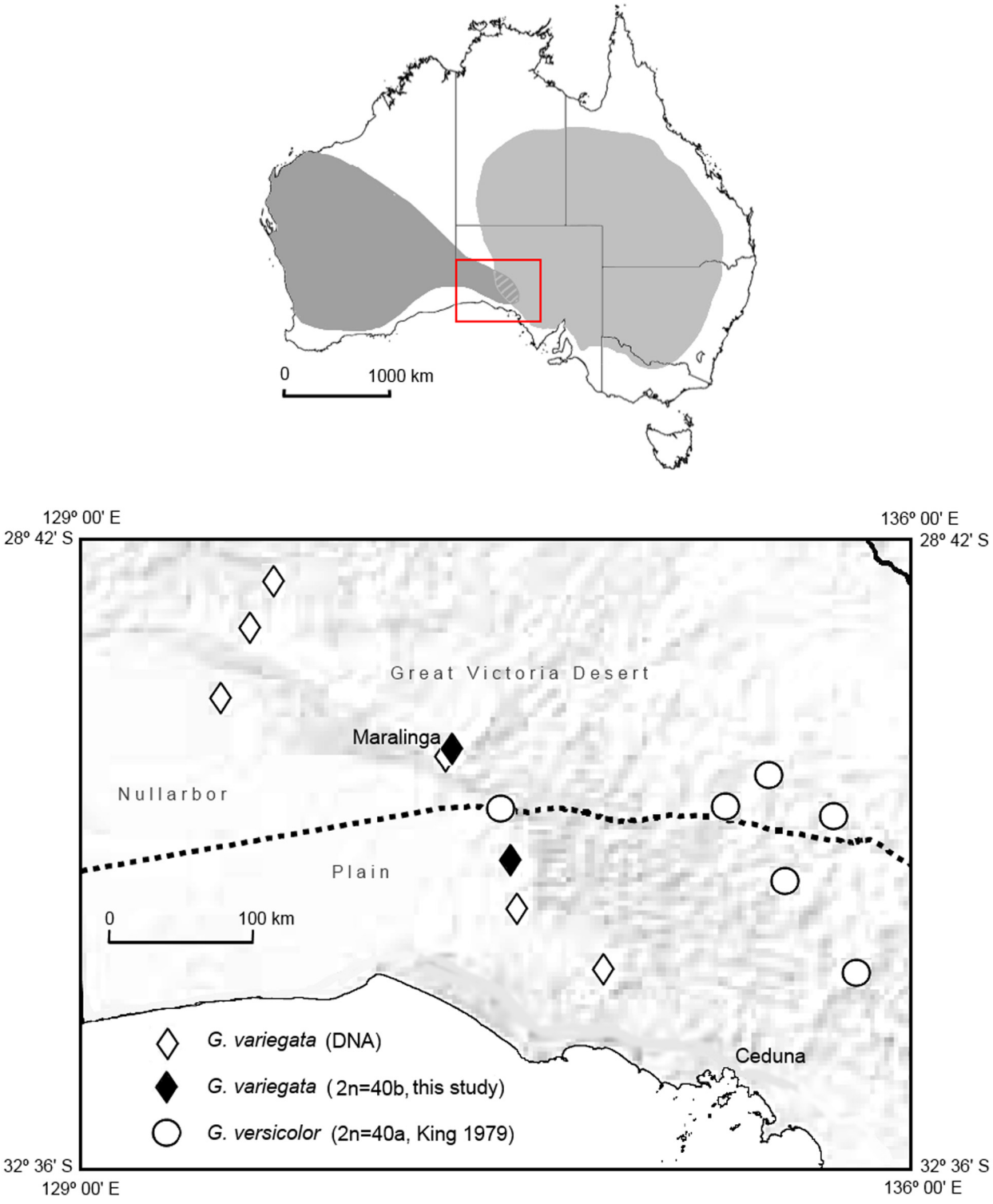

FIGURE 6. Map showing the documented occurrence of *G. variegata* (dark grey) and *G. versicolor* **sp. nov.** (light grey). The inset shows the western part of the state of South Australia where distributions of the two species approach one another. Dashed line indicates the transcontinental railway line.

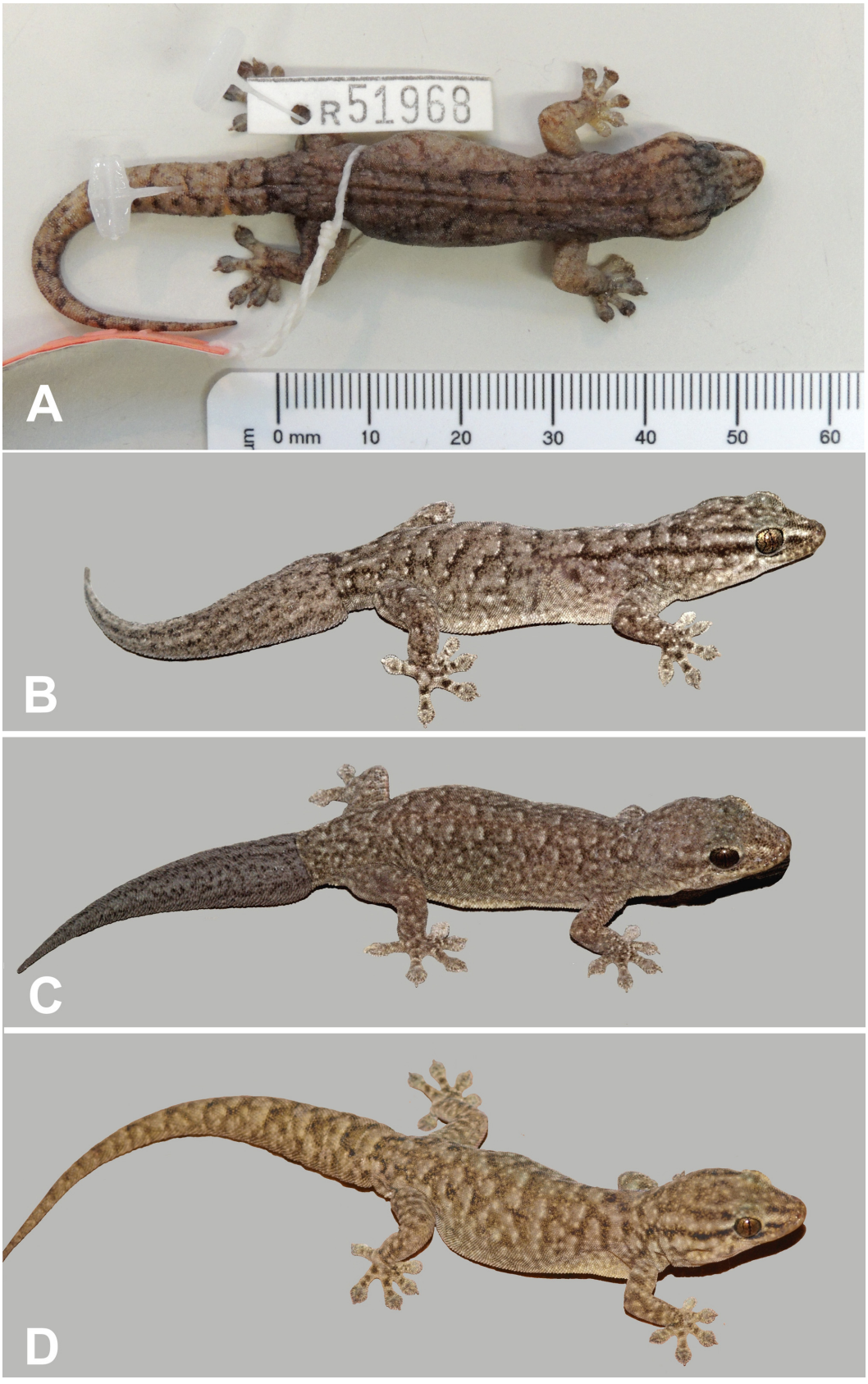

FIGURE 7. *Gehyra versicolor* **sp. nov.**. A. Holotype, SAMA R51968, adult male from 1.9 km SW of Reedy Hole Springs, Flinders Ranges, South Australia. B and C, adult females, SAMA R63187 and 63185 (respectively), from arboreal microhabitats at New Year's Gift Bore, 9.6 km SW of Bopeechee, South Australia, showing strong and weak pattern variants typical of both inter- and intra-population variation for this species. D, adult male, SAMA R65588, from Witchelina Station, South Australia, with speckled patterning sometimes seen in rock dwelling populations.

Etymology. The specific name chosen here is from the Latin meaning 'variable in colour', appropriate for a species that shows considerable individual and geographic variation. Given the very wide distribution of the species it is somewhat surprising that no older name appears to be available for it in the synonymy of *G. variegata*. Cogger *et al*. (1983) listed several synonyms of *Gehyra variegata*. Subsequently, these have proven to be based on specimens attributable to other Australian *Gehyra* species groups, especially eastern species related to *G. australis* (Bauer & Henle 1994; Shea 1995). Other possible synonyms were discussed by Sistrom *et al.* (2009) in reference to *G. lazelli*; none apply to *G. versicolor*.

Gehyra montium Storr, 1982

Figs 3, 8.

Gehyra montium Storr, 1982: p. 56. Holotype: WAM R31732, from Mt Lindsay [Watarru], Birksgate Range, north-western South Australia (27º 02'S, 129º 53'E).

Specimens scored for morphology (n=29; all genotyped as 'montium clade'): SAMA: R44368–69, 14 km ENE Mt Cooparinna, SA (26º 20'S, 130º 06'E), R44407, 8.4 km NW Mt Kintore, SA (26º 30'S, 130º 26'E), R46107, 21 km ENE Pipalyatjara, SA (26º 07'S, 129º 22'E), R46134–36, 16 km E Pipalyatjara, SA (26º 10'S, 129º 33'E), R46139, 40 km NE Pipalyatjara, SA (25º 59'S, 129º 29'E), R46168, 26 km S Pipalyatjara, SA (26º 24'S, 129º 08'E), R48718, 4 km W Mt Lindsay, SA (27º 02'S, 129º 50'E), R48731–33, Mount Lindsay, SA (27º 02'S, 129º 53'E), R56451, R56497, 5.6 km W Mount Hoare, SA (27º 03'S, 129º 39'E), R61922–24[K], Morgan Range, WA (25º 53'S, 128º 23'E). WAM: R90848, Woodstock Station, WA (21º 37'S, 119º 01'E), R90903, Woodstock homestead, WA (21º 37'S,118º 57'E), R98094, Warburton, WA (26º 08'S, 126º 34'E), R125475, 30km E Newman, WA (23º 19'S, 120º 02'E), R132553, De Grey River Station, WA (20º 16'S, 119º 12'E), R154518, R154523, 156679, Yarri Mining Camp, WA (20º 36'S, 120º 19'E), R156317, Chichester Range, WA (22º 14'S, 118º 58'E , R166317, R166321, Morgan Range, WA (25º 53'S, 128º 23'E).

Diagnosis. Distinguished from other Australian *Gehyra* by a combination of modally seven divided scansors under the expanded portion of the fourth toe, small to moderate size, generally two pairs of enlarged chin shields, second infralabial notched, a dorsal colour pattern combining pinkish brown to rufous colouring (in life) usually patterned by small pale spots interspersed in a continuous network of irregular, dark lines, and a karyotype of 2n=42a (illustrated in King 1979, fig. 9; Moritz 1986, fig. 3). Distinguished from some other rock dwelling species (*G. minuta*, *G. moritzi* **sp. nov.** and *G. pulingka* **sp. nov.**) by more reticulate dorsal pattern and often weak contrast of pale spots. Most similar to *G. variegata* and *G. versicolor* **sp. nov.** but somewhat smaller and usually more rufous in colouring with dorsal white markings consisting of small poorly contrasting dots (readily lost in preservative) that are not consistently coordinated with the dark markings.

This diagnosis applies to populations of *Gehyra* genetically assignable to the "*montium* clade" of Sistrom *et al*. (2013).

Description. Adult snout-vent length 36–51 mm (mean = 41.7 mm, n = 29). Length of original tail 41–58 mm (mean = 113% SVL, n = 9).

Nostril bordered by rostral, first supralabial, supranasal and two post nasals, the upper usually markedly larger than the lower. None to three (modally 1) moderate internasal scales separate the supranasals above the rostral. Supralabials 8–11 (mode 8). Infralabials 7–9 (mode 8). Consistently two pairs of chin shields, anterior pair in contact with only the first infralabial. Chin shields separated from the third and succeeding infralabials by the interpolation of a series of enlarged scales (parinfralabials) that margin the ventral edge of the infralabials. Second infralabial notched where this parinfralabial scale row starts. Scansors under pad of fourth toe divided, 7–8 (mode 7). Precloacal pores in males 10–13, (mean = 11.3, n = 16).

The karyotype is 2n=42a, a karyotype that is shared with a number of *Gehyra* species, including *G. minuta* and some populations that are morphologically distinct from *G. montium* (King 1979, fig. 13a) and currently assigned to *G. punctata* (Fry, 1914) in Western Australia .

In life, dorsally light grey-brown to reddish brown to pinkish, the entire dorsal surface patterned by a strong to weak reticulum of blackish grey (Fig. 8). Scattered over the dorsal surface are small circular pale spots, often only contrasting weakly with the dorsal background colour. In preservative any rusty colour tones and pale spots tend to disappear leaving the specimens greyish with a dark reticulum.

FIGURE 8. *Gehyra montium* Storr, 1982. A. Adult male, SAMA R61924, from Morgan Range, Western Australia. B. Adult female (not collected) from Uluru, Northern Territory. Note reticulate dark markings, reddish body colour and small, weakly contrasting pale spots that do not margin the dark markings.

Distribution. The western portion of the Australian arid zone, from the north-west of South Australia, and south-east of the Northern Territory, north-west to the Pilbara Region of Western Australia.

Comments. Throughout arid areas of central and northern Australia, rocky outcrops may harbour relatively small *Gehyra* species, typically with rufous colouring and a pattern including pale spots. The name *G. montium* has often been applied to many such populations, but our study reveals that this species only just extends east of the Western Australian border, to the Tomkinson Ranges and Birksgate Ranges (east to Mt Kintore) in South Australia and is probably restricted in the Northern Territory to the far south-west corner (Uluru and the Petermann Ranges). The fact that the species was not recognised hitherto as extending westward as far as the Pilbara possibly reflects a tacit assumption that *G. montium* was a central Australian species, as well as the similarity of colour pattern in preserved *G. montium* and *G. variegata*. This similarity is such that individuals of the two species will continue to be difficult to separate by morphology alone

In the adjacent rocky ranges of north-west South Australia and the southern and central Northern Territory, *G. montium* is replaced by geckos of Clades 2 and 1 (Sistrom *et al*. 2013), respectively, and these are described below as new species.

Populations we have assigned to this species require further study in several areas. Colour and pattern as described here is based on central Australian populations for which we had freshly collected material of known genotype; preserved specimens examined by us suggest that this colour pattern extends to Pilbara populations, but in this region the species is more variable in colour pattern. Animals of known genotype from this area include not only animals with a dark dorsal network, but also almost plain individuals, grey in preservative but possibly rusty in life, with no more than scattered small black speckles. Three specimens genotyped as *G. montium* by Sistrom *et al.* (2013) are from areas to the south and west of the species' main distribution, apparently in areas of sandy desert rather than rocky ranges. Further collection and typing of specimens from these populations is needed to confirm that these seemingly atypical records are correctly documented, and that there are populations of *Gehyra* from these areas that pertain to this species.

When describing this species Storr (1982) suggested it might represent the 2n=38 karyotypic group of King (1979). However, the data of Moritz and our own checks of karyotype show that populations conspecific with the type population of *montium* have the 2n=42a karyotype.

Gehyra minuta King, 1982

Fig. 3.

Distinguished from other Australian *Gehyra* by a combination of modally 7 divided scansors under the expanded portion of the fourth toe, generally two pairs of enlarged chin shields, with the median (postmental) pair being relatively small, second infralabial notched and often in contact with postmental, low numbers of labial scales (nine or fewer supralabials, eight or fewer infralabials), a dorsal colour pattern combining pinkish brown to rufous colouring (in life) patterned by circular whitish spots and irregular short black flecks, and a karyotype of 2n=42a (King 1982).

This diagnosis applies to populations of *Gehyra* genetically assignable to the "*minuta* clade" of Sistrom *et al*. (2013).

Comments. King described his new species from a small number of localities and more recent knowledge has not suggested any broader distribution for this species. We did not have significant sampling of this species and so suggest that until further data prove the contrary, it should be regarded as an endemic inhabitant of the scattered rocky ranges centred around Tennant Creek, Northern Territory. King's description reveals this species as very short-faced compared to the other species described here, with a reduced labial count (as few as six and not exceeding nine) and relatively small chin shields crowded by the short snout so that the postmentals are often in contact with the second infralabials (a very rare exception among the other species treated here). In colour pattern it is most similar to *G. pulingka* **sp. nov.** of the Central Ranges around Northern Territory-South Australia-Western Australia border region. That species is further distinguished from *G. minuta* in generally having three pairs of enlarged chin shields and the third infralabial notched. Nearby populations of *G. moritzi* **sp. nov.** can be distinguished by their finely spotted colour pattern (both black and white markings in the form of small circular spots),

Gehyra moritzi sp. nov

Figs 3, 9.

Gehyra 2n=44 "*nana-montium*" Moritz, 1986: p. 48.

Holotype: SAMA R65941[K], adult male from Corroboree Rock, East MacDonnell Ranges, Northern Territory (23° 44' 23.0" S, 133° 57' 02.5" E), collected by M. Hutchinson, P. Oliver, G. Armstrong and S. South on 9 January 2011 (Fig 9A–B).

Paratypes (n=17; all genotyped as 'Clade 1'): MAGNT: R14356, R15356, 6 km SSW Claraville HS, NT (23° 25'S, 134° 44'E), R18310, Palm Valley Gas Well, Finke Gorge NP, NT (24° 01'S, 132° 37'E), R20664, Finke Gorge, NT (24° 08'S, 132° 49'E). SAMA: R65935[K]–36, Rainbow Valley, NT, R65896–900, R65937[K]–38, Emily Gap, NT (23° 44'S, 133° 57'E), R65895, Corroboree Rock, NT (23° 44' 23" S, 133° 57' 03" E, R65881, R65945[K]–46, 20 km S of Barrow Creek, NT (21° 38'S, 133° 44'E).

Diagnosis. Distinguished from other Australian *Gehyra* by a combination of either 7 or 8 divided scansors under the expanded portion of the fourth toe, small to moderate size, generally two pairs of enlarged chin shields, second or third infralabial notched, dorsal colour pattern combining pinkish grey to rufous colouring (in life) patterned entirely by black and whitish spots, and a karyotype of 2n=44 (Moritz 1986). Distinguished from most central Australian species (*G. versicolor*, *G. purpurascens* and *G. montium*) by its strongly white-spotted pattern with dark markings also forming discrete spots rather than wavy lines or continuous networks. Distinguished from *G.minuta* and *G. pulingka* **sp. nov.** by having black spots rather than short black wavy lines, normally two rather than three pairs of chin shields (*G. pulingka* **sp. nov.**), and higher numbers of labial scales (*G. minuta*).

This diagnosis applies to populations of *Gehyra* genetically assignable to "Clade 1" of Sistrom *et al*. (2013).

Description. Adult snout-vent length 36–49 mm (mean = 42.0 mm, n = 19). Length of original tail 38–51 mm (mean = 106% SVL, n = 5).

Nostril bordered by rostral, first supralabial, supranasal and two subequal postnasals. Either a single internasal scale separates the supranasals above the rostral (n= 9) or supranasals in median contact (n= 9). Supralabials 8–10 (mode 9). Infralabials 7–9 (mode 8). Two, less frequently (6/19) three, pairs of chin shields, anterior pair in contact with only the first infralabial. Chin shields separated from the fourth, or third, and succeeding infralabials by the interpolation of a series of enlarged scales (parinfralabials) that margin the ventral edge of the infralabials. Third, less frequently (7/19) second, infralabial notched where this parinfralabial scale row starts. Scansors under pad of fourth toe divided, 7–8 (mode 8). Precloacal pores in males 11–16 (mean = 14.4, n = 11).

The karyotype is 2n=44 , regarded as the plesiomorphic karyotype for the *Gehyra variegata* species group by King (1979) and Moritz (1986), but see Sistrom *et al*. (2013) for cautionary remarks on this assumption.

In life, dorsally light pinkish grey to reddish brown, the entire dorsal surface patterned by spots. Dark spots are larger and more irregular, pale spots tend to be more precisely circular in shape.

Distribution. Rocky mountain ranges of the south-central Northern Territory centred on the MacDonnell Ranges and south to the James Range, west to the Kings Canyon area and north to the Devils Marbles.

Comments. The above description refers to specimens from the central and southern parts of the species' range. The northernmost sample (SAMA R65875-80, 65943-44), from rocky hills south of the Devils Marbles, is distinctly different in morphology but is not distinguishable by either DNA sequence data or karyotype (SAMA R65943: 2n = 44). This series of eight specimens is consistently smaller (largest specimens only 40 mm SVL), males have fewer precloacal pores (range 8–11) and the spotted colour pattern consists of relatively very small spots, each covering only a few dorsal scales. All have seven enlarged scansors rather than the eight usual for the other populations. The small size, spotted pattern and rock dwelling habits of these animals are reminiscent of *G. minuta* which occurs close by, but that species has a dorsal pattern with larger pale spots and irregular black flecks rather than spots, lower infralabial counts and frequent contact between the postmental and second infralabial. For the present we refer this sample to *G. moritzi* but exclude it from the paratype series. Further genetic studies of gecko populations along the Northern Territory portion of the Stuart Highway would be useful to clarify the genetic relationships among *G. moritzi* populations and the pattern of occurrence of the rock dwelling *Gehyra* of this region.

The prominently spotted colour pattern of *G. moritzi* is very similar to that of some Western Australia rock-dwelling populations of *Gehyra*. They are quite genetically distinct ('punctata clade' of Sistrom *et al.* 2013), but the species delineation modeling indicates that they are likely sister taxa. Current chromosomal data (King 1979, Moritz 1986) suggests a further distinction (2n=44 for *G. moritzi*, 2n=42a for *G. 'punctata'*), but the precise relationships will require further work on Western Australian populations where multiple species are likely present in the Pilbara and adjacent areas. The strong similarity in colour pattern suggests selection for camouflage against rocks, but given their relationships this could be due to common ancestry rather than convergence.

Etymology. The specific name recognises the contribution of Dr Craig Moritz (Australian National University, Canberra, and University of California, Berkeley) in revealing the high level of karyotypic and morphological diversity among central Australian populations of *Gehyra*.

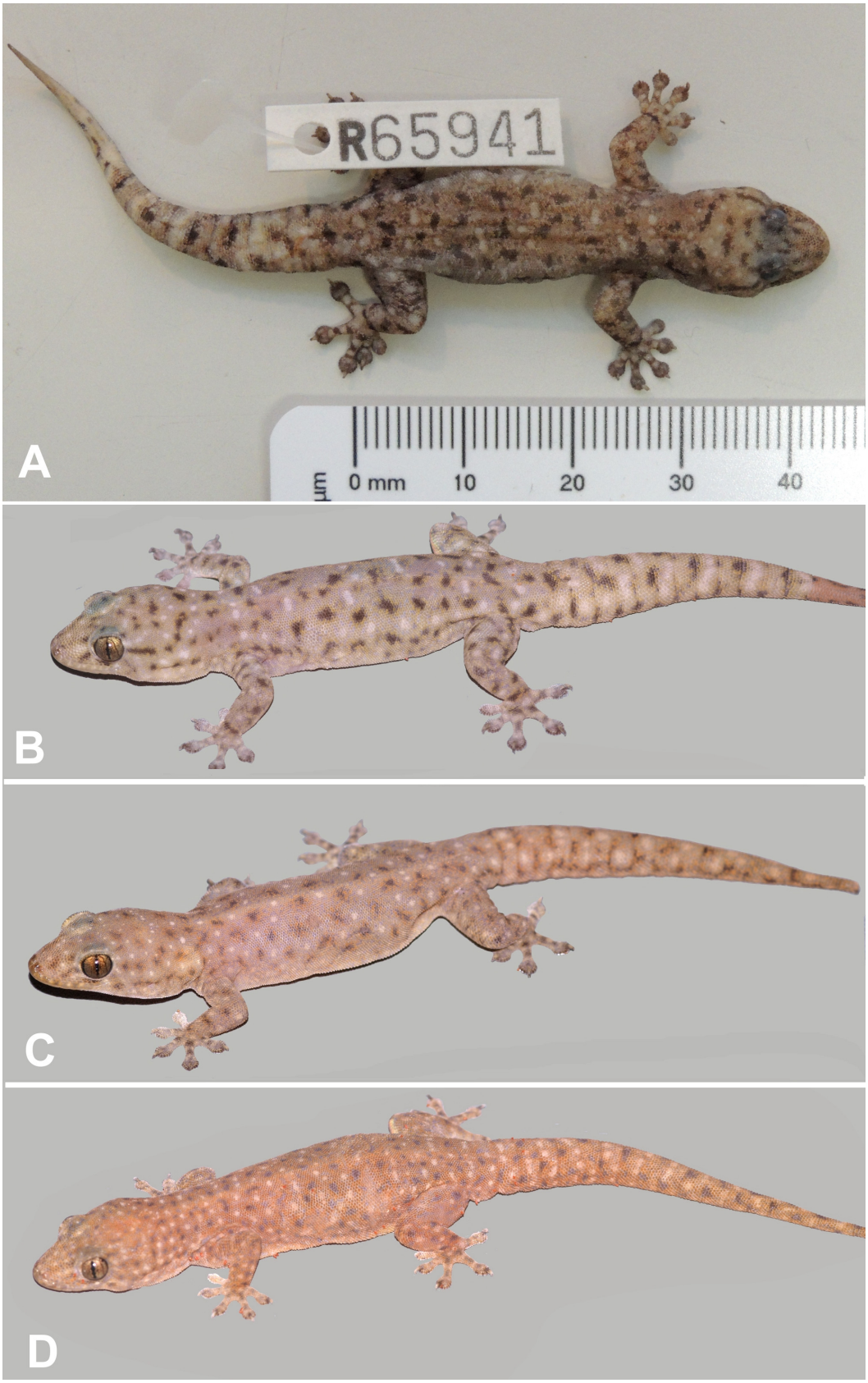

FIGURE 9. *Gehyra moritzi* **sp. nov**. A and B. Holotype, SAMA R65941, adult male from Corroboree Rock, Northern Territory, showing a strongly contrasting variant of the colour pattern, shown as preserved and in life. C. Adult female paratype, SAMA R65937, from Emily Gap, Northern Territory, showing a weakly contrasting variant of the colour pattern. D. Adult male, SAMA R65943, from 2 km S of Devils Marbles, Northern Territory, with a pattern of light and dark markings that are smaller relative to the pattern in specimens from the MacDonnell Ranges as exemplified by specimens A and B.

***Gehyra pulingka* sp. nov**
Figs 2B, 3, 4B, 10.

Gehyra 2n=42b "*nana-montium"* Moritz, 1986: p. 48.

Holotype: SAMA R65248, from Umuwa, Musgrave Ranges, South Australia (26° 28' 45" S, 133° 57' 02" E), collected by M. Hutchinson, on 26 May 2010, (Fig. 10 A–B).

Paratypes *(n=16; all genotyped as 'Clade 2')*: SAMA: R28265, Kulgera, NT (25° 50'S, 133° 18'E), R28322–23, between Victory Well and Betty Well, Everard Ranges, SA (27° 03'S, 132° 28'E), R41876–77, 15km W Mimili, SA (27° 01'E , 132° 34'E), R42069, 29 km SW Illintjitja, SA (26° 20'S, 130° 10'E), R44892, 8 km SE Mitchell Knob, SA (26° 11'S, 131° 53'E), R50119, 0.9 km SE Sentinel Hill, SA (26° 05'S, 132° 27'E), R51536–37[K], R51540[K], R51565[K], R51574[K], 35 km ESE Amata, SA (26° 15'S, 131° 29'E), R54751, Mt Howe, SA (26° 16'S, 133° 26'E), R61926[K], Kurtjurntari Rockhole, WA (24° 53'S, 128° 46'E). WAM: R166314, Kurtjurntari Rockhole, WA (24° 53'S, 128° 46'E).

Diagnosis. Distinguished from other Australian *Gehyra* by a combination of modally 7 or 8 divided scansors, small to moderate size, generally three pairs of enlarged chin shields, third infralabial notched, dorsal colour pattern a light to medium brown (in life) patterned by irregular thin black lines and circular pale spots, and a karyotype of 2n=42b (Fig. 2B) (Moritz 1986). Distinguished from most central Australian species (*G. variegata, G. versicolor* ***sp. nov.***, *G. purpurascens* and *G. montium*) by its strongly white-spotted pattern with dark markings forming short, wavy lines rather than discrete spots or continuous networks. Distinguished from *G. moritzi* by having short, black wavy lines rather than black spots, and from *G. minuta*, which has a similar colour pattern, by having the third, rather than second, infralabial notched.

This diagnosis applies to populations of *Gehyra* genetically assignable to "Clade 2" of Sistrom *et al*. (2013).

Description. Adult snout-vent length 38–49 mm (mean = 43.3 mm, n = 14). Length of original tail 43–56 mm (mean = 117% SVL, n = 6).

Nostril bordered by rostral, first supralabial, supranasal and two subequal postnasals. Usually a single internasal scale (occasionally two or none) separates the supranasals above the rostral. Supralabials 7–10 (mode 8). Infralabials 7–9 (mode 8). Three pairs of chin shields, outer (third) pair small (absent in three specimens), anterior pair in contact with only the first infralabial. Chin shields separated from the fourth and succeeding infralabials by the interpolation of a series of enlarged scales that margin the ventral edge of the infralabials. Third infralabial notched (all specimens) where this parinfralabial scale row starts (Fig. 4B). Scansors under pad of fourth toe divided, 7–8 (mode 8). Precloacal pores in males 12–16 (mean = 13.9, n = 7).

The karyotype (2n=42b) is unique for this species, differing from the 2n=42a karyotype via a secondary constriction on pair 11 (Moritz 1986).

In life, dorsally pinkish grey to reddish brown, the entire dorsal surface patterned by light spots that are generally strongly contrasting and precisely circular in shape, sometimes forming rather regular transverse series. The pale spots are interspersed with short dark irregular lines, which are more elongate and irregular than the pale spots.

Distribution. Rocky mountain ranges of north-western South Australia, extending into adjacent areas of Western Australia (northwest to the eastern Rawlinson Range) and far southern Northern Territory (Kulgera area).

Comments. Long included in *G. montium*, *G. pulingka* is consistently distinguishable in morphology, karyotype and DNA sequence data. The two species show overlap in distribution, although no cases of strict syntopy are known as yet. In the field, the colour pattern of blackish squiggles and prominent spots can be used to distinguish this species from true *G. montium*, which has a more continuous black dorsal network and small, weakly contrasting spots. Additional distinctions in chin shields (three versus two pairs), having the third, rather than second, infralabial notched and higher male precloacal pore counts will provide extra support if genetic data are lacking.

Etymology. The specific name is from the Pitjantjatjara language (Goddard 1996) from the roots *puli*, rock, or rocky hill, and the suffix *-ngka* meaning pertaining to, alluding to the habits of the species and its distribution, which is confined to the desert areas occupied by the speakers of Pitjantjatjara and related dialects. Specific name would not change with gender of the genus.

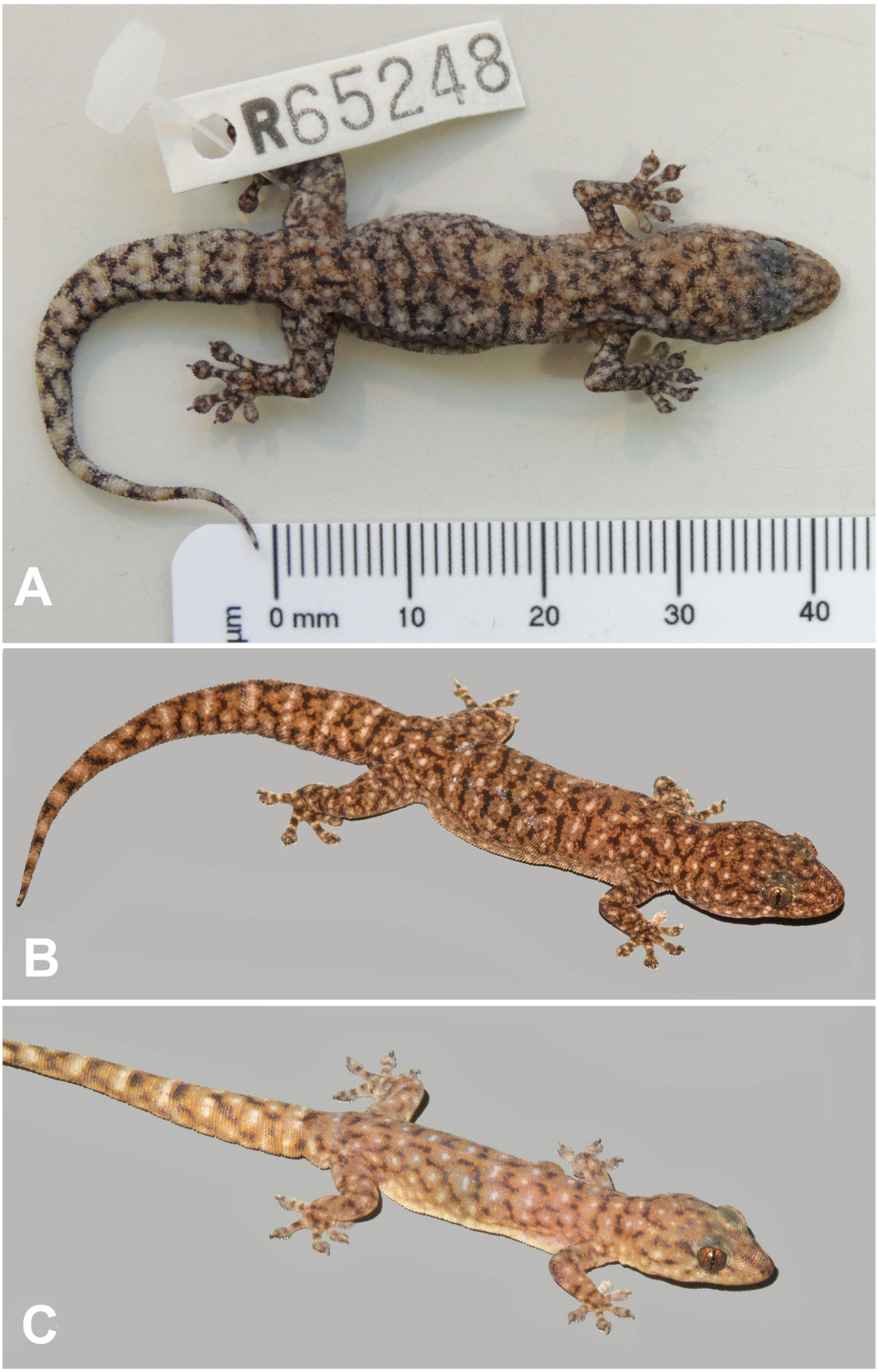

FIGURE 10. *Gehyra pulingka* **sp. nov**. A and B. Holotype, SAMA R65248, adult female from Umuwa, South Australia, showing a variant of the species' colour pattern with dense patterning of dark and light markings, shown as preserved and in life. C. Adult male, SAMA R61926, from Kutjurntari Waterhole, Western Australia, showing a sparse patterning of larger, more widely scattered light and dark markings.

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