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A new species of *Oligosoma* (Squamata: Scincidae) from the northern North Island, New Zealand

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Abstract

New Zealand is home to a diverse cool temperate assemblage of skinks, with 60+ identified taxa (genus *Oligosoma* Girard), of which only 50 have been formally described. Here we describe a new species (*Oligosoma kakerakau* **sp. nov.**) from Bream Head Scenic Reserve, near Whangārei Heads, Northland. This species is considered to be conspecific with a single specimen (*Oligosoma* "Whirinaki") previously reported (in 2003) from Whirinaki Te Pua-a-Tāne Conservation Park ~370 km further south. *Oligosoma kakerakau* **sp. nov.** can be distinguished from all other members of the genus by a combination of a distinctive "teardrop" marking below the eye, a distinctive mid-lateral stripe, and the colouration and pattern on its ventral surface. Our phylogenetic analyses indicate that *Oligosoma kakerakau* **sp. nov.** is most closely related to *O. zelandicum* (Gray), and more distantly to *O. striatum* (Buller) and *O. homalonotum* (Boulenger). Sea level changes during the Pliocene, such as the formation of the Manawatū Strait, may have contributed to the divergence between *Oligosoma kakerakau* **sp. nov.** and *O. zelandicum*. We discuss the distribution, ecology and conservation of *Oligosoma kakerakau* **sp. nov.**, and outline future research and conservation priorities for the species.

Key words: Kakerakau skink, conservation, morphology, *Oligosoma kakerakau* **sp. nov.**, Bream Head, Whirinaki, taxonomy

Introduction

New Zealand has the most diverse skink assemblage of any cool temperate region in the world (Chapple 2016). Skinks are thought to have colonised proto New Zealand during the early Miocene (16–22.6 mya; Chapple *et al*. 2009), and subsequent speciation was driven by climatic and tectonic processes. These processes led to sea level changes, with water barriers such as the Manawatu Strait having come and gone (Chapple & Hitchmough 2016; Trewick & Bland 2012). Alpine barriers including the Southern Alps have arisen, leading to strong gradients in altitude, rainfall, vegetation and substrate over very short distances (Chapple & Hitchmough 2016). Furthermore, the country is long and narrow, leading to substantial north–south differentiation in climate. These processes were more dramatic in the South Island, therefore total skink diversity, and skink diversity per unit area, is greatest in the South Island (van Winkel *et al*. 2018).

The number of skink species discovered in New Zealand has been steadily growing, and 15 new species have been described in the last 10 years alone (Chapple *et al*. 2011; Jewell 2017, 2019; Melzer *et al*. 2017, 2019; Patterson *et al*. 2013; Patterson & Hitchmough 2021; Whitaker *et al.* 2018) bringing the total number of recognised species to 50. An additional 15 proposed species have been informally identified, bringing the diversity recognised by van Winkel *et al*. (2018) to 65 species. Since 2018, a further three morphologically distinct potential new species have

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been discovered, and the discovery of sympatry of distinct clades within widespread species has also suggested a need for additional taxonomic splits. This diversity includes many morphologically distinctive species, as well as cryptic species complexes such as the *O. infrapunctum* complex (Melzer *et al*. 2019), that have been revealed through molecular techniques. New species are being found with surprising frequency in the South Island, but new discoveries are rare in the North Island.

In 2003, a skink was found in an outdoor hand basin in the middle of mature podocarp forest in Whirinaki Te Pua-a-Tāne Conservation Park, near Minginui by Andy Blick. A video recording was made of the skink before it was released. Expert opinion at the time considered this individual was likely of an undescribed species, although its phylogenetic associations were not immediately clear (the late Tony Whitaker, pers. comm.). It was assigned the tag name *Oligosoma* "Whirinaki" and classified as Data Deficient under the New Zealand Threat Classification System. Subsequent surveys conducted for this species in Whirinaki Te Pua-a-Tāne failed to locate further individuals (Barr 2014).

In February 2013, three individuals of a previously unknown skink taxon were discovered in Bream Head Scenic Reserve in the Whangārei Heads, Northland (~370 km north of the Whirinaki Te Pua-a-Tāne Conservation Park) by Cathy and Peter Mitchell during routine reptile monitoring. Exotic mammals are controlled to low densities within Bream Head Scenic Reserve. Monitoring has continued at the site, and the population appears to be locally abundant, albeit with a very restricted range covering <1 ha. Preliminary molecular and morphological data suggested that the Bream Head population represented an undescribed taxon, most closely related to the glossy brown skink, *O. zelandicum*. Morphological evidence indicated that the individual found in Whirinaki may be from a disjunct population of the Bream Head taxon. Here we describe this species, and discuss its distribution and phylogenetic affinities in the context of the New Zealand skink fauna and current biogeographical understanding.

Materials and methods

Morphological analyses. We examined preserved specimens of the Bream Head taxon, along with specimens of the closely related *O. zelandicum*, from the Museum of New Zealand Te Papa Tongarewa. The following morphological descriptions and measurements were taken from each individual, as outlined in Patterson & Daugherty (1990), Patterson *et al*. (2013) and Whitaker *et al*. (2018). Unless stated, bilaterally present characters were taken from the right side. Longitudinal midbody scale rows were counted at the midpoint between the fore- and hind limbs, ventral scales were counted in a line between the mental scale and the vent (including the mental and one preanal scale), subdigital lamellae were counted on the fourth hind toe (right foot) from the tip to the base of the toe, the number of dorsal scale rows including full and half scales between the outer edges of the dorsolateral stripe were also counted. Nine variable head scale categories were counted: nuchal scale pairs, supraoculars, supraciliaries, upper and lower ciliaries, infra and supra labials, posterior and anterior suboculars as outlined in Hardy (1977). Measurements (to 0.1 mm) were taken of the snout-vent length (SVL), snout to ear (anterior margin) (SE), snout to axilla (the junction of the posterior margin of the forelimb with the body wall) (SF), head length (HL) from tip of snout to posterior extremity of the interparietal, head width (HW) between the lateral edges of the left and right parietals, axilla to groin (junction of the anterior margin of the hindlimb with the body wall) (AG), ear (posterior margin) to axilla (EF), intact tail length (TL), hindlimb length (HLL) from the groin to the tip of the fourth toe including nail, forelimb length (FLL) from the axilla to the tip of the fourth finger including nail, and the length of fourth toe (FTL). Pattern elements (e.g. dorsolateral, mid-lateral stripe) follow naming conventions from van Winkel *et al.* (2018: p. 159).

Molecular analyses. To confirm the distinctiveness of the Bream Head taxon, and determine its phylogenetic position, we sequenced the mitochondrial DNA gene (mtDNA), ND2. Previous studies have found this mtDNA region to be phylogenetically informative for taxonomic and phylogeographic studies of New Zealand skinks (Chapple & Patterson 2007; Chapple *et al*. 2008a,b,c, 2009, 2011, 2012; Greaves *et al*. 2007, 2008; Hare *et al*. 2008; Liggins *et al*. 2008a,b; Melzer *et al*. 2019; Miller *et al*. 2009; O'Neill *et al*. 2008; Patterson *et al*. 2013; Whitaker *et al*. 2018). ND2 sequences from the three Bream Head samples were produced by EcoGene Ltd, following the protocols of Greaves *et al*. (2008), and were compared to previously published ND2 sequences across the range of *O. zelandicum* (Figure 1; O'Neill *et al*. 2008).

Sequences were edited and aligned (using default parameters of Clustal W; Larkin *et al*. 2007) in Geneious 7.1.5 (Kearse *et al*. 2012). We translated all coding region sequences in MEGA X (Kumar *et al*. 2018) to ensure none contained premature stop codons. Based on preliminary analysis of the Bream Head sequences, they were found to

group within Clade 5 of *Oligosoma* (Chapple *et al*. 2009), therefore samples from *O. homalonotum* and *O. striatum*, the other two species in that clade, were also included (Table 1). Single specimens of two skink species from New Caledonia (*Nannoscincus mariei* Bavay, *Marmorosphax tricolor* Bavay) were included as outgroups (Table 1). The Bream Head sequence data were deposited in GenBank under the accession numbers listed in Table 1. We used jModelTest 2.1.10 (Darriba *et al*. 2012) to identify the most appropriate model of sequence evolution based on the Bayesian Information Criterion (BIC). This model was then implemented in MEGA X to generate a Maximum Likelihood (ML) tree. The node support was estimated using 1000 bootstrap replicates. Model-corrected genetic distances among the Bream Head taxon, and closely related *Oligosoma* species, were calculated in MEGAX.

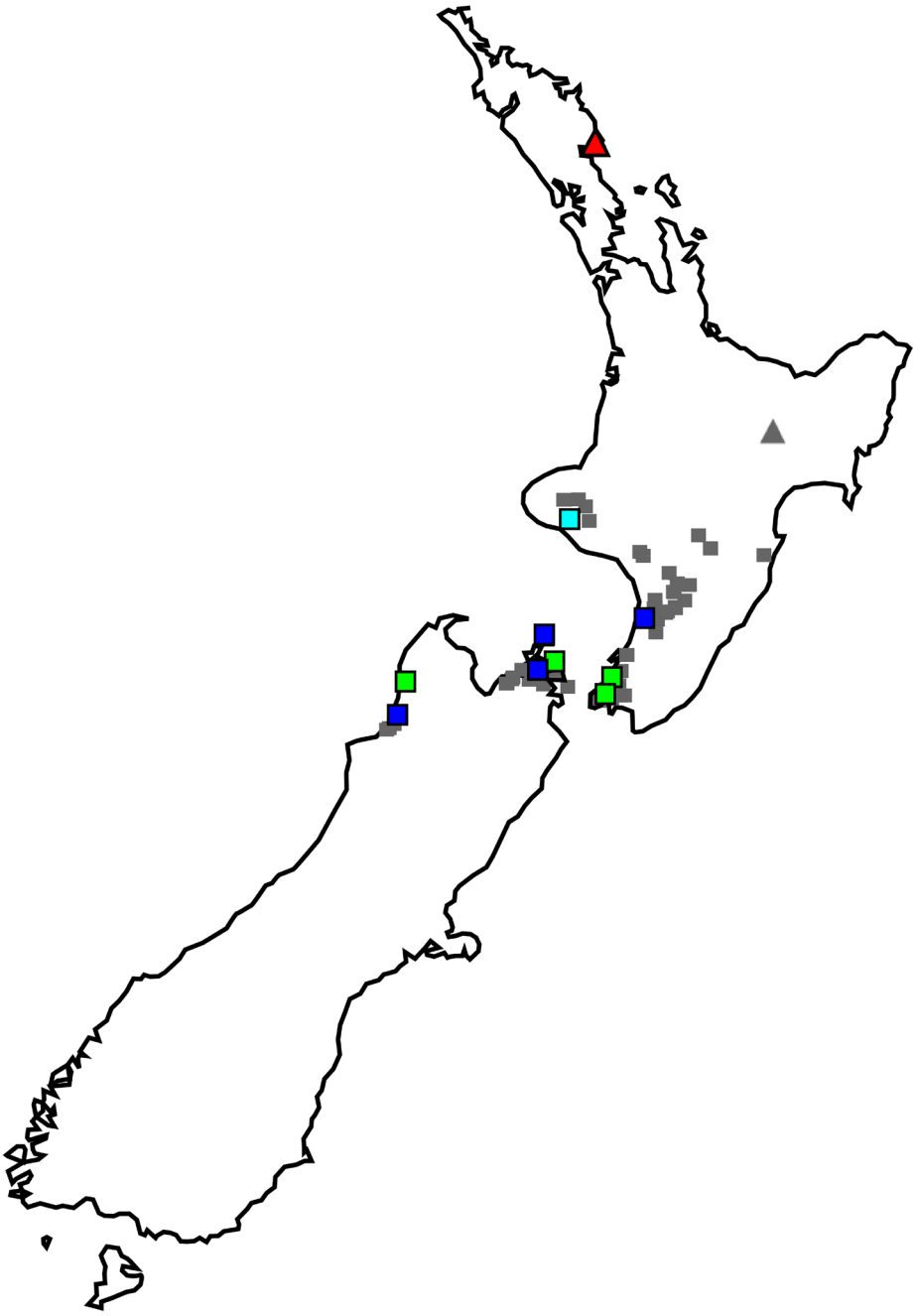

FIGURE 1. Distribution map of *O. kakerakau* **sp. nov.** and *Oligosoma zelandicum* and in New Zealand. Red triangle—location of *O. kakerakau* **sp. nov.** population in Bream Head Scenic Reserve and specimens used in morphological and molecular analyses. Grey triangle—specimen with strong affinities to *O. kakerakau* **sp. nov.** found in Whirinaki Te Pua-a-Tāne Conservation Park in 2013. Grey squares—*O. zelandicum* records from NZ herpetofauna database, dark blue squares—*O. zelandicum* specimens used in morphological and molecular analyses, green squares—*O. zelandicum* specimens only used for molecular analysis, light blue squares—*O. zelandicum* specimens only used for morphological analysis.

Results

Molecular analyses. The edited alignment comprised 507 bp of ND2, with 143 (28%) variable and 84 (17%) parsimony-informative sites. For the ingroup (*Oligosoma* clade 5), the alignment comprised 76 (15%) variable characters and 73 (14%) parsimony informative sites. The BIC from jModelTest supported the HKY+I substitution model for our data set. Parameters estimated under this model were: relative substitution rates (A↔C = 2.316, A↔G = 17.632, A↔T = 1.000, C↔G = 2.316, C↔T = 17.623, relative to G↔T = 1.000), and proportion of invariant sites (0.655). We present the optimal ML tree (-ln L = 1659.61), with ML bootstraps indicating branch support (Figure 2).

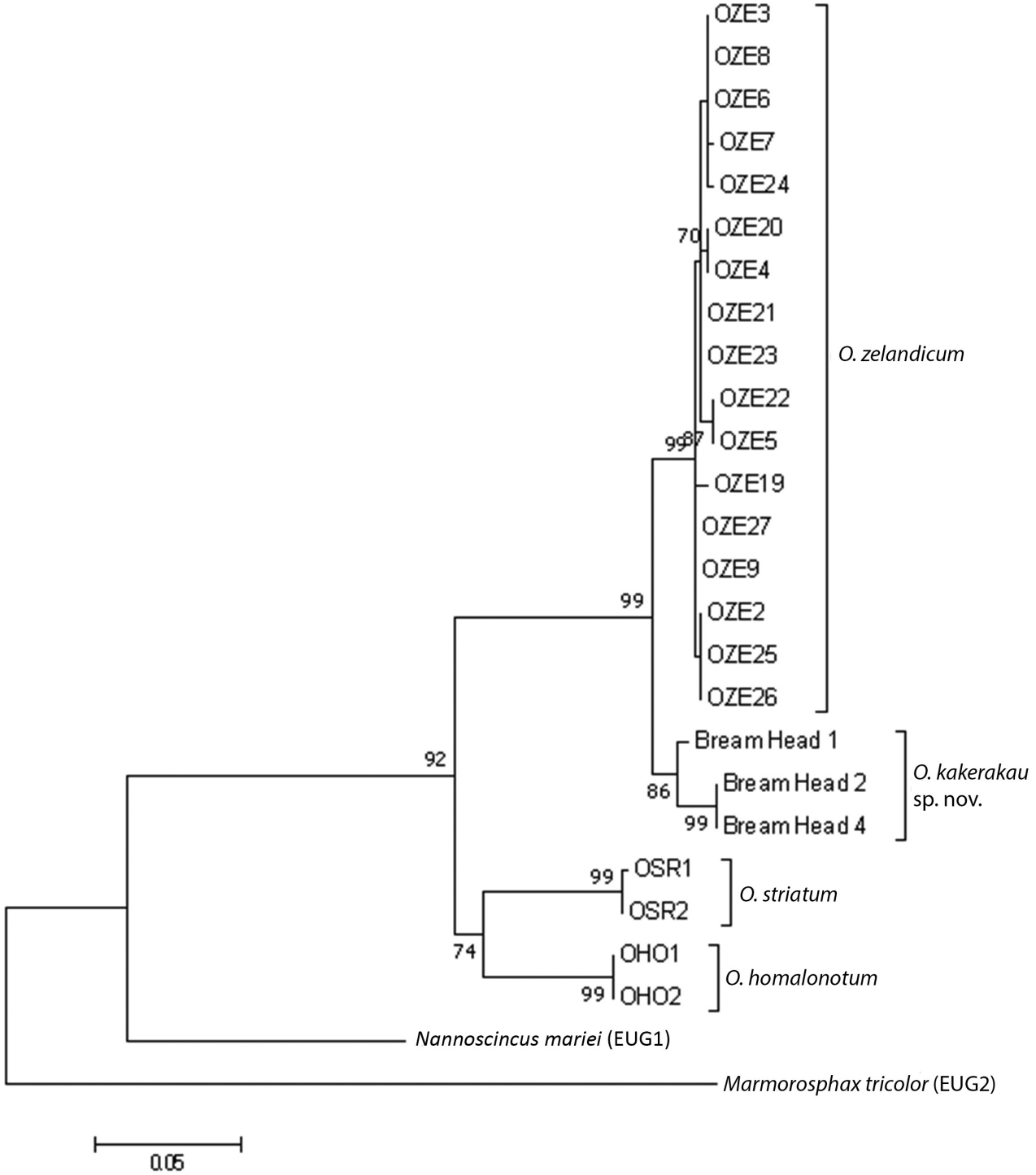

FIGURE 2. Maximum likelihood (ML) phylogenetic tree, with 1,000 bootstraps, for *Oligosoma* clade 5 (Chapple *et al*. 2009), indicating the phylogenetic affinities of the Bream Head taxon. Well-supported nodes (i.e. bootstrap support >70) are indicated.

The Bream Head taxon (86% bootstrap support [BS], n = 3) was most closely related to *O. zelandicum* [99% BS, n = 17], and more distantly related (92% BS) to other members of *Oligosoma* clade 5, *O. homalonotum* (n = 2) and *O. striatum* (n = 2)(Figure 2). All members of clade 5, including the Bream Head taxon, are cryptic forest dwelling species with arboreal tendencies (Hitchmough *et al*. 2016; Neilson *et al*. 2004). The Bream Head taxon is 3.2% divergent (~2.4 mya, based on the evolutionary rate for ND2 calculated in O'Neill *et al*. 2008) from *O. zelandicum*, and 10.4% (8 mya) divergent from *O. homalonotum* and 11.0% (8.5 mya) divergent from *O. striatum*. The intraspecific divergence within *O. zelandicum* is 1.2% (O'Neill *et al*. 2008).

Decisions on whether allopatric populations justify formal taxonomic recognition are essentially subjective and therefore problematic, however *O. kakerakau* **sp. nov.** meets all the criteria used by Patterson & Hitchmough (2021) to justify species status for *O. kahurangi. Oligosoma kakerakau* **sp.nov.** has a genetic divergence from its sister species slightly higher than *O. kahurangi*, and similarly multiple diagnostic morphological differences from its sister species. Finally, *O. kakerakau* **sp.nov.** and *O. zelandicum* are ecologically somewhat different, *O. kakerakau* **sp.nov.** occupying forest rather than forest margins, and they occupy different and well supported biogeographic regions.

TABLE 1. Locality information and GenBank accession numbers for the samples used in the phylogenetic analyses. Samples with CD or FT codes were obtained from the National Frozen Tissue Collection (NFTC) housed at Victoria University of Wellington, New Zealand. Samples with RE codes were obtained from ethanol preserved specimens housed at Te Papa Tongarewa, National Museum of New Zealand, Wellington. NR codes are from the Australian Museum, Sydney.

Species	Sample code	Museum Code	Locality	GenBank Accession No.
Oligosoma kakerakau **sp. nov.**	Bream Head 1	RE7383	Bream Head Scenic Reserve, Whangārei	MT661457
Oligosoma kakerakau **sp. nov.**	Bream Head 2	RE7384	Bream Head Scenic Reserve, Whangārei	MT661458
Oligosoma kakerakau **sp. nov.**	Bream Head 4	RE7386	Bream Head Scenic Reserve, Whangārei	MT661459
Oligosoma zelandicum	OZE2	FT6516	Pukerua Bay	EF447181
Oligosoma zelandicum	OZE3	FT3814/RE5508	Mokihinui River Mouth	EF033057
Oligosoma zelandicum	OZE4	CD331/RE5478	Maud Island	EF447183
Oligosoma zelandicum	OZE5	CD542/RE5483	Stephens Island	EF447184
Oligosoma zelandicum	OZE6	CD1951	Outer Chetwode Island	EF447185
Oligosoma zelandicum	OZE7	FT3743/RE5337	Gentle Annie	EF447186
Oligosoma zelandicum	OZE8	FT3773	Scotts Beach, Heaphy Track	EF447187
Oligosoma zelandicum	OZE9	FT6526	Johnsonville	EF447188
Oligosoma zelandicum	OZE19	RE1594	Foxton area	EF447189
Oligosoma zelandicum	OZE20	CD335	Maud Island	EF447190
Oligosoma zelandicum	OZE21	CD543/RE5484	Stephens Island	EF447191
Oligosoma zelandicum	OZE22	CD554/RE5485	Stephens Island	EF447192
Oligosoma zelandicum	OZE23	CD1952	Outer Chetwode Island	EF447193
Oligosoma zelandicum	OZE24	FT3744/RE5338	Gentle Annie	EF447194
Oligosoma zelandicum	OZE25	FT6517	Pukerua Bay	EF447195
Oligosoma zelandicum	OZE26	FT6518	Pukerua Bay	EF447196
Oligosoma zelandicum	OZE27	FT6526	Johnsonville	EF447197
Oligosoma homalonotum	OHO1	FT6290	Shoal Bay, Great Barrier Island	EF447146
Oligosoma homalonotum	OHO2	FT6291	Tryphena, Great Barrier Island	EU567724
Oligosoma striatum	OSR1	FT3301	Waipuku, Taranaki	EF447147
Oligosoma striatum	OSR2	FT3296	Little Barrier Island	EU567725
Nannoscincus mariei	EUG1	NR9809	New Caledonia	EU423132
Marmorosphax tricolor	EUG2	NR9800	New Caledonia	EU423133

Species description

Genus *Oligosoma* Girard, 1857

Oligosoma kakerakau sp. nov.
(Figure 3)

Oligosoma "Whirinaki" Hitchmough *et al*. (2016)

Holotype. NMNZ RE007385 (adult male); Bream Head Scenic Reserve, Whangārei, New Zealand; E1742432 N6031080; 460m; collected by B.P. Barr, 15 January 2014.

Paratypes (3 specimens). NMNZ RE007383; adult male; same collection data as holotype. NMNZ RE007384; adult female; same collection data as holotype. NMNZ RE007386; adult female; same collection data as holotype.

Morphological characters of the type series are presented in Table 2.

Diagnosis. *Oligosoma kakerakau* **sp. nov.** can be distinguished from other *Oligosoma* species by the following combination of characters: the combination of the distinctive teardrop marking under the eye on the supralabials and the distinctive mid-lateral stripe distinguish *O. kakerakau* **sp. nov.** from all other *Oligosoma* except *O. zelandicum* and *O. microlepis* (Patterson & Daugherty). *Oligosoma kakerakau* **sp. nov.** can be distinguished from *O. microlepis* by its speckled ventral surface versus pale cream or white, and by fewer midbody scales (n=4, 26–30) versus *O. microlepis* (n=9, 38–44). *Oligosoma kakerakau* **sp. nov.** can be distinguished from *O. zelandicum* by: (a) the heavily flecked venter versus uniform or fine flecking in *O. zelandicum*; (b) relatively long hindlimb length with no overlap in HLL/SVL ratio; (c) relatively long 4th hind toe length with no overlap in FTL/SVL; (d) subdigital lamellae count usually >20 versus usually <21 in *O. zelandicum* (e) mid-lateral stripe always broken above forelimb versus infrequently broken in *O. zelandicum* (f) larger midbody scales with midbody scale rows usually <31 versus usually >30 in *O. zelandicum*; (g) dorsal scale rows always 6 and two half scales versus usually 8 and two half scales in *O. zelandicum*; (h) ventral scales usually <76 versus usually >73 in *O. zelandicum* (Table 3).

Although sample sizes are unavoidably small because *Oligosoma kakerakau* **sp. nov.** is a threatened species with a very small known population, confidence is greatly increased by the close agreement of the Whirinaki specimen with the Bream Head individuals in all characters visible in the video of the former. *Oligosoma zelandicum* is a common, well-known species and the characters used have proven reliable for many specimens handled at various field localities.

Description of Holotype. Body elongate, oval in cross-section; limbs well-developed, pentadactyl; hindlimbs 38% of SVL and 1.5x length of forelimbs; adpressed limbs meeting; digits sub-cylindrical; third front digit shorter than the fourth; ear opening moderately large and rounded.

Lower eyelid with a transparent palpebral disc surrounded either side and below with granules; snout moderately blunt; nostril centred just below middle of nasal, not touching bottom edge of nasal; nasals entire; supranasals absent; rostral broader than deep; frontonasal broader than long, narrow contact with frontal; frontal longer than broad, shorter than frontoparietal and interparietal together, in contact with 2 anteriormost supraoculars; supraoculars 4, the second largest; preoculars 2, the upper one larger; frontoparietals distinct, larger than interparietal; a pair of parietals meeting behind interparietal, the left overlapping the right, and are bordered posteriorly by a pair each of nuchals and temporals, also in broad contact with interparietal, frontoparietal, 2 postoculars, and narrow contact with 4th supraocular; nuchals 2 pairs; loreals 2, similar size; anterior loreal in contact with first and second supralabial, posterior loreal, prefrontal, frontonasal and nasal; posterior loreal in contact with second and third supralabial, first subocular, upper and lower preocular, prefrontal and anterior loreal; supralabials 7, the sixth the largest; fifth supralabial below centre of eye; infralabials 6, 2–4 are similar in size; mental broader but shallower than rostral; subocular row interrupted by 5th supralabial; postmental larger than mental; chinshields 3 pairs, the second pair the largest; anterior chinshields separated by one scale width, contact 2nd and 3rd infralabial; second chinshields separated by one scale width but two scales deep, contact 3rd and 4th infralabial; posterior chinshields separated by 4 gular scales, contact 4th and 5th infralabials; ear with several moderate triangular projecting lobules on the anterior margin; one primary temporal, dorsal scales largest, weakly striate; ventral scales smooth; subdigital lamellae smooth.

Measurements (in mm; holotype with the variation shown in the type series in parentheses): SVL 58.4 (mean 56.2, range 51.3–60.4), SE 11.4 (mean 10.7, range 10.3–11.4), SF 23.9 (mean 22.6, range 21.5–23.9), HL

9.7 (mean 9.1, range 8.3–9.7), HW 3.9 (mean 3.7, range 3.2–4.1), AG 26.5 (mean 28.4, range 25.5–33.2), EF 13.0 (mean 12.1, range 11.1–13.0), TL 77.0 (mean 77.9, range 74.4–82.5), HLL 22.3 (mean 21.4, range 20.4–22.3), FLL 14.6 (mean 14.1, range 12.6–15.2), and FTL 7.7 (mean 7.3, range 7.0–7.7).

FIGURE 3. Adult male holotype of *Oligosoma kakerakau* **sp. nov.** (RE 007385): A.) dorsal, B.) ventral and C.) lateral views. [*Photographs: Jean-Claude Stahl*].

TABLE 2. Variation in morphological measurements, meristic counts and ratios of *Oligosoma kakerakau* **sp. nov.** and *O. zelandicum*. Measurements are presented in millimeters (mm).

		***O. kakerakau* sp. nov.**												
		Holotype	**Paratypes**			***O. zelandicum***								
	Museum code	**RE7385**	**RE7384**	**RE7383**	**RE7386**	**RE5337**	**RE5508**	**RE5485**	**RE5484**	**RE4537**	**RE5483**	**RE5338**	**RE5478**	**RE1594**
Morphological measures	SVL	58.4	60.4	54.8	51.3	58.6	60.3	57.0	49.8	69.7	56.0	60.4	50.7	56.4
	Tail length	77.0	82.5	74.4	77.8	-	-	-	-	-	-	-	-	-
	Axilla-groin length	26.5	33.2	28.2	25.5	32.2	30.7	29.0	23.6	36.0	29.3	32.9	27.6	29.8
	Ear-axilla length	13.0	12.8	11.1	11.3	11.6	12.0	11.9	10.7	15.6	10.1	11.7	10.3	10.7
	Snout-ear length	11.4	10.5	10.7	10.3	10.6	10.6	11.2	9.8	12.4	10.7	10.7	10.0	10.8
	Snout-axilla length	23.9	22.7	22.4	21.5	21.5	22.5	23.5	20.4	26.6	20.7	22.2	19.7	21.4
	Head length	9.7	9.4	8.8	8.3	8.9	8.8	9.5	8.3	9.8	8.6	9.1	9.0	8.5
	Hindlimb length	22.3	21.9	20.8	20.4	17.7	17.8	18.0	16.9	22.6	17.7	18.2	17.0	17.4
	Forelimb length	14.6	15.2	14.1	12.6	12.7	12.2	13.8	11.4	14.2	12.6	14.3	12.2	12.5
	Head width	3.9	4.1	3.7	3.2	3.8	3.9	4.5	3.6	4.3	4.0	3.9	3.9	3.8
	Fourth hind toe length	7.7	7.4	7.0	7.2	6.2	6.6	6.8	4.9	7.2	6.2	6.2	4.9	6.2
Meristic counts	No. of anterior suboculars	2	2	3	2	3	3	3	3	3	3	3	4	3
	No. of posterior suboculars	3	3	3	3	3	3	3	3	3	3	3	3	3
	No. of supralabials	7	7	7	7	7	7	7	7	7	7	7	7	7
	No. of infralabials	6	6	6	6	6	6	6	6	6	6	6	6	6
	No. of upper ciliaries	8	9	8	8	9	7	8	7	8	7	7	9	8
	No. of lower ciliaries	12	12	13	10	12	11	12	11	12	10	11	13	11
	No. of supraciliaries	5	6	7	6	5	5	6	6	6	6	4	6	5
	No. of nuchal scale pairs	2	2	3	3	3	4	1	1	-	1	1	1	3
	No. of subdigital lamellae	26	23	24	20	19	19	16	19	21	19	19	17	19
	No. of midbody scale rows	30	29	28	26	32	31	33	32	30	31	32	34	38
	No. of dorsal scale rows	6.5	6.5	6.5	6.5	8.5	8	8.5	8.5	6.5	8.5	8.5	8.5	8.5
	No. of ventral scales	75	71	67	67	80	79	80	77	74	81	77	80	75

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TABLE 2. (continued)

		O. kakerakau sp. nov.												
		Holotype	**Paratypes**			***O. zelandicum***								
	Museum code	**RE7385**	**RE7384**	**RE7383**	**RE7386**	**RE5337**	**RE5508**	**RE5485**	**RE5484**	**RE4537**	**RE5483**	**RE5338**	**RE5478**	**RE1594**
ratios	Snout-forelimb/axilla-groin	0.90	0.68	0.79	0.84	0.67	0.73	0.81	0.74	0.86	0.71	0.67	0.71	0.72
	Snout-ear/ear-forelimb	0.88	0.82	0.96	0.91	0.91	0.88	0.94	0.79	0.92	1.06	0.91	0.97	1.01
	Hindlimb length/snout-vent	0.38	0.36	0.38	0.40	0.30	0.30	0.32	0.32	0.34	0.32	0.30	0.34	0.31
	Hind toe length/snout-vent	0.13	0.12	0.13	0.14	0.11	0.11	0.12	0.10	0.10	0.11	0.10	0.10	0.11
	Head width/snout-interparietal	0.40	0.44	0.42	0.39	0.43	0.44	0.47	0.44	0.43	0.47	0.43	0.43	0.45
	Head width/snout-vent	0.07	0.07	0.07	0.06	0.06	0.06	0.08	0.06	0.07	0.07	0.06	0.08	0.07
	Head length/ snout-vent	0.17	0.16	0.16	0.16	0.15	0.15	0.17	0.14	0.17	0.15	0.15	0.18	0.15

Scalation (holotype with the variation shown in the type series in parentheses): Upper ciliaries 8 (mean 8.3, range 8–9); lower ciliaries 12 (mean 11.8, range 10–13); nuchals 2 pairs (mean 2.5 pairs, range 2–3 pairs); midbody scale rows 30 (mean 28.3, range 26–30); ventral scale rows 75 (mean 70.0, range 67–75); subdigital lamellae 26 (mean 23.3, range 20–26); supraciliaries 5 (mean 6.0, range 5–7), anterior suboculars 2 (mean 2.3, range 2–3), posterior suboculars 3 (mean 3, range 3–3). Anterior loreal in contact with first and second supralabial. Posterior loreal in contact with second and usually third supralabial. Supralabials 7. Infralabials 6. One primary temporal. Third front digit usually shorter than the fourth. Maximum SVL 60.4 mm. Ratios for morphological measurements (± SD): SF/AG 0.90 (± 0.09); SE/EF 0.88 (± 0.06); HLL/SVL 0.38 (± 0.01); FTL/SVL 0.13 (± 0.01); HW/HL 0.40 (± 0.02); HW/SVL 0.07 (0.00); HL/SVL 0.17 (± 0.00).

Colouration. Dorsal surface brown with occasional dark brown and light brown flecks, especially on the head. A cream "tear-drop" marking is below the eye, edged in dark brown. No mid-dorsal stripe. A cream dorsolateral stripe with a distinct lower edge that undulates, sometimes strongly. Dorsolateral stripe fades out gradually. A cream mid-lateral stripe, two half-scale rows wide, extends from the eye to the forelimb and sometimes beyond (although it is always broken above the forelimb) breaking posteriorly into irregular blotches that are on the same plane. Top of the mid-lateral stripe passes through ear. A cream dorsoanterior stripe runs down forelimb on brachium and antebrachium and can be broken. Upper lateral zone between the dorsolateral and mid-lateral stripe is dark brown and unmarked and extends from the nostril, through the eye and down the body and tail. Chin grey and speckled. Throat and belly are brown or dark red-orange, heavily speckled with black flecks aligned as broken stripes. Soles of the feet are dark brown to black. There does not appear to be sexual dimorphism in colour patterns. Juvenile colouration similar to that in adults.

Etymology. The specific name is from the te reo Māori words kake, meaning to climb or scale, and rākau, meaning tree. These are in reference to the tree climbing behaviour of this species. This name was gifted by kaumātua of Ngātiwai, the mana whenua of Bream Head Scenic Reserve, where the type locality resides.

TABLE 3. Comparison of the morphological characters of *Oligosoma kakerakau* **sp. nov.** (n = 4) and *O. zelandicum* (n = 9). All measurements are presented in millimeters (mm).

Species	SVL	Hind limb length	Fourth hind toe length	Subdigital lamellae	Midbody scale rows	Dorsal scale rows	Ventral scales	SVL/ hind limb length	SVL/ hind toe length
O. kakerakau **sp.nov.**	51.3–60.4	20.4–22.3	7.0 –7.7	20–26	26–30	6.5	67–75	2.5–2.8	7.1–8.2
O. zelandicum	49.8–60.4	16.9–18.2	4.9–6.8	16–19	31–38	8–8.5	75–81	2.9–3.4	8.4–10.3

Ecology. Currently, *O. kakerakau* **sp. nov.** is known only from a small extant population in Bream Head Scenic Reserve in Northland, and a probable single observation in Whirinaki Forest Park, near Minginui (~370 km south of Bream Head) in 2003, which is assumed on the basis of examination of photographs to be conspecific. At Bream Head, *O. kakerakau* **sp. nov.** occupies a 1.8 ha 100% mimimum convex polygon (Wiles 2014). Large areas within this MCP are apparently unoccupied, therefore the true area of occupancy is likely to be <1 ha (Hitchmough *et al*. 2016).

Oligosoma kakerakau **sp. nov.** is diurnal and strongly heliothermic, and is most often observed basking or foraging in light wells (Figure 4), particularly during humid conditions (Gillanders 2017). The habitat within its area of occupancy is a mixture of broadleaf forest, low scrub and low groundcover (Wiles 2014). *Oligosoma kakerakau* **sp. nov.** occurs in all of these habitats, but is most common in low scrub and groundcover probably because these habitats provide a greater number of basking opportunities (Barr 2014; Wiles 2014). Similarly they are known to occur only on the ridgetop and north facing slopes, and have never been detected on the shady south facing slopes at Bream Head (Wiles 2014).

While most often observed on the ground, *O. kakerakau* **sp. nov.** individuals are also frequently observed climbing and basking in trees and vines. This arboreal behaviour is similar to other members of clade 5, *O. striatum* and *O. homalonotum* (Hitchmough *et al*. 2016; Neilson *et al*. 2004). Indeed their ability and propensity to climb trees and other vegetation is quite remarkable. Individual skinks have been observed actively foraging and chasing cave

weta spp. on the trunk of *Cyathea dealbata*, and foraging and basking up to 4 m high on a variety of other species including: *Ripogonum scandens*, *Freycinetia banksii*, *Cyathea medullaris* and *Olearia furfuracea*. In addition, *O. kakerakau* **sp. nov.** have been observed catching flies (Diptera spp.), native bush cockroaches (Blattidae spp.), a honeybee (*Apis mellifera* Linnaeus) and a wasp (*Vespula* sp.).

FIGURE 4. Forested habitat at the type locality Bream Head Scenic Reserve, Whangārei, March 2019 showing typical light wells similar to those frequented by *Oligosoma kakerakau* **sp. nov.** [*Photograph: Ben Barr*].

FIGURE 5. Wild *Oligosoma kakerakau* **sp. nov.** in damp leaf litter habitat at Bream Head Scenic Reserve, Whangārei, November 2013 [*Photograph: Dylan van Winkel*].

At Bream Head Scenic Reserve *O. kakerakau* **sp. nov.** are known to be syntopic with four other skinks: *O. aeneum* (Girard), *O. ornatum* (Gray), *O. moco* (Duméril & Bibron) (Barr 2019; Gillanders 2017, 2018) and as of 2016 the introduced plague skink, *Lampropholis delicata* (De Vis) (Gillanders 2017); and one gecko: *Mokopirirakau*

granulatus (Gray). Three other gecko species (*Dactylocnemis pacificus* (Gray), *Naultinus elegans* Gray and *Woodworthia maculata* (Gray)) occur in the reserve. *Oligosoma kakerakau* **sp. nov.** are the most frequently observed of all the species (Barr 2019; Gillanders 2017, 2018). Despite having a very similar niche to *O. moco* and *L. delicata*, and being syntopic with *O. aeneum* and *O. ornatum*, interspecific aggression is observed infrequently (B. Barr unpubl. data). Rather, *O. kakerakau* **sp. nov.** is regularly observed in close proximity with the other species sometimes not interacting at all; for example, an *O. aeneum* was observed walking on top of a basking *O. kakerakau* **sp. nov.** which remained motionless (unpubl. data). However, *O. kakerakau* **sp. nov.** has been observed 'snapping' at *L. delicata*, and *L. delicata* has been observed 'startling' *O. kakerakau* **sp. nov.**. Similarly, intra-specific aggression has been observed, albeit infrequently (Unpubl. data).

The maximum SVL recorded for this species is 67 mm, the most common size category is 51–60 mm (Wiles 2014). It is viviparous. Young appear to be born in late summer, but the litter size is unknown.

Conservation Status. *Oligosoma kakerakau* **sp. nov.** is currently listed under the New Zealand National Threat Classification System as 'Nationally Critical' by Hitchmough *et al*. (2016). This listing uses criterion A(3) on the basis that the total known area of occupancy (AOO) is ≤ 1 ha (0.01 km^2), and the qualifiers Conservation Dependent, Range Restricted, and Sparse (Townsend *et al*. 2008) also apply. The species potentially qualifies for listing as Critically Endangered under the IUCN Red List criteria (IUCN 2012). Its AOO and Extent of Occurrence (EOO) are both <4 km^2, and it has 2 known locations, which are severely fragmented. Invasive mammalian predators are inferred to be a source of past, current and ongoing decline in EOO, AOO, and number of mature individuals. Thus, the species may be listed as Critically Endangered B1ab(i,ii,v)+B2ab(i,ii,v).

Discussion

Our morphological and molecular phylogenetic data provide evidence that *O. kakerakau* **sp. nov.** is a distinct species nested within clade 5 of the New Zealand skink fauna (Chapple *et al*. 2009), and sister to *O. zelandicum*. We include the Whirinaki record in *O. kakerakau* **sp. nov.** on the basis that all observable and described characters of the individual skink found in Whirinaki Te Pua-a-Tāne match the characters of the Bream Head population and the type series: speckled ventral surface, distinctive cream coloured teardrop under the eye, distinct dorsolateral stripe, distinct mid-lateral stripe that passes through the ear and is broken above the forelimb, upper lateral zone between the dorsolateral and mid-lateral stripe is dark brown and unmarked, cream dorsoanterior stripe running down forelimb. In contrast there are notable differences with all other known taxa (the late Tony Whitaker, pers. comm.). Although the lone Whirinaki individual is separated from the Whangārei population by ~370 km, it is probable that historically *O. kakerakau* **sp. nov.** was widespread in the northern North Island biogeographic region (Chapple & Hitchmough 2016). Its southern boundary is likely to be the diffuse biogeographic boundary widely referred to as the "Taupo line" (Chapple & Hitchmough 2016), which is associated with the location of the "Manawatu Strait" during the Pliocene. Therefore *O. kakerakau* and *O. zelandicum* occupy different biogeographic regions of the New Zealand North Island which have largely non-overlapping faunas (Chapple & Hitchmough 2016), and the distance between the two species is much smaller that the extent of each species (Figure 1).

This pattern of distribution is shared with many New Zealand lizard species including: *Naultinus elegans, Mokopiriraku granulatus, Dactylocnemis pacificus, Toropuku inexpectatus* Hitchmough *et al*., *O.* oliveri (McCann), *O. robinsoni* (Wells & Welington), *O. striatum, O. suteri* (Boulenger), *O. moco, O. smithi* (Gray) and *O. townsi* (Chapple *et al.*) (van Winkel *et al*. 2018). The apparent absence of *O. kakerakau* **sp. nov.** across the majority of its range is likely due to range contractions brought about by introduced mammalian predators, as well as habitat alteration and fragmentation (Towns & Daugherty 1994). However, it is also possible that other populations exist but have remained undetected because of the cryptic nature of this species and/or due to their remoteness.

The genetic divergence of *O. kakerakau* **sp. nov.** and *O. zelandicum*, and the estimated divergence times support the idea of speciation either side of the Manawatu Strait. This strait is believed to have formed during the Opoitian (5.33–3.7 mya) during the Tangahoe pull down event (Milner 2017) that would have inundated the lower North Island. The divergence times of *O. kakerakau* **sp. nov.** and *O. zelandicum* are slightly more recent than this (~2.4 mya); however, Trewick & Bland (2012) suggest that Manawatu strait probably did not exist as a single, wide, long-lived entity as sometimes suggested (e.g. Bunce *et al*. 2009), but rather a dynamic system of narrow (<20 km wide) and relatively short-lived (c. 2–5 my) features. Thus, precisely identifying the time and place of reproductive

isolation is difficult. Subsequent to the final closure of the Manawatu Strait and the uplift of the Lower North Island (Milner 2017), *O. zelandicum* is thought to have colonised the Lower North Island from a single colonisation event from the South Island (0.46 mya) using the initial landbridge across the Cook Strait (O'Neill *et al*. 2008). Future studies should complete more detailed sampling across the North Island, and include nuclear datasets, to investigate the potential for contact and introgression between *O. kakerakau* **sp. nov.** and *O. zelandicum*. This additional sampling will undoubtedly improve our understanding of the taxonomic relationships, and evolutionary history of these taxa.

Exotic predator control and population monitoring should continue at Bream Head. Passive sampling techniques such as tracking tunnels could be deployed arboreally to detect the population at Whirinaki, and possible additional populations between these two known localities. To lower the extinction risk, a wild to wild translocation to a predator free island could be undertaken to create a second population.

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