Article

A new species of scincid lizard in the genus *Caledoniscincus* (Reptilia: Scincidae) from northwest New Caledonia

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Abstract

A new species of skink in the genus *Caledoniscincus* is described from the northwest region of New Caledonia. It is known from two locations, one on the coast at Pointe de Vavouto north of Koné, the other on the slopes of the Massif d'Ouazangou, an isolated mountain 30 km to the north. Typical of all members of the genus, adult males and females of the new species are sexually dichromatic. The new species, *Caledoniscincus constellatus* **sp. nov.**, has a bold, white midlateral stripe, a feature which distinguishes it from most other species of *Caledoniscincus* except the regionally sympatric *C. haplorhinus* (Günther) and *C. austrocaledonicus* (Bavay), from which it can be distinguished by a unique pattern of contact between the pale midlateral stripe and the ear. DNA sequence data for the ND2 mitochondrial gene identifies a high level of genetic differentiation between the new species and all other *Caledoniscincus*, further supporting its distinctiveness as an independent evolutionary lineage. The species is of high conservation concern given its restricted distribution in a region that has been, and will continue to be, heavily impacted by human occupation, and would be ranked as Critically Endangered under IUCN criteria.

Key words: New Caledonia, Scincidae, Endangered

Résumé

Une nouvelle espèce de scinque du genre *Caledoniscincus* est décrite du nord-ouest de la Nouvelle-Calédonie. Elle est à présent connue de deux localités, l'une côtière à la Pointe de Vavouto au nord de Koné, l'autre sur les pentes du Massif d'Ouazangou, une montagne isolée située 30 km plus au nord. Comme tous les autres membres du genre, les mâles et les femelles adultes de cette nouvelle espèce sont sexuellement dichromatiques. La nouvelle espèce, *Caledoniscincus constellatus* **sp. nov.**, présente une bande médio-latérale nette ; cette caractéristique la différencie de la majorité des autres espèces de *Caledoniscincus*, sauf des deux espèces sympatriques régionales *C. haplorhinus* (Günther) and *C. austrocaledonicus* (Bavay), desquelles elle peut cependant être distinguée par son patron unique de contact entre la bande médio-latérale pâle et l'oreille. Les données concernant l'ADN séquencé pour le gène mitochondrial ND2 permettent de mettre en évidence un niveau élevé de différentiation génétique entre la nouvelle espèce et tous les autres *Caledoniscincus*, confortant ainsi son statut de lignée évolutive indépendante. L'espèce présente un statut de conservation particulier du fait de sa répartition limitée dans une région qui a été et qui continue d'être largement impactée par l'occupation humaine, ce qui la place dans la catégorie '*en danger critique d'extinction*' selon les critères de l'UICN.

Introduction

The last 25 years has seen a dramatic increase in the richness and diversity of the New Caledonian scincid lizard fauna, with over half of the 50 described species first recognized in this period. In particular, field studies undertaken between 2001 and 2003 in the central-west and north-west regions of the Grande Terre (Whitaker *et al.* 2004), an area dominated by a chain of isolated, near-coastal, ultramafic massifs, nearly all of which had never been investigated for lizards, proved to be exceptionally rich in new species.

One of the features to emerge from this recent phase of investigation is the extent of regional and narrow-range endemism in the skink fauna of the territory. Some of the recently described skinks from these western ultramafic ranges have distributions that span two or more massifs (*Kanakysaurus zebratus*—Sadlier *et al*. 2009a) and sometimes extend into adjacent non-ultramafic habitats (*Kanakysaurus viviparus*—Sadlier *et al*. 2004a, 2009b), but the majority have very narrow ranges and appear to be restricted to single massifs (*Nannoscincus manautei* and *Lioscincus vivae*—Sadlier *et al*. 2004b; *Marmorosphax* three species—Sadlier *et al*. 2009). This has also been the case for some diplodactylid geckos, and is typified in the recognition of nine new species in these regions in the newly created *Dierogekko* and *Oedodera* (Bauer *et al*. 2006a, 2006b), most of which are restricted to a single massif. As such, the presence of a number of endemic species in the central-west/north-west ultramafic region identifies this as distinctive biogeographic zone for lizards.

Caledoniscincus is the most diverse of the New Caledonian skink lineages. The genus contains a suite of several wide-ranging taxa, *C. austrocaledonicus*, *C. haplorhinus*, *C. atropunctatus* (Roux), and *C. festivus* (Roux), and a number of recently recognized regionally endemic species (Sadlier *et al*. 1999; Bauer & Sadlier 2000). Most of the restricted-range species occur in the central and northern regions of Grand Terre in forested habitats on the ranges and adjacent lowlands of the Chaîne Centrale: *C. cryptos* Sadlier, Bauer & Colgan, *C. renevieri* Sadlier, Bauer & Colgan, *C. chazeaui* Sadlier, Bauer & Colgan in the central-eastern region; *C. aquilonius* Sadlier, Bauer & Colgan in the north-east and north-west regions; and *C. auratus* Sadlier, Bauer & Colgan in the north-west and central-west regions. By contrast, only a single undescribed species is endemic to southern Grande Terre (Sadlier *et al*. in prep.), and one, *C. bodoi* Borner, to Ile des Pins. The new species described has a localized distribution in the north-west and central-west regions. It differs from the other restricted range species of *Caledoniscincus* in habitat preference, being known only from seasonally dry sclerophyll forests and shrubland of maquis and *Acacia* on both ultramafic and non-ultramafic surfaces.

Material and methods

Acronyms: Specimen abbreviations are prefixed as follows: AMS Australian Museum, Sydney; MNHN Museum National d'Histoire Naturelle, Paris; QM Queensland Museum, Brisbane; CAS California Academy of Sciences, San Francisco..

Measurements: The following characters were scored for each specimen where possible: snout to vent length—measured from tip of snout to caudal edge of anal scales; axilla to groin distance —measured from middle of base of the forelimb to middle of base of hindlimb; forelimb to snout length—measured from tip of snout to middle of base of forelimb; hindlimb length - measured from middle of base of hindlimb to tip of fourth toe including nail; tail length—measured from caudal edge of anal scales to tip of tail, on complete original tails only. Body measurements are expressed as percentages of snout to vent length (SVL) in the taxon accounts.

Scalation: Terminology for head scalation follows Sadlier (1987). For characters used in Table 1 the abbreviation is given in parentheses: midbody scale rows (MBR)—number of longitudinal scale rows around body counted midway between axilla and groin; dorsal scale rows (DSR)—number of scales in a row from first scale posterior to parietal scale to last scale at the level of vent opening; fourth finger (FFS) and toe (FTS) scales—umber of dorsal scales on fourth digit of hand and foot, distal scale contains claw and basal scale broadly contacts adjacent basal scale of third finger or toe; fourth finger (FFL) and toe (FTL) lamellae - number of ventral scales on fourth digit of hand and foot, distal scale contains claw and basal scale is last largely undivided scale at a point level with intersection of third and fourth digits. Bilateral scalation characters were scored on both sides and the mean value used; in the holotype description these values are presented as left/right values. Variation between species and populations was assessed using independent two-sample *t*-tests for size and scalation characters.

Osteology: Specimens were *X*-rayed to determine the number of premaxillary teeth, presacral and postsacral vertebrae, and the phalangeal formulae for the manus and pes; other skeletal details were determined by dissection. Molecular Phylogenetics: We obtained sequence data from a 514 bp fragment of the mitochondrial NADH dehydrogenase 2 (ND2) gene. Four specimens from Pointe de Vavouto initially determined on morphological criteria as *Caledoniscincus* sp., and 20 samples representing all described species of *Caledoniscincus* constituted the ingroup. Outgroups were selected on the basis of a broader phylogenetic analysis of New Caledonian skinks by Smith *et al*. (2007) and sequences for these were obtained from Genebank.

Total Genomic DNA was isolated from liver or skeletal muscle specimens stored in 95% ethanol using the Qiagen DNeasy™ tissue kit (Valencia, CA, USA). The target gene was amplified using a double-stranded Polymerase Chain Reaction (PCR). Included in the reaction were 2.5 µl genomic DNA, 2.5 µl light strand primer MET F6 L4437 5'-AAGCTTTCGGGCCCATACC-3' (Macey *et al*., 1997), 2.5 µl heavy strand primer TRP R3 H5540 5'-TTTAGGGCTTTGAAGGC-3' (Macey *et al*., 1997), 2.5 µl dinucleotide pairs, 2.5 µl 5x buffer, MgCl 10x buffer, 0.18 µl Taq polymerase, and 9.82 µl H$_2$O. All reactions were executed on an Eppendorf Mastercycler gradient thermocycler under the following conditions: initial denaturation at 95ºC for 2 min, followed by a second denaturation at 95ºC for 35 s, annealing at 50-54ºC for 35 s, followed by a cycle extension at 72ºC for 35 s, for 31 cycles. PCR products were visualized on 1.5% agarose gel electrophoresis.

PCR products were purified using AMPure magnetic bead solution (Agentcourt Bioscience, Beverly, MA, USA) to remove any impurities in the PCR products. Purified PCR products were then sequenced using DYEnamic™ ET Dye Terminator kit (GE Healthcare, Piscataway, NJ, USA). Products were purified using a Cleanseq magnetic bead solution (Agentcourt Bioscience, Beverly, MA, USA). Purified sequence reactions were analyzed using an ABI 3730XL automated sequencer. Sequences were analyzed from both the 3' and the 5' ends independently. Both the contiguous and the complimentary strands were uploaded and edited in Genious™ version 5.4 (Drummond *et al*. 2011), ambiguous bases were corrected. After editing the sequences they were initially aligned by eye. MacClade v4.08 (Maddison & Maddison 2005) was used to check for premature stop codons and to ensure that the alignment was in the correct amino acid reading frame.

For our phylogenetic analyses we applied a pluralistic approach using both model-based (Maximum Likelihood-ML and Bayesian Inference-BI) and character-based methods (Maximum Parsimony-MP). MP was implemented in PAUP* v4.0 (Swofford 2002). The heuristic search algorithm was used with a starting tree obtained by stepwise addition. One thousand random addition replicates were carried out with a TBR branch swapping algorithm. Branch lengths of zero were collapsed to yield polytomies and gaps were treated as missing data. Bootstrap support values (Felsenstein 1985) for nodes in MP trees were calculated using 1000 pseudo-replicates each including 50 random addition-sequence replicates.

The Akakine Information Criterion (AIC) as implemented in ModelTest v3.7 (Posada & Crandall 1998) was used to calculate the best-fit model of evolution for both ML and BI. For both model-based approaches we partitioned our data set by codon position. The General Time Reversal (GTR) plus (I) for proportional sites plus (G) for gamma distribution among site variation was applied for all codon positions

Maximum Likelihood analysis was performed using RAxML HPC v7.2.3 (Stamatakis *et al*. 2008). The analysis was performed using the above model of evolution. Gaps were treated as missing data and for clade confidence we applied 1000 bootstrap pseudoreplicates via the rapid hill-climbing algorithm (Stamatakis *et al.,* 2008).

The Bayesian analysis was carried out in MrBayes v3.1 (Huelsenbeck & Ronquist 2001; Ronquist & Huelsenbeck 2003) using default priors. The GTR+I+G model was applied to each codon position. Two simultaneous runs were performed with 4 chains per run, three hot and one cold following default settings. The analysis was run for 10,000,000 generations and sampled every 1000 generations from the Markov Chain Monte Carlo (MCMC). The analysis was halted after 10,000,000 generations if the average standard deviation split frequency was below 0.01. The program Are We There Yet? (AWTY) (Nylander *et al*. 2008) was used to plot the log likelihood scores against the number of generations to assess convergence and to determine the appropriate burn-in. A consensus tree from the two runs was built using TreeAnnotator v1.6.1 (Drummond & Rambaut 2006). Nodes that had posterior probabilities above 0.95 were considered significantly supported.

The following species and specimens of *Caledoniscincus* were used in the genetic analyses: *Caledoniscincus* **sp. nov.** AMS R171470, R171496-97 Pointe de Vavouto; *Caledoniscincus* sp. AMS R172613 Mt Humbolt; R172648 Yaté Barrage; *Caledoniscincus auratus* AMS R157910 Forêt Tia, R144298 (holotype) Grottes de Koumac; *Caledoniscincus cryptos* AMS R135141 Col d'Amieu; *Caledoniscincus chazeaui* AMS R138515 Koulnoué; *Caledoniscincus terma* CAS 198680 Mt Mandjélia; *Caledoniscincus aquilonius* CAS 231935 Riviére Nehoué, AMS R150712 Hienghène; *Caledoniscincus orestes* AMS R149926 Mé Adéo, AMS R149983 Mt Panié; *Caledoniscincus festivus* AMS R161882 Kwa Né Mwa, AMS R165885 Pouembout; *Caledoniscincus haplorhinus* AMS R161077 Ile Art, CAS 231888 Ilot Brosse; *Caledoniscincus austrocaledonicus* AMS R153713 Mt Taom, AMS R172661 Chutes de la Madeleine.

Results

Tests for differences in scalation between the new species of *Caledoniscincus* and four populations of *C. haplorhinus* (the species with which it is most likely to be confused) showed significant differences (P<0.05) in number of scales above ($\bar{x}$ = 18 *vs* 16.7, t_{68} = 2.632, P = 0.010) and below ($\bar{x}$ = 31.9 *vs* 27.7, t_{69} = 2.219, P = 0.030) the longest (4th) digit of the pes (Table 1), although these characters show some degree of overlap in the range of values, and in the number of midbody scale rows ($\bar{x}$ = 28.5 *vs* 29.9, t_{69} = -2.460, P = 0.016). However, a comparison of the new species and syntopic *C. haplorhinus* (n = 6) on Pointe de Vavouto failed to support this level differentiation for these characters.

TABLE 1. Values for number of midbody scale rows (MBR), dorsal scale rows (DSR), fourth finger (FFS) and toe (FTS) scales, and fourth finger (FFL) and toe (FTL) lamellae between samples of *Caledoniscincus constellatus* **sp. nov.**, *C. haplorhinus* from the west coast of New Caledonia (five separate populations including the sympatric population from Pointe de Vavouto) and for the syntopic population of *C. haplorhinus* from Pointe de Vavouto. Significant differences in character values between taxa (P values) relate to independent *t*-tests between samples of *C. constellatus* **sp. nov.** and *C. haplorhinus* (five separate populations), and between *C. constellatus* **sp. nov.** and the sympatric population from Pointe de Vavouto only.

.	*C. constellatus* **sp. nov.** Pointe de Vavouto N = 4	*C. haplorhinus* west coast N.C. N = 61	*C. haplorhinus* Pointe de Vavouto N = 6
MBR			
range	28–30	28–30	28–30
mean ± sd	28.5 ± 1.00	29.9 ± 1.09	29.0 ± 1.09
		t_{69} = -2.460 P = **0.016**	t_8 = -0.730 P = 0.486
DSR			
range	61–65	59–67	61–66
mean ± sd	63.0 ± 1.63	63.0 ± 1.63	63.0 ± 1.67
		t_{69} = 0.036 P < 0.972	t_8 = 0.0 P = 1.000
FFS			
range	10–12	10–13	10–13
mean ± sd	11.0 ± 0.82	10.9 ± 0.68	11.7 ± 0.88
		t_{68} = 0.150 P = 0.881	t_8 = -1.209 P = 0.261
FFL			
range	16–17	14–20	15–20
mean ± sd	16.5 ± 0.71	15.9 ± 0.83	16.75 ± 1.66
		t_{68} = 1.335 P = 0.186	t_8 = -2.2739 P = 0.787
FTS			
range	17–19	14–20	16–20
mean ± sd	18.0 ± 0.81	16.7 ± 0.98	17.6 ± 1.28
		t_{68} = 2.632 P = **0.010**	t_8 = 0.571 P = 0.583
FTL			
range	31–33	25–34	27–34
mean ± sd	31.877± 0.85	28.1 ± 1.59	29.7.1 ± 2.68
		t_{68} = 4.681 P = **0.000**	t_8 = 1.569 P = 0.155

For the parsimony analysis of 514 bp of ND2, 38 sites were variable but uninformative and 171 were informative. The score of the best likelihood tree was –ln L5513.133258.

The ND2 sequence data gave strong support for the monophyly of the samples identified as the new species on morphological criteria (Figure 1). The new species shows a high level of genetic differentiation from both *Caledoniscincus haplorhinus* (18.2–19.9%) and *C. austrocaledonicus* (18.8–20.6%), the two species with which it is morphologically most similar in sharing a pale midlateral stripe. Further, the genetic data placed the new species at the base of the genus as the sister species to a moderately well supported group comprising all other *Caledoniscincus* (pP 0.98; ML 54%).
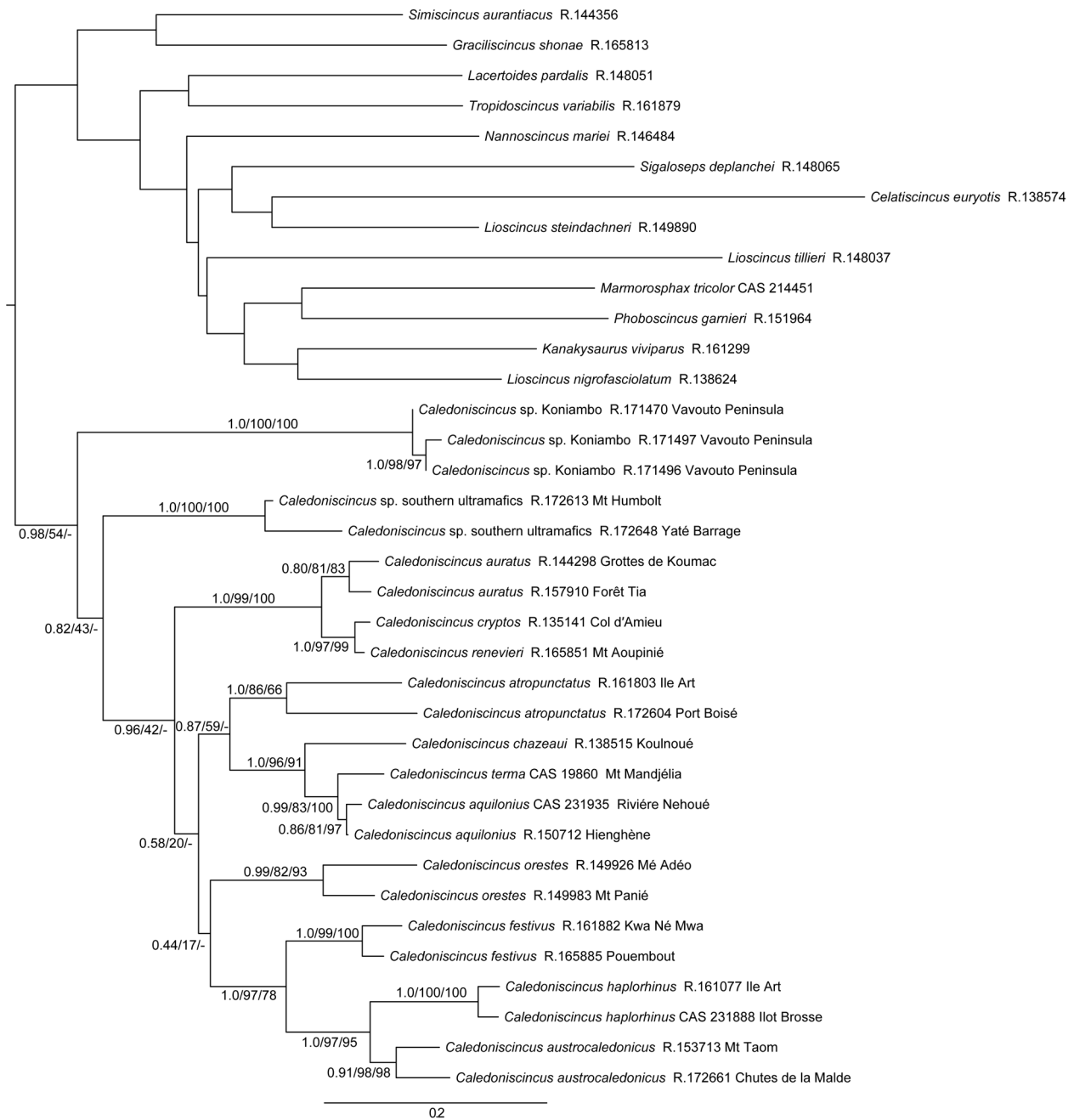
FIGURE 1. Phylogenetic relationships of *Caledoniscincus constellatus* **sp. nov.** relative to each species within the genus. This is a likelihood topology with Bayesian posterior probabilites and ML and MP support values.

Systematics

The species of *Caledoniscincus* range from moderately small (*C. chazeaui* maximum SVL 43 mm) to moderately large in size (*C. festivus* maximum SVL 72 mm) with well developed limbs and digits, and a moderately long tail (~150% of SVL). In scalation and osteology they share the following suite of characters (apomorphic character states for genus denoted by asterisk; polarities from Sadlier 2010): *dorsal body scales with three strong keels; no distinct supranasals; *nasal scales with a post-nasal crease; frontonasal broader than long; *prefrontals reduced in size and widely separated; frontal nearly as broad as long; four supraoculars; *frontoparietals fused; interparietal distinct; parietals in broad contact behind interparietal, and each bordered by a single nuchal and upper secondary temporal scale; primary temporal single; lower secondary temporal single; two tertiary temporal scales; postlabials

two; nasals moderately to widely separated; anterior loreal higher than wide; supraciliaries seven; upper labials seven with the fifth subocular and contacting the lower eyelid; postmental contacting first and second lower labial; three transversely enlarged chinshields, first pair in broad contact, second pair separated by one scale, third pair separated by three scales; 11 premaxillary teeth; altantal arches of first cervical vertebrae fused to the *intercentrum; 29 presacral vertebrae; phalangeal formula for the manus 2.3.4.5.3 and for the pes 2.3.4.5.4.; two pairs of mesosternal ribs contacting the mesosternum; *hemipenes distinctly bifurcated (in those taxa examined).

The species of *Caledoniscincus* are conservative in morphology with minimal diagnostic differentiation in scalation and to a lesser extent body proportions (see Sadlier *et al*. 1999), the most notable difference between species being in adult male colouration. Adult female *Caledoniscincus* typically retain a colour and pattern similar to that of juveniles, whereas males change in pattern and often develop a different ventral colouration to the females.

Caledoniscincus constellatus sp. nov.
Figs. 1–5

Holotype. MNHN 2011.0228 (formerly AMS R171497) Pointe de Vavouto, Province Nord, New Caledonia 21°00'39.8"S 164°41'04.3"E (collected R.A. Sadlier and A.H. Whitaker 27 Jan. 2009).

Paratypes. AMS R171496 Pointe de Vavouto 21°00'35.1"S 164°41'02.0"E (collected R.A. Sadlier and A.H. Whitaker 27 Jan. 2009); AMS R171470 Pointe de Vavouto 21°00'40.3"S 164°41'07.9"E (collected R.A. Sadlier and A.H. Whitaker 26 Jan. 2009); AMS R171471 Pointe de Vavouto 21°00'34.5"S 164°41'02.0"E (collected R.A. Sadlier and A.H. Whitaker 26 Jan. 2009).

Additional material examined. QM J.58022 Massif d'Ouazangou 20°44'34"S 164°28'03"E collected R. Raven 14 May 1992.

Etymology. The species epithet is Latin for studded with stars and refers to the pattern of white specks on the dorsal surface of males of the species.

Diagnosis. *Caledoniscincus constellatus* sp. nov. can be distinguished from the other species of *Caledoniscincus* by the following combination of characters: (a) moderately small size (adult male 46–57mm SVL; adult female 57mm SVL); (b) tail long, approximately 2.0+ longer than body; (c) the fourth toe being covered with 17–19 scales above and 31–33 lamellae below; (d) a broad pale midlateral stripe; (e) bright yellow ventral colour in adults of both sexes.

FIGURE 2. Orientation and contact of the pale midlateral stripe around the ear opening in *Caledoniscincus constellatus* **sp. nov.** (A), *C. haplorhinus* (B), and regionally sympatric *C. austrocaledonicus* (C).

The presence of a pale midlateral stripe in *Caledoniscincus constellatus* **sp. nov.** will distinguish it from all other species of *Caledoniscincus* except *C. haplorhinus* and populations of *C. austrocaledonicus* from the central and northern regions of New Caledonia, both of which also have this character state, and which also occur in the northwest region of New Caledonia. *Caledoniscincus constellatus* **sp. nov.** is sympatric with *C. haplorhinus* on the Pointe de Vavouto, and locally sympatric with both *C. haplorhinus* and *C. austrocaledonicus* which occur on the Massif d'Ouazangou-Taom. The general pattern of *C. constellatus* **sp. nov.** and *C. haplorhinus* are similar to each other in that the males and females are two-toned with a light dorsal surface contrasting with a noticeably darker upper lateral surface which is bordered below by a pale midlateral stripe. The most consistent difference between the two species, and with *C. austrocaledonicus*, is in the positioning of the pale midlateral stripe where it contacts the back of the ear opening (Fig. 2): in *C. constellatus* **sp. nov.** the pale midlateral stripe is broad, meets most of the posterior

edge of the ear and then continues broadly from the anterior edge of the ear unbroken to the anterior-most upper labials; in *C. haplorhinus* the pale midlateral stripe is narrow, joins the upper posterior edge of the ear and forms a pale edge over the ear and continues anteriorly as a row of broken pale markings to the anterior upper labials; in *C. austrocaledonicus* the pale midlateral stripe is narrow, follows a line anteriorly towards the middle of the rear edge of the ear opening, but loses definition approaching the ear opening. The tail of *C. constellatus* **sp. nov.** (208% SVL) is also longer than that of *C. haplorhinus* (maximum 173% SVL) or *C. austrocaledonicus* (~150% SVL).

There are also marked differences in ventral colouration between these three species. Adult male and female *C. constellatus* **sp. nov.** have bold yellow ventral surfaces which distinguish them from *C. haplorhinus* (adult males moderate yellow; adult females pale yellow) and from *C. austrocaledonicus* (adult males orange; adult females moderate yellow). Further, the reticulate pattern of narrow, bicoloured transverse bars in adult male *C. constellatus* **sp. nov.** is unique and readily distinguishes them from adult male *C. haplorhinus* which lack any transverse markings on the dorsal surface, and male *C. austrocaledonicus* which has a pale vertebral marking (rough stripe or variably connected blotches) down the centre of the back.

In scalation there is highly significant levels of difference ($t < 0.005$) between *C. constellatus* **sp. nov.** and *C. haplorhinus* (all populations included) in toe scalation and number of midbody scale rows (Table 1). However, there is overlap in range of values for these characters and they are not significantly different when compared with syntopic *C. haplorhinus*, limiting their usefulness diagnostic markers in the identification of individuals.

Description. Based on three adult males (46–52mm SVL), one adult female (57mm SVL) from Pointe de Vavouto. Measurements: adult size 46–57mm SVL; distance from axilla to groin 58.6–63.2% SVL ($\bar{x} = 61$); distance from forelimb to snout 30.7–35.4% SVL ($\bar{x} = 33.9$); hindlimb length 43.9–47.5% SVL ($\bar{x} = 45.3$); tail length of individual with most complete tail 208.1% SVL.

Scalation: midbody scale rows 28–30 ($\bar{x} = 28.5$, sd = 1.00); dorsal scale rows 61–65 ($\bar{x} = 63.0$, sd = 1.63); scales on top of fourth finger 10–12 ($\bar{x} = 11$, sd = 0.81); lamellae beneath fourth finger 16–18 ($\bar{x} = 16.5$, sd = 0.7); scales on top of fourth toe 17–19 ($\bar{x} = 18.0$, sd = 0.82); lamellae beneath fourth toe 31–33 ($\bar{x} = 31.9$, sd = 0.85).

Osteology: presacral vertebrae 28 (n = 1) – 29 (n = 3); postsacral vertebrae 43 (n = 1) for individual with longest tail, tip (19%) reproduced.

Colour and pattern in life (Fig. 3): Dorsal surface of males predominately light brown (larger individuals) to grey-brown (smallest individual) with a reticulate pattern of narrow (one scale width), bicoloured transverse bars, the individual scales of which are black with one to several small white spots medially within the scale and/or along its anterior edge, and the scales making up the of lighter interspaces between the dark transverse bars are densely peppered with minute black spots. Top of head bearing a mix of grey and light brown (larger individuals) or more uniformly grey-brown (smallest individual). Lateral surface of body and head black with a bold white midlateral stripe that extends along the side of the head from the anterior labials to the anterior edge of the ear, and then along the neck from the lower and posterior edge of the ear opening and passing above the forelimb and along the body as a continuous stripe (one scale width) to the edge of the hindlimb, continuing along the hindlimb as a lighter and narrower grey stripe bordered below by a continuation of the black lower lateral colour. The light dorsal and dark lateral surfaces are well differentiated and highly contrasting, the dorsolateral edge is irregular and defined by a pale narrow stripe that is cream with brown suffusion between the naris and eye, white between the eye and level of the forelimb, and of variable in width and clarity of colour along the remainder of the body being narrow (half scale width) and variably suffused with brown to wide (one scale width) and white in colour, with the wider and paler areas appearing more as a series of white blotches. Tail grey-brown above with some continuation medially of the light brown dorsal colouration of the body. Lateral surface of the tail dark basally but mid-brown over the remainder of its length and bordered above by a very narrow, unbroken, black edge along the dorsolateral margin. Undersurface of body and neck white and strongly contrasting with the dark lower lateral surface, the body with a bold yellow flush anteriorly to the level of the forelimbs. Lower labials each with large dark markings, scales along inner edge of jaw line also with scattered dark markings, and the mental scale with dark blotches and numerous minute dark specks to give an overall blackish appearance.

Adult female with the dorsal surface grey-brown above with a series of small, widely separated dark blotches along the vertebral line of the neck, body and base of tail, continuing as a narrow dark vertebral streak along the remainder of the tail. Lateral surface as for males but with the pale dorsolateral markings usually white, near continuous and narrow (1/2 scale width).

Details of Holotype: Adult male (MNHN 2011.0228); size 49.5 mm SVL; tail length 103 mm (19.5 mm of tip

reproduced). Midbody scale rows 28; dorsal scale rows 61; dorsal scales of fourth finger 11/11; lamellae of fourth finger 16/16; dorsal scales of fourth toe -/18; lamellae of fourth toe -/31.

FIGURE 3. Adult male *Caledoniscincus constellatus* **sp. nov.**, holotype (MNHN 2011.0228) dorsal (A) and ventral (B) coloration.

Comments. The single juvenile specimen in the Queensland Museum from the Ouazangou massif is assigned to *C. constellatus* **sp. nov.** on the basis of having the black upper and lower lateral colouration (including the side of the head) and distinctive broad, pale midlateral stripe and the contact of this stripe with the ear opening diagnostic of

the population at the type locality. However, this specimen is poorly preserved and the scalation characters are difficult to assess thus not allowing comparison with the type series from Vavouto with any confidence, although it does appear to have a shorter tail (166% versus 208% SVL) indicating the possibility of some regional differentiation, the significance of which can only be assessed with more samples.

Distribution and biology. *Caledoniscincus constellatus* **sp. nov.** occurs in the northwest coast of the Grande Terre on Pointe de Vavouto and on the Massif d'Ouazangou. The site at Vavouto is mostly covered by disturbed vegetation but there is a mixture of dense to open maquis and *Acacia* shrubland on the coastal hills and remnant sclerophyll forest ('Formation Jaffré') in the gully. This site is unique for the occurrence of sclerophyll forest on serpentine. The new species was found in both habitats, and was syntopic with *Caledoniscincus haplorhinus* which was more abundant. Sclerophyll forest habitat is extremely restricted in distribution, but the mosaic of maquis and acacia shrubland is widespread and extends to the adjacent coastal hills and low-elevation slopes and valleys at the base of the Massif de Koniambo. Investigation of maquis and acacia shrubland at the base of Massif de Koniambo did not record *C. constellatus* **sp. nov.**, but did record *C. haplorhinus*. The single juvenile from Massif d'Ouazangou was collected in an insect pitfall trap set in *Acacia* shrubland in a west-facing gully around 400 m elevation.

Conservation status. Potential threats to the species preferred habitats includes an array of low- to moderate-level human-mediated impacts, including: extensive loss and fragmentation of sclerophyll forest, near coastal maquis and *Acacia* shrubland on the central-west and north-west coast from clearing for ranching and agriculture; a decline in the extent and quality of remaining sclerophyll forest, maquis and *Acacia* shrubland in the long-term from repeated wildfires and, where they occur on ultramafic massifs, from activities associated with nickel mining; a potentially very high risk of a decline in quality (and consequently in extent) of the remaining sclerophyll forest fragments at Pointe de Vavaouto from the immediate proximity of the infrastructural development associated with the Koniambo mine processing facility; a potentially severe negative impact from the invasive little red fire ant (*Wasmannia auropunctata*) in sclerophyll as indicated by studies on congeners (Jourdan *et al*., 2001).
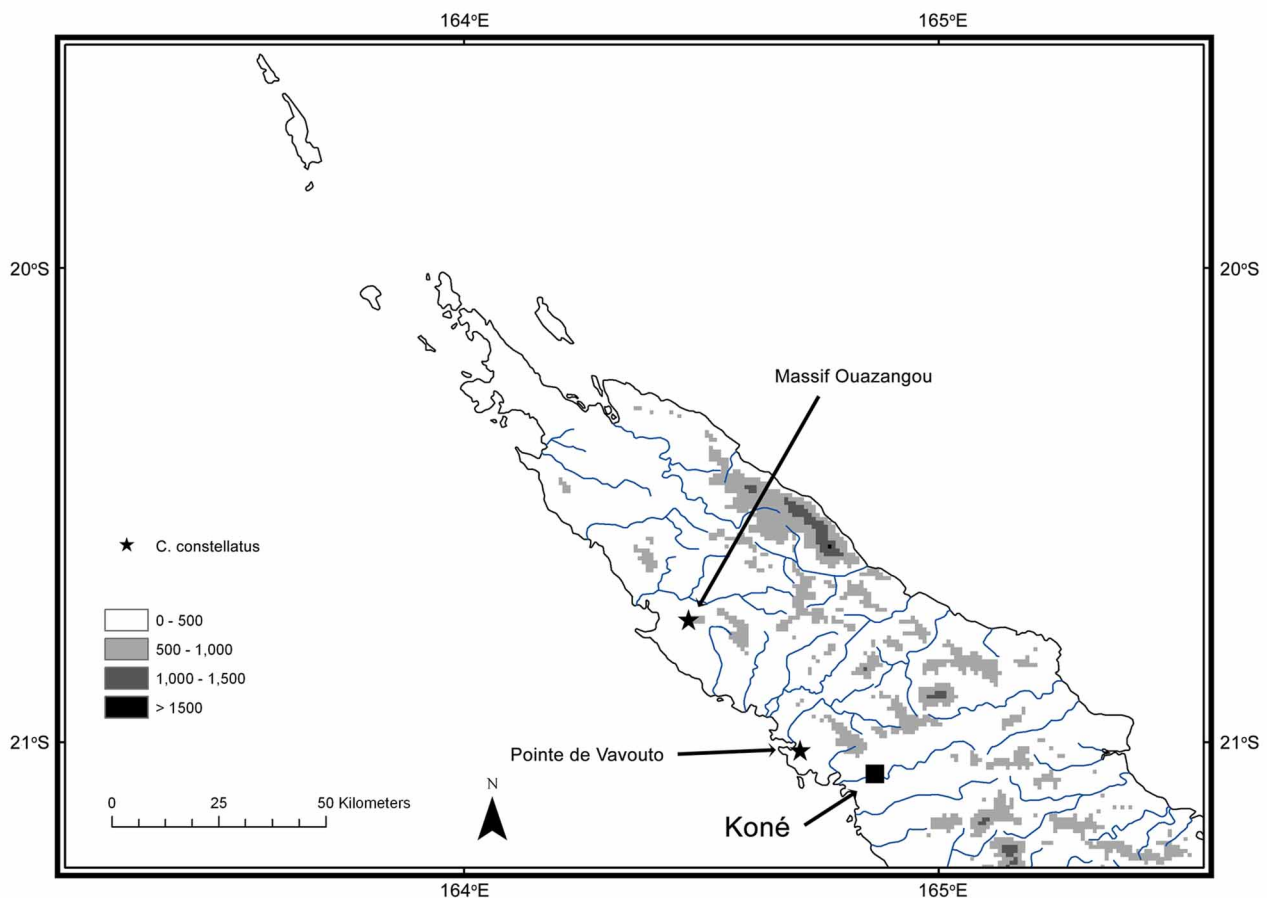

FIGURE 4. Distribution of *Caledoniscincus constellatus* **sp. nov.** (star) in north-west New Caledonia. Note that Pointe de Vavouto is the type locality for the species.

FIGURE 5. Maquis/*Acacia* shrubland ('Formation Jaffré') on Pointe de Vavouto (A) and interior of remnant sclerophyll forest (B).

Based on the threats identified above, the species extremely restricted range and its occurrence at only two locations, *C. constellatus* **sp. nov.** is ranked as Critically Endangered on IUCN Red List criteria (IUCN 2001).

Comparative material examined. The following specimens of *Caledoniscincus haplorhinus* were used in the morphological comparisons: AMS R77407, R77409, R77427, R77429, R77437, R77449–52, R78319–20, R78322, R78326-28 Nouméa, Fambourg Blanchot 22°18'S 166°27'E; AMS R135119-23 Nouville, Isle Nou 22°16'S 166°24'E; R146433–4, CAS 198763–71 Plage de Ouano 21°50'43"S 165°48'33"E; AMS R144257–58, R144284–89 Grottes de Koumac, 9km E of Koumac 20°33'18"S 164°21'49"E; AMS R146459–70, R146472 Pindaï, Plage de Pindaï 21°21'26"S 164°57'11"E; AMS R171478–81 Pointe de Vavouto 21°00'40.3"S 164°41'07.9"E; AMS R171483 Pointe de Vavouto 21°00'36.4"S 164°41'8.6"E; AMS R171491 Pointe de Vavouto 21°00'17.8S 164°46'7.5E.

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