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A new species of bandy-bandy (*Vermicella*: Serpentes: Elapidae) from the Weipa region, Cape York, Australia

CHANTELLE M. DEREZ[1], KEVIN ARBUCKLE[2], ZHIQIANG RUAN[3], BING XIE[3,4], YU HUANG[3,5], LAUREN DIBBEN[6], QIONG SHI[3,5], FREEK J. VONK[7,8] & BRYAN G. FRY[1,8]

[1]*Venom Evolution Laboratory, School of Biological Sciences, University of Queensland, St. Lucia, Qld 4067, AUSTRALIA*
[2]*Department of Biosciences, College of Science, Swansea University, Swansea SA2, 8PP, UK*
[3]*Shenzhen Key Lab of Marine Genomics, Guangdong Provincial Key Lab of Molecular Breeding in Marine Economic Animals, BGI Academy of Marine Sciences, BGI Marine, BGI, Shenzhen 518083, China;*
[4]*Institute of Biology Leiden (IBL), Leiden University, 2333 BE, Leiden, The Netherlands*
[5]*BGI Education Center, University of Chinese Academy of Sciences, Shenzhen 518083, China*
[6]*Ecotone Flora and Fauna Consultants, PO Box 9, Yungaburra, Qld 4884, Australia*
[7]*Naturalis Biodiversity Center,Darwinweg 2, Postbus 9517, 2300 RA Leiden, The Netherlands*
[8]*Corresponding authors. E-mail: bgfry@uq.edu.au, freek.vonk@naturalis.nl*

Abstract

Bandy-bandies (genus *Vermicella*) are small (50–100cm) black and white burrowing elapids with a highly specialised diet of blindsnakes (Typhlopidae). There are currently 5 recognized species in the genus, all located in Australia, with *Vermicella annulata* the most encountered species with the largest distribution. Morphological and mitochondrial analyses of specimens collected from the Weipa area, Cape York, Queensland reveal the existence of a new species, which we describe as *Vermicella parscauda* **sp. nov.** Mitochondrial DNA analysis (*16S* and *ND4*) and external morphological characteristics indicate that the closest relatives of the new species are not *V. annulata*, which also occurs on Cape York, but rather species from Western Australia and the Northern Territory (*V. intermedia* and *V. multifasciata*) which, like *V. parscauda,* occupy monsoon habitats. Internasal scales are present in *V. parscauda* **sp. nov.**, similar to *V. annulata*, but *V. intermedia* and *V. multifasciata* do not have nasal scales. *V. parscauda* **sp. nov.** has 55–94 black dorsal bands and mottled or black ventral scales terminating approximately 2/3^{rds} of the body into formed black rings, suggesting that hyper-banding is a characteristic of the tropical monsoon snakes (*V. intermedia*, *V. multifasciata* and *V. parscauda*). The confined locality, potential habitat disruption due to mining activities, and scarcity of specimens indicates an urgent conservation concern for this species.

Key words: Australian Monsoonal Tropics, mtDNA, taxonomy, *Vermicella parscauda* **sp. nov.**

Introduction

Vermicella are small (50–100cm), black and white banded burrowing oviparous elapid snakes, incorporating significant premaxilla and tooth reductions which are proposed as modifications for the stenophagous diet of blindsnakes (Typhlopidae) (Keogh *et al.* 1998; McDowell 1970; Sanders *et al.* 2008; Shine 1980). *Vermicella* are generally nocturnal hunters, following prey via a chemical trail and examinations of museum specimens show blind snakes of the genus *Anilios* as specialised prey (Shine 1980; Shine & Keogh 1996; Greenlees *et al*. 2005). The dorsal black and white bands are hypothesized by Shine (1980) to create a 'flicker fusion' effect confusing predators and allowing escape. In this study we compare the Cape York bandy-bandy (*Vermicella parscauda* **sp. nov.**) morphologically and genetically to other *Vermicella* species. This is the first study to look at the genetics of the *Vermicella* genus, with all extant species represented. We found the Cape York bandy-bandy to be morphologically and genetically distinct to currently recognized *Vermicella* taxon and therefore formally describe this novel taxon below.

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Material and methods

Morphology. We obtained external morphological data from two specimens, one collected by FJ Vonk and BG Fry in April 2014 and the other by LD in July 2016; and further examined two specimens already in museum collections. LD also provided photographs of two additional individuals previously encountered in January 2005 and December 2011 but not recognized at the time as a potentially new species and the photographs were uncovered in retrospective analyses of images from the region. The morphological dataset of *Vermicella* collected by Keogh and Smith (1996) was obtained for analytical comparison. Morphological data was collected by CD from an additional 35 preserved specimens of *V. intermedia* (n = 13), *V. multifasciata* (n = 6), *V. snelli* (n = 10) and *V. vermiformis* (n = 6), housed at Museum and Art Gallery of Northern Territory (MGNT) and Western Australian Museum (WAM) (Appendix I). Calipers were used to take head and body measurements in mm. Snout-vent length (SVL) was recorded by aligning a string along the ventral surface of the snake from the tip of the snout to the vent before transferring to a ruler for measurement.

Meristic measurements of each specimen and photographed individuals included the number of black bands/ white bands on the body and tail. Scalation characteristics of the two specimens were recorded following Keogh & Smith (1996) with definitions from Cogger (2014) and Maddock *et al.* (2015) (Table 1). For head measurements the right side of the animal was used. Missing scores for specimens were excluded in the analysis. Potential differences between the species were tested by ANOVA and significant results were further tested with a pot hoc Tukey analysis, with species as the independent variable. The two initial specimens were accessioned to the Queensland Museum (QM) upon completion of this study as specimens J95678 and J95679.

Molecular genetics. Mitochondrial DNA was extracted from muscle tissue for 23 *Vermicella* samples (Appendix I) using Isolate II Genomic DNA kit (Bioline, Australia) following standard kit directions. Small subunit ribosomal RNA (*16S*) and NADH-ubiquinone oxidoreductase chain 4 (ND4) were targeted as they are the most widely sampled genes for elapid snakes (Keogh *et al.* 1998; Maddock *et al.* 2015; Sanders *et al.* 2008, 2012; Ukuwela *et al.* 2013). The extracted DNA was isolated and amplified using a polymerase chain reaction (PCR) and a TaKaRa Ex Taq kit (Takara, USA), with a total volume of 25 mL. PCR reaction consisted of ddH_20 15.875 mL; buffer 2.5 mL; dNTPS + $MgCl_2$ 2.0 mL; primers x2 1.25 mL (Table 2); Taq 0.125 mL and DNA 2.00 mL. Amplification conditions involved an initial incubation period of 95°C for 3 min, 35 cycles of denaturing at 95°C for 45 s; annealing at 50°C for 50 s; extension at 72°C for 1min30s and concluding extension of 72°C for 5 mins to finalize each reaction. Sequencing was undertaken by BGI, Hong Kong. Genbank accession codes for the sequences are given in Table 3 along side the museum accession codes for the specimens examined.

Phylogenetic analysis. Additional *Vermicella* sequences from were obtained from GenBank (Appendix I), along with *Neelaps* to be used as the outgroup as it is from the same burrowing clade as *Vermicella* (Keogh 1999; Keogh *et al.* 1998). Sequences were edited, aligned by eye and concatenated in Geneious (version 10.05 http://www.geneious.com) (Kearse *et al*. 2012). Phylogenetic analyses were conducted in maximum likelihood (ML) and Bayesian inference (BI) frameworks using a general time reversible substitution model with rates, a gamma parameter for rate heterogeneity, and proportion of invariant sites estimated in analyses. This model was chosen as it is highly general and can incorporate a wide range of substitution patterns, which is advantageous for non-coding sequences such as those included here.

ML analyses were conducted in FastTree 2.1.10 (Price *et al.* 2010) with a combination of NNI and SPR search strategies and node support assessed with SH-like values. BI analyses were conducted using MCMC in MrBayes 3.2.6 (Ronquist *et al.* 2012) and summarized as a majority rule consensus tree with posterior probabilities as node support values. Four independent runs each including four chains were ran for 10,000,000 generations, sampled every 2000 generations, and the first 10% of samples were discarded as burnin. The temperature parameter was set to 0.2 and convergence was assessed using the standard deviation of split frequencies and log-likelihoods across runs. The phylogenies presented herein were prepared using FigTree 1.4.3.

Finally, evolutionary divergence between species was assessed in MEGA 7.0.26 (Kumar *et al.* 2016) by calculating the mean proportion of base differences per site between each species pair (and also between individual samples within each species) from the concatenated alignment.

TABLE 1. Morphological characters measured in this study.

Character	Description
ToL	Total body length, from snout to tail tip
SVL	Snout-vent Length, from anterior point of snout to posterior edge of anal scale
TailL	Tail length, from anterior edge of first subcaudal scale to tail tip
HeadL	Head length, from tip of snout to posterior margin of the quadrate
HeadW	Head width, widest point, posterior to eyes
HeadH	Head height, just posterior to the eye
SnoutL	Snout length, from anterior edge of the eye to anterior tip of nose
MouthL	Mouth length, from posterior corner of the mouth to anterior tip of nose
IN	Internasal scales, on top of snout between nasal scales, behind rostral scale
NOS	Position of nostril inside nasal scale
PreO	Preoccular scale, from front margin of the eye
PosO	Postoccular scale, region of head behind eye
AntT	Anterior temporal scales, between parietal scales and supralabials scales
PosT	Posterior temporal scales, vertical scales behind postoccular scales
SubLab	Supralabial scales, series scales on upper lip
InfLab	Infralabial scales, series of scales on lower lip
NeckH	Neck height, one head length posterior to the head
NeckW	Neck width, one head length posterior to the head
ED	Eye diameter, from left to right
VS	Ventral scales, counted from anterior ventral to anal scale
ScST	Subcaudal scales total, from first subcaudal posterior to vent to posterior most scale on tip, including paired scales
DSR	Dorsal scale rows, one head length posterior to the neck
MBSR	Dorsal scale rows, mid-body
VSR	Dorsal scale rows, one head length anterior to vent
MBW	Mid-body width
MBH	Mid-body height
VSW	Vent scale width

TABLE 2. Elapid snake primers used during PCR (Sanders *et al*. 2008).

Primer Name Primer (5'–3')
16s
M1272 CGCCTGTTTATCAAAAACAT
M1273 CCGCTCTGAACTCAGATCACGT
ND4
M245 TGA CTA CCA AAA GCT CAT GTA GAA GC
M246 TAC TTT TACC TTG GAT TTG CAC CA

TABLE 3. Genbank accession codes obtained in this study

Species	Museum voucher	Genbank
V. annulata	SAM_66008	16S = MH198560
V. annulata	SAM_66008	ND4 = MH198561
V. annulata	SAM_53540	16S = MH198562
V. annulata	SAM_53540	ND4 = MH198563

.....continued on the next page

TABLE 3. (Continued)

Species	Museum voucher	Genbank
V. annulata	SAM_50226	16S = MH198564
V. annulata	SAM_50226	ND4 = MH198565
V. annulata	SAM_24269	16S = MH198566
V. annulata	SAM_24000	16S = MH198567
V. intermedia	SAM_29783	16S = MH198552
V. intermedia	SAM_29783	ND4 = MH198553
V. intermedia	SAM_27282	16S = MH198554
V. intermedia	SAM_27282	ND4 = MH198555
V. intermedia	SAM_25672	16S = MH198556
V. intermedia	SAM_25672	ND4 = MH198557
V. intermedia	MGNT_35501	16S = MH198558
V. intermedia	MGNT_35501	ND4 = MH198559
V. multifasciata	MGNT_18760	16S = MH198550
V. multifasciata	MGNT_18760	ND4 = MH198551
V. multifasciata	*WAM*_156263	ND4 = MH198568
V. parscauda Nsp 1	QMJ95807	16S = MH198531
V. parscauda Nsp 1	QMJ95807	ND4 = MH198532
V. parscauda Nsp 2	QMJ95808	16S = MH198533
V. parscauda Nsp 2	QMJ95808	ND4 = MH198534
V. snelli	WAM_165995	16S = MH198540
V. snelli	WAM_165995	ND4 = MH198541
V. snelli	WAM_164336	16S = MH198542
V. snelli	WAM_164336	ND4 = MH198543
V. snelli	WAM_164326	16S = MH198544
V. snelli	WAM_164326	ND4 = MH198545
V. snelli	WAM_163637	16S = MH198546
V. snelli	WAM_163637	ND4 = MH198547
V. snelli	WAM_114082	16S = MH198548
V. snelli	WAM_114082	ND4 = MH198549
V. vermiformis	MGNT_36249	16S = MH198535
V. vermiformis	MGNT_36248	16S = MH198536
V. vermiformis	MGNT_36248	ND4 = MH198537
V. vermiformis	MGNT_36176	16S = MH198538
V. vermiformis	MGNT_35706	16S = MH198539

Results

Morphology. All specimens of *V. parscauda* **sp. nov.** had internasal scales present. Dorsal coloration starting at the tip of the nose to the tip of the tail shows 55–92 black bands and 54–95 white bands present in the 6 individuals. All individuals display white dorsal banding which do not fully surround the body, resulting in more complete black bands than white bands. White scales in the bands are either outlined in black or do not have a sharp boundary with dark scales (Figure 1). Ventral scales specimens ranged from 213–230 in the four specimens. Snout vent length (SVL) ranged from 267 mm to 357 mm indicating a small species within the *Vermicella* genus but further sampling is required to ascertain if this is a consistent trend. Specimen QM J95678 was damaged during the mining

workplace activities which uncovered it, which precluded several measurements such as head height, eye diameter and neck height. Two males were determined by the presence testes present in QM J95678 and everted formed hemipenes in QM J95679. Specimen CSIRO R02719 was the only female, identified by 3 egg follicles ranging from 1.53 mm to 2.49 mm. Tail lengths of 21 mm and 31 mm were recorded for the male specimens (7.61% and 8.68% of SVL) and 22mm (6.62% of SVL) for the female specimen. The last specimen (AM R94413) examined was not assigned a sex due to the damage the specimen would sustain but suspected to be a male, with a tail length of 7.86 % of the SVL. All specimen exhibited either mottled or dark ventrals that terminated to black rings on the underside of the body (3, 10, 10, 12 rings) and continued on the tail (7, 6 + 3 incomplete rings, 6, 7 respectively). Each black ventral ring covered 2–3 scales and 1–2 white scales in between the black rings. See Appendix II for full details.

FIGURE 1. Dorsal and head view of *Vermicella parscauda* **sp. nov.** holotype QM J95678. Male collected from boat ramp Weipa, Cape York, Queensland -12°31'53" S 141°50'51"E in August 2014 by FJ Vonk and BG Fry. Photos by FJ Vonk.

Molecular genetics. Molecular phylogenetic analyses recovered *V. parscauda* sp. nov. as a distinct and strongly supported monophyletic group sister to a clade containing both *V. multifasciata* and *V. intermedia* (Figure 2; sequences available via Genbank accession codes in Table 3). All other species were also recovered as strongly supported monophyletic entities except *V. intermedia* and *V. multifasciata*, which were strongly supported as a clade but not as two monophyletic groups within that clade. Thus further work is required to ascertain if *V. intermedia* and *V. multifasciata* are two distinct species or a single species with isolated populations due to vicariance events resulting in discontinuous tropical monsoon habitats.

Measures of genetic differentiation within and between species also support *V. parscauda* sp. nov. as a distinct species (Table 4). Intraspecific differentiation ranges from 0 to 0.013, whereas the interspecific differentiation ranges from 0.012 to 0.104 within the genus. Note that there is almost no overlap in intraspecific and interspecific differentiation, and the one interspecific value that causes slight overlap (0.012) is between *V. multifasciata* and *V. intermedia*, consistent with these two species not being recovered as distinct species in our phylogenies (Figure 2). The intraspecific differentiation of *V. parscauda* **sp. nov.** (0.002) is at the lower end of the range, whilst its interspecific differentiation includes the highest value measured (0.104) and its differentiation from its closest relatives (*V. multifasciata* and *V. intermedia*) is 0.038 and 0.039, three-fold higher than the highest intraspecific variance.

Specimen misidentifications. Five individuals examined during this study were diagnosed as misidentified *Vermicella* specimens based on morphological characteristics (Appendix III). Specimens AM R94413 and CSIRO R02719 labelled as juvenile *V. annulata,* match many of the characteristics of the new *Vermicella* species *V. parscauda* (band markings, band counts, head size, ventral scale count) in addition to both being from Weipa.

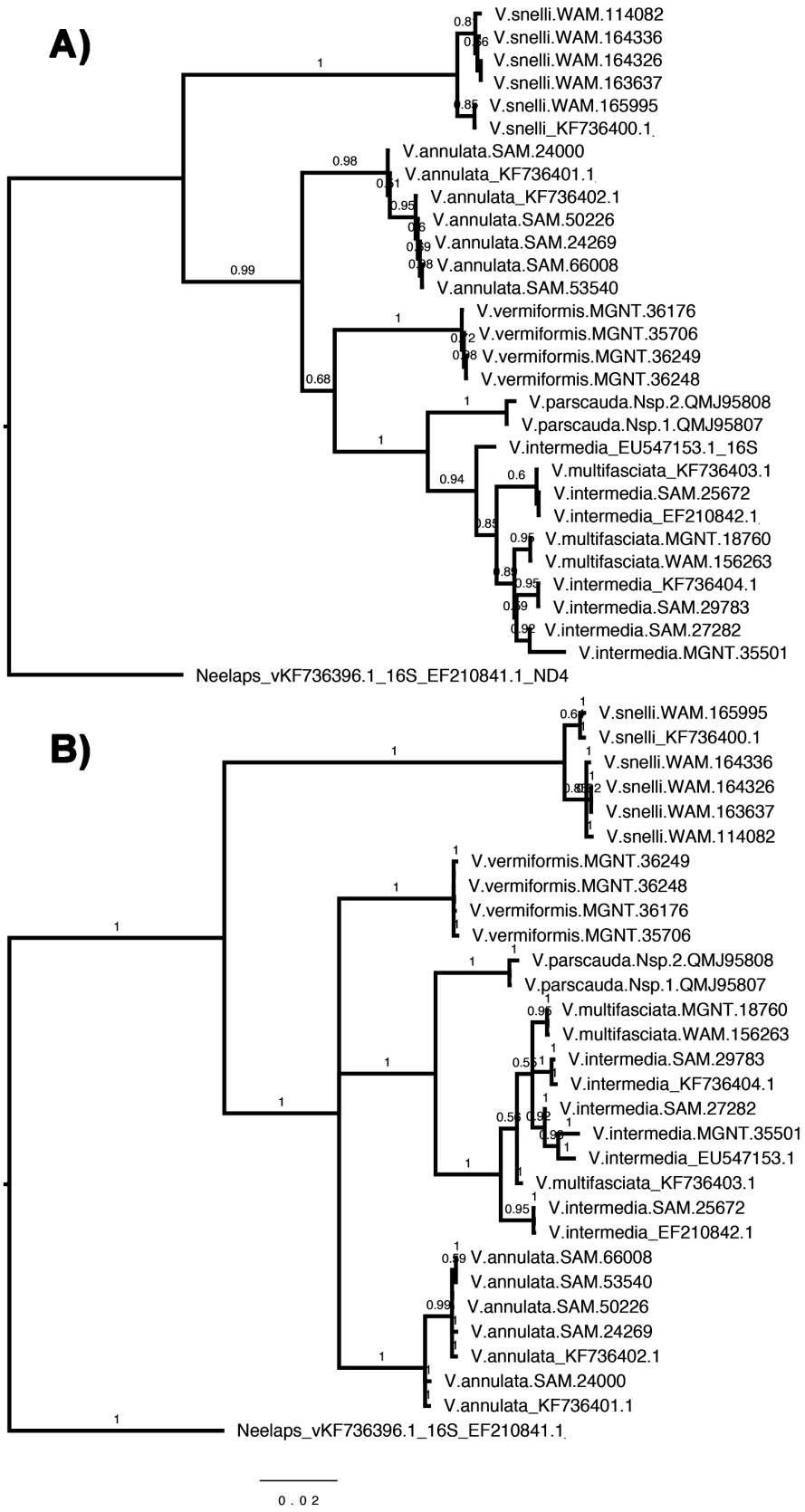

FIGURE 2. Phylogeny of *Vermicella* estimated from concatenated mitochondrial *16S* and *ND4* sequences using (A) ML and (B) BI. Node support values on each branch represent SH-like support and posterior probabilities for the ML and BI trees respectively. The BI tree is a majority rule consensus of the posterior distribution, such that nodes with posterior probabilities ≤0.5 are collapsed. Branch lengths represent expected substitutions per site. The trees were rooted using *Neelaps calonotos* as a designated outgroup.

Based on morphological characteristics of 80 black bands, specimens MGNT R37121 and WAM R156263 should be labeled as *V. multifasciata* instead of *V. intermedia*. Specimen MGNT R28112, currently listed as *V. multifasciata*, should be *V. intermedia* based on 63 black bands (Cogger 2014; Keogh & Smith 1996). This information was integrated into the dataset used by this study.

TABLE 4. Estimates of evolutionary divergence over sequence pairs between species*

	annulata	intermedia	multifasciata	*parscauda* sp nov	snelli
intermedia	0.05				
multifasciata	0.054	0.012			
parscauda **sp. nov.**	0.048	0.039	0.038		
snelli	0.07	0.09	0.096	0.104	
vermiformis	0.041	0.058	0.06	0.059	0.089

* The number of base differences per site from averaging over all sequence pairs between groups are shown. The analysis involved 30 nucleotide sequences. All ambiguous positions were removed for each sequence pair. There were a total of 1268 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [Kumar *et al*. 2016).

Discussion

Descriptions of each of the currently recognized *Vermicella* species can be found in Keogh and Smith (1996), with their study identifying two more species within *Vermicella*; *V. intermedia* and *V. vermiformis*, previously identified as variations of *V. multifasciata* and *V. snelli*. Four species (*V. annulata, V. intermedia, V. multifasciata*, and *V. vermiformis*) all occur in delineated distributions across the tropical monsoon zone and *V. annulata* has the largest distribution, found across many habitats in northern and eastern Australia, including Cape York (Figure 3). Molecular phylogenetic analysis supports vicariant speciation events in Australia as a response to barriers, like the Carpentarian Gap and the Great Dividing Range which runs down Cape York Peninsula, dividing two biomes, resulting in colder climates on the ridge which may exclude reptiles and thus preclude genetic exchange between east and west coast (Bowman *et al.* 2010; Marin *et al.* 2013). Two specimens found on the west coast of Cape York were previously identified as juvenile *V. annulata* but have now been identified as part of the new taxon *V. parscauda*, suggesting *V. annulata* may be restricted to the east of the Great Dividing Range on Cape York and the new taxon to the west. Specimen MGNT R37121 from Bathurst Island, within the Tiwi Islands of Northern Territory is now identified as *V. multifasciata*, removing *V. intermedia* from species found on the islands, however *V. multifasciata* has been recorded on a neighboring island (Atlas of Living Australia 2016). Based on genetics, habitat and morphology, the basal hyper-banded monsoon specialist form is represented by *V. parscauda,* with *V. intermedia/V. multifasciata* subsequently evolving due to isolation as a consequence of ecological vicariance events resulting the once continuous northern tropics becoming isolated zones. Internasals were lost in the common ancestor of *V. intermedia* /*V. multifasciata* prior to population isolations as a consequence of ecological vicariance events splitting the tropical monsoon habitats.

Comparison with other *Vermicella* species. *V. parscauda* **sp. nov.** has internasals present like *V. annulata* however band/head characteristics are more similar to *V. intermedia* and *V. multifasciata* (Table 5). Using a Tukey post hoc test*, V. parscauda* **sp. nov.** showed a difference in the number of black bands when compared to all *Vermicella* species (Tukey F = 0.001, P = <0.001), with slightly less difference compared to *V. snelli,* which has the closest number of black bands (Tukey F = 0.02065, P = <0.01). *Vermicella parscauda* **sp. nov** has a larger number of black and white bands than *V. annulata* (ANOVA, F=0.00568, P = <0.01). Snout vent length for *V. parscauda* **sp. nov.** was smaller than other *Vermicella*—roughly 23% smaller than the largest species *V. annulata* and 9% smaller than *V. multifasciata*, the previously smallest species within the genus. However examination of further specimens will be required to confirm this trend.

As there was only 1 female out of the 4 individuals examined of *V. parscauda* **sp. nov.**, and ages unknown for all, it remains unknown if this species is sexually dimorphic. Females attaining larger body size has been shown for *V. annulata* (Shine 1980) and *V. intermedia* (Keogh & Smith 1996). In addition, fossorial species have shorter tails than snakes occupying other ecological niches, tail length dimorphism persists (King 1989). *Vermicella*

multifasciata and *V. snelli* were shown to have a distinct tail to body ratio that does not overlap between the sexes and is larger in males (Clarke & How 1995). However this was prior to the species separation of *V. multifasciata* and *V. snelli* into *V. intermedia, V. multifasciata, V. snelli* and *V. vermiformis* and thus the data may be a species mixture. Keogh & Smith (1996) showed males having larger tail ratio is still true for *V. snelli* and *V. vermiformis* but this has not been tested for *V. multifasciata.* Keogh & Smith (1996) found the proportional tail length to be the highest in the sexual dimorphic *V. annulata* with males averaging tails 7.63% of body length and females 6.14% of body length. In the current study with 4 *V. parscauda* **sp. nov.** individuals shows a mean of 8.05% for males and the single female's ratio of 6.62%. While these results indicate *V. parscauda* **sp. nov.** may have the amongst longest relative tail length within the genus, more specimens would need to be examined to support this. The ring count on the underside of the body, ranging from 9–17 black rings was not identified different due to sex of the individual as the single female count was within the range of the males.

Vermicella parscauda **sp. nov.** also exhibits a low number of ventral scales 222 ± 9, which is fixed at birth (Aubret *et al.* 2004) and lower than all species (ANOVA, F = 0.433, P = <0.001) except *V. annulata* (ANOVA, $F_{1.5}$ = 211.8, P = 0.433) which for this study showed a mean of 220 ventrals (N = 355), differing by 3 ventrals more when compared to Keogh & Smith (1996). As *V. annulata* is the largest growing species within the *Vermicella* genus but has the least amount of ventral scales, these results do not support the findings of Lee *et al.* (2016a) who found in a general population trend of nightsnakes (Genus: *Hypsiglena*), those with higher number of ventral scales grow larger than conspecifics. *Vermicella intermedia* has 251 ± 5 ventral scales and *V. multifasciata* has 268 28 ventral scales, resulting in similar figures to Keogh & Smith (1996) and an 8.6% and 8.3% higher difference when compared to *V. parscauda* **sp. nov.** When comparing ventral scale counts of all species, there is overlapping ranges, suggesting this may not be a reliable characteristic to identify each species alone.

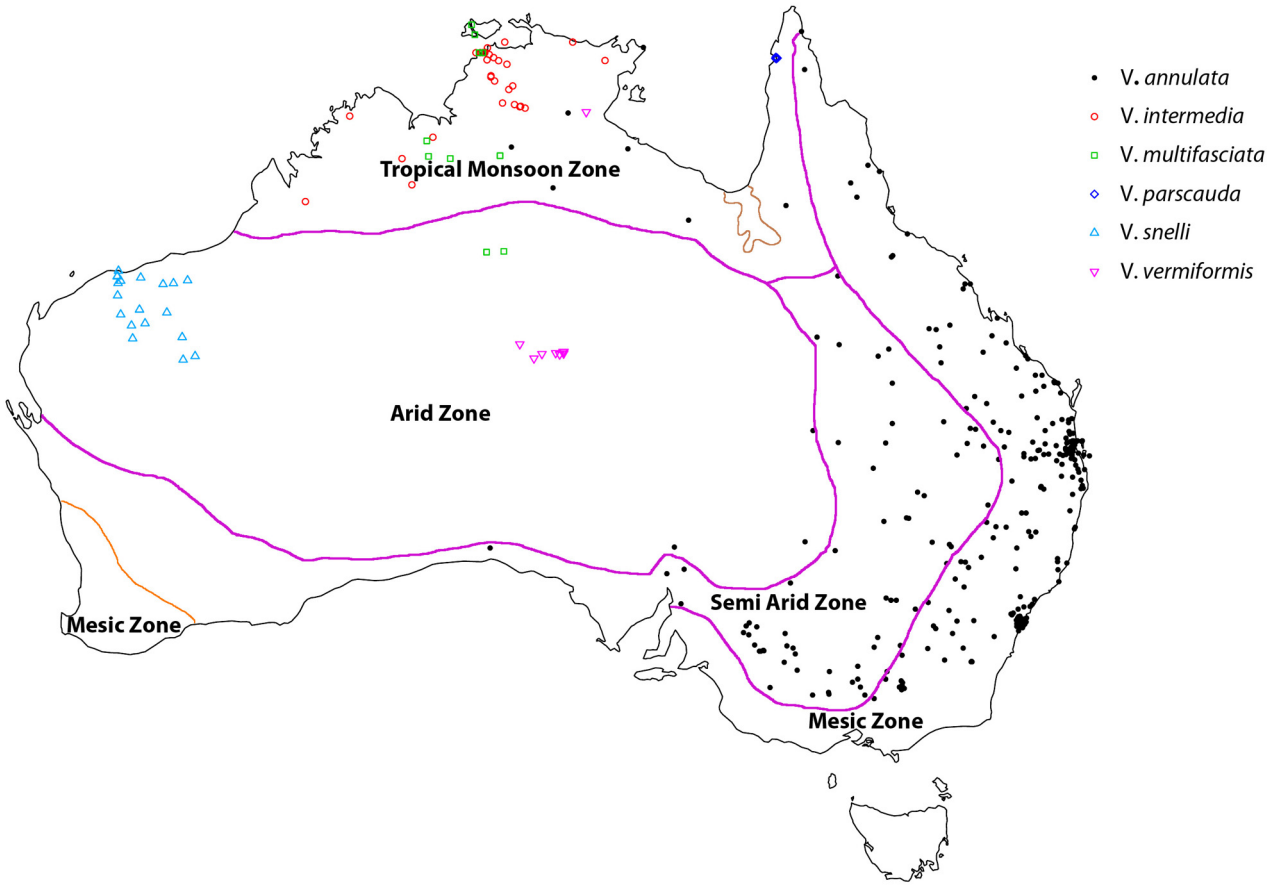

FIGURE 3. Localities of examined *Vermicella* specimens, including the new species *Vermicella parscauda* ***sp. nov.***. Climatic zones outlined in yellow adapted from Marin *et al*. (2013), indicating geographic barriers and the Carpentarian Gap outlined in brown, as a potential geographic barrier to Cape York (Bowman *et al.* 2010).

Vermicella parscauda **sp. nov.** *, V. annulata*, *V. snelli* and *V. vermiformis* all exhibit internasal scales, which are absent in *V. intermedia* and *V. multifasciata.* However, like *V. parscuada, V. intermedia/V. multifasciata* are hyper-banded specialists for the northern tropical monsoon zones, with *V. intermedia/V. multifasciata* occurring in the tropical monsoonal zone of Western Australia and Northern Territory while *V. parscauda* is known only form the northern monsoon zone of Cape York. Head length and head width average showed similarities between *V. parscauda* **sp. nov.** to *V. multifasciata* and *V. snelli* (Table 5) and just under half the head length of *V. annulata* (ANOVA, $F_{5,441} = 20.37$, $P = < 0.01$) and head width (ANOVA, $F_{5, 438} = 14.28$, $P = < 0.05$).

Previously Keogh & Smith (1996) examined the holotypes QM J 192 of *V. latizonatus* (DeVis, 1905) 'possibly from Herberton', Queensland and AM R 131709 of *V. lunulata* (Krefft, 1869) from near Townsville, Queensland and found them be variations of *V. annulata*, disregarding the resurrection of the two species by Wells & Wellington (1983). The locations of these specimens are not on the Cape York peninsula and photographs of the specimen QM J 192 on the database website Atlas of Living Australia (2017) show an individual with *V. annulata* band characteristics. We therefore conclude *Vermicella parscauda* **sp. nov.** is a new species and not a previous species to be resurrected.

TABLE. 5. Summary of characters and ratios measured for analysis of *Vermicella* genus. All measurements in mm. Mean±S.D. (range). Number of specimens examined. Internasals present (p)/absent (a). SVL = Snout Vent Length, TL = Tail Length, HL = Head Length, HW = Head Width, VS = Ventral Scales. Sample size listed for each character.

	V. parscauda **sp. nov.**	*V. annulata*	*V. intermedia*	*V. multifasciata*	*V. snelli*	*V. vermiformis*
Character	N = 4-6	N =332–356	N = 47–49	N = 11	N = 19–21	N = 19
Black body bands	70 ± 18 (52–87) N = 6	36 ± 1 (35–37) N = 352	53 ± 3 (50–56) N = 49	93 ± 17 (776119) N = 11	56 ± 8 (48–64) N = 21	43 ± 3 (40–46) N = 19
White body bands	70 ± 19 (51–89) N = 6	37 ± 1 (36–38) N = 352	53 ± 3 (50– 53) N = 48	93 ± 16 (77–109) N = 11	56 ± 8 (48–64) N = 21	43 ± 2 (41–45) N = 19
Internasals	p	p	a	a	p	p
SVL	318 ± 47 (271–364) N = 4	412 ± 21 (391–433) N = 356	375 ± 33 (342–408) N= 48	346 ± 66 (280–412) N = 11	347 ± 47 (300–395) N = 21	394 ± 67 (327–462) N = 19
TL	25 ± 5 (20–30) N = 4	28 ± 1 (27–29) N = 351	22 ± 2 (20–24) N = 48	20 ± 4 (16–24) N = 11	17 ± 3 (14–20) N = 21	24 ± 5 (20–29) N = 19
HL	7 ± 1 (6–8) N = 4	13 ± 1 (12–14) N= 347	9 ± 1.0 (8–10) N = 48	8 ± 1 (7–9) N = 11	7 ± 1 (6–8) N = 20	10 ± 1 (9–11) N = 19
HW	4 ± 2 (2–6) N = 4	7 ± 1 (6–8) N = 346	5 ± 1 (4–6) N = 47	4 ± 1 (3–5) N =11	4 ± 1 (3–5) N = 19	5 ± 1 (4–6) N = 19
VS	222 ± 9 (213–231) N = 4	218 ± 2 (216–220) N = 355	251 ± 5 (246–256) N = 48	268 ± 28 (240 –296) N = 11	282 ± 20 (262–302) N = 21	272 ± 9 (263–281) N = 19

Genetics

Vermicella. parscauda **sp. nov.** is supported as a distinct clade in our phylogenetic analyses and exhibits patterns of intraspecies and interspecific genetic differentiation consistent with other species in the genus, corroborating the morphological distinction of the new species.

The mitochondrial phylogenies show *Vermicella parscauda* **sp. nov.** is most closely related to *V. intermedia* and V. *multifasciata*, found in the Northern Territory/Western Australian, than to the widely distributed *V. annulata* that also occurs on Cape York (Figure 3). The phylogenetic relationships we found were consistent with those found by Lee *et al.* (2016b) for species included in that study (the only previous study to include most *Vermicella* species). It is notable that *V. intermedia* and *V. multifasciata* were not recovered as two distinct reciprocally monophyletic species, however the relationships within this clade are not strongly supported. Nevertheless, this result is consistent with the patterns of genetic differentiation in these two species, which are only differentiated

from each other to a degree typical of intraspecific variation in this genus, and also with the overall morphological similarity which has led to taxonomic confusions (see 'Specimen Misidentifications' above). Hence, we suggest that sampling of additional genes and specimens of *V. intermedia* and *V. multifasciata* is worthwhile to confirm the validity of *V. intermedia* as a distinct species or if *V. multifasciata* occupies disjunct populations due to ecological vicariance events causing a discontinuity of the tropical monsoon ecology.

These results suggest the hypothesis that *Vermicella* may have radiated from Cape York before vicariance occurred between Queensland and Northern Territory, also supporting the hypothesis that colonization of Australian elapid snakes occurred from a single Melanesian ancestor (Keogh *et al*. 1998 ; Grundler & Rabosky 2014).

Systematics

Vermicella parscauda sp. nov.

Holotype. QM J95678, large male collected from boat ramp Weipa, Cape York, Queensland 12°31'53" S 141°50'51"E in August 2014 by B.G. Fry and F.J. Vonk. Fixed in 10% formalin, stored in 70% ethanol at QM.

Paratypes. QM J95679, small male squashed during mining company workplace activities, Evans Landing, Weipa, Qld (1240'21"S, 14152'09"E); AM R94414, unsexed individual, Mission River, Weipa, Qld (1240'59"S, 14152'59"E); CSIRO R02719, adult female, Rocky Point, Weipa, Qld (1237'00"S, 14152'00"E).

Diagnosis. A small *Vermicella* to total 388 mm in length. Distinguished from all other Australian *Vermicella* by a combination of 55–92 black bands, white bands mottled posterior of scale, SVL 267–357 mm, tail length 21–31 mm, 213–230 ventral scales, head length 5–8 mm, head width 3–5 mm and present internasal scales (Figure 1). Ventrals dark black or mottled with distinct black rings on the posterior body and tail, each ring covering 2–3 divided caudal scales and 1–2 white divided caudal scales in between the black rings.

Description of holotype (QM J95678). Measurements and counts: ToL 388mm; SVL 357; TaiL 31 mm (8.68% of SVL); HeadL 8mm; HeadW 4mm; HeadH 4mm; SnoutL 4mm; MouthL 6mm; ED 0.9mm; NeckH 4.5mm; NeckW 3mm; MBW 5mm, MBH 5.5mm, VS 230; VSW 4mm. Internasals present with undivided nasal scales, 6 supralabials, 6 infralabials, 0 anterior temporals, 3 posterior temporal scales. Fifteen dorsal scale rows present along the body, 27 total divided subcaudal scales and a ventral scale width of 4mm. Colouration: Neck scales: 6 black scales, 2 white scales; mid body scales: 5 black scales, 1 white scale; vent scales 5 black, 1 white scale. Ventral view mottled black for 2/3^{rds} of body, ending with 17 black rings; 8 on the body and 9 on the tail.

Coloration. Colour and pattern of dorsal and lateral surfaces of live specimen alternate black and white bands. White banding begins on the head including white markings classed as bands on the nasal scales and parietal scales. White bands are 1–2 white scales wide with mottling around each white scale resulting in white bands of smaller width that do not have a defined edge. Dark or mottled ventrals that terminate to black rings. Frozen and preserved specimens lose the white vibrancy, resulting in a yellowish tinge and brownish bands under light.

Variation. SVL up to 357 mm; TailL 6–8% of SVL, mean 7% (N=4); 213–230 Ventral scales (N=4), Ventrals dark or mottled with 3–10 distinct posterior black rings terminating to 6–7 rings on the tail (N=4). The ring count on the underside of the body was not identified different due to sex of the individual as the single female count was within the range of the males.

Distribution and habitat. *V. parscauda* may to restricted to the Western side of Cape York as current individuals were all found between the Weipa (museum specimens AM R94413, CSIRO R02719, QM J95678 and QM J95679) and Mapoon areas (photographed individuals). The surrounding vegetation is woodlands dominated by *Eucalyptus tetrodonta* and *Eucalyptus miniata*, with the soil classed as deep or gradational soils of red massive earth with concretions (Fox *et al*. 2001).

Comparison with other species.

- *Vermicella parscauda* **sp. nov.** is considered geographically distant from other *Vermicella* species and show the following morphological differences:
- *V. annulata* (Grey, 1841) has the largest distribution through NT, QLD, NSW, VIC and SA, including Cape York), white bands can be larger (1–4 scales vs. 1–2) with a distinct edge and often a larger SVL (155–760mm vs. 267–357mm).

- *V. intermedia* (Keogh & Smith, 1996), from northern WA to northern NT, has fewer black bands (37–65 vs. 55–92) and no internasal scales.
- *V. multifasciata* (Longman, 1915), from north-eastern WA to northern NT, including Tiwi Islands, has no internasal scales and more ventral scales (231–350 vs. 213–230).
- *V. snelli* (Storr, 1968) from Pilbara region of WA, with a smaller tail length (9–23mm vs. 21–31mm) and normally higher ventral scale count (173–315 vs. 213–230).
- *V. vermiformis* (Keogh & Smith, 1996) from a localized population in southern Arnhem Land in NT and central Australia, lower number of black rings (38–51 vs. 55–92), with more ventral scales (253–303 vs. 213–230) and ring patterning on ventral scales.

Etymology. The specific epithet is modified from the Latin words *pars* (part) and *cauda* (tail) in reference to the tail length and formed bands on the tail.

Conservation Status. Only 6 individuals of *Vermicella parscauda* **sp. nov.** have been recorded and the presumed habitat on Cape York is the site of broad-scale mining. Activities that disturb the soil, such as commercial digging for mining purposes, may adversely affect *V. parscauda*, given the burrowing behavior of the *Vermicella* genus. A detailed assessment on abundance, distribution and potential threats to the species will clarify the need for listing by the International Union for Conservation of Nature (IUCN) as a species requiring protection under legislation.

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