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## A new skink species (*Oligosoma taumakae* sp. nov.; Reptilia: Scincidae) from the Open Bay Islands, New Zealand

DAVID G. CHAPPLE\*

Allan Wilson Centre for Molecular Ecology and Evolution  
School of Biological Sciences  
Victoria University of Wellington  
PO Box 600  
Wellington 6140, New Zealand

GEOFF B. PATTERSON

149 Mairangi Road  
Wilton  
Wellington 6140, New Zealand

\*Present address: David Chapple, Museum Victoria, Herpetology Section, GPO Box 666, Melbourne Victoria 3001, Australia. dchapple@museum.vic.gov.au

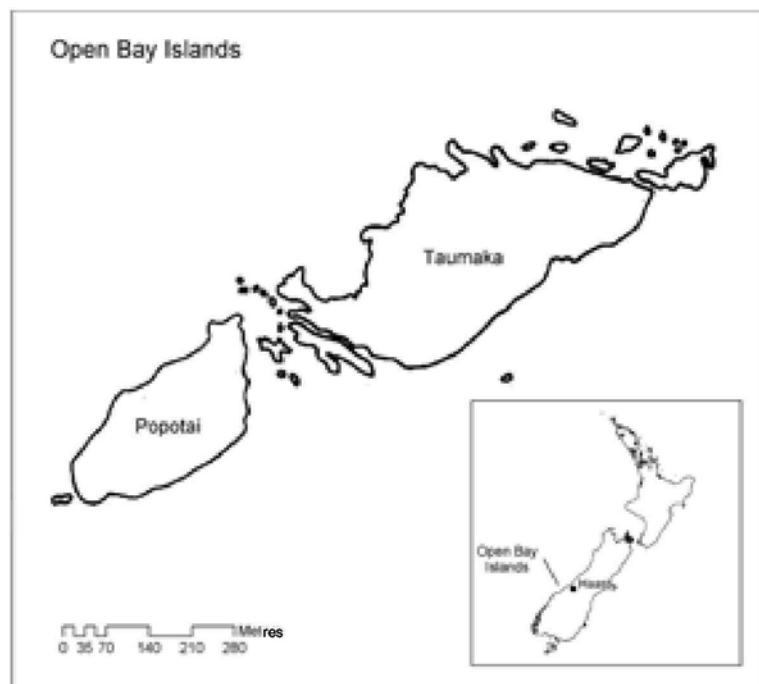
**Abstract** We describe a new skink species (*Oligosoma taumakae* sp. nov.) from the Open Bay Islands, New Zealand. This species is diagnosed on the basis of several morphological characteristics, and its specific status is supported by mitochondrial sequence data (ND2, ND4). The new species appears to be most closely related to *O. acrinasum*, *O. infra-punctatum*, *O. ottagense* and *O. waimatense*. The new taxon appears to be rare and endemic to the island of Taumaka in the Open Bay Islands (off the west coast of the South Island). Predation by a flightless rail (weka, *Gallirallus australis*), native to New Zealand but introduced to the Open Bay Islands, is a major conservation concern.

**Keywords** mitochondrial DNA; morphology; ND2; ND4; Scincidae; taxonomy

### INTRODUCTION

The New Zealand archipelago supports a diverse endemic skink fauna, given the cool temperate climate, latitude, and relatively small land area (Daugherty et al. 1990; Hickson et al. 2000; Gill & Whitaker 2001). At present there are 28 described species in two genera, *Oligosoma* (22 species) and *Cyclodina* (six species) (Gill & Whitaker 2001). However, the morphological conservatism evident within the New Zealand skink radiation conceals the complex taxonomic history and true diversity of this group (Hardy 1977; Patterson & Daugherty 1990, 1995). Molecular studies have provided substantial insight into the taxonomy of New Zealand skinks, revealing a high incidence of cryptic species (e.g., Daugherty et al. 1990; Hickson et al. 2000). In addition, putative new species continue to be discovered in remote regions of the country (Patterson 2002; Jewell & Tocher 2005). Although many of these undescribed species have been known for some time, they are yet to be formally described (Patterson 2002). Here we describe a new skink species from the Open Bay Islands, off the west coast of the South Island of New Zealand.

The Open Bay group comprises two main islands (plus several smaller islets and rocks), Taumaka and Popotai. They are located approximately 5 km offshore of the Okuru River mouth, near Haast (Fig. 1, 2). Taumaka is the larger island (c. 20 ha, 660 m long and 260 m wide) and is separated from Popotai (400 m long and 200 m wide) by a narrow channel (Craig Miller 1997, 1999). The bedrock is comprised of indurated, semi-crystalline contorted, Oligocene limestone with layers of muddy limestone, which is overlaid by a shallow (1.5–12 m) sheet of glacial till (Mutch & McKellar 1964; Burrows 1972; Craig Miller 1997, 1999). The summit of Taumaka is a shrub covered plateau approximately 21 m above sea level, with large glacial boulders scattered across the island (Burrows 1972). The vegetation on both islands is dominated by a dense cover of shrubs (kiekie, *Freyinetia banksii*), and small trees (mahoe, *Melicytus ramiflorus*) (Cockayne 1904; Burrows



**Fig. 1** Map of the Open Bay Islands (Taumaka and Popotai), with the inset indicating their location off the coast of Haast in the South Island of New Zealand (adapted from Craig Miller 1999).

1972). A native climber (pohuehue, *Muehlenbeckia australis*) is widespread on the edges of the shrubland and within the canopy. Detailed surveys of the fauna of the Open Bay Islands have been limited to birds (Stirling & Johns 1969) and arachnids (Skeel 1974). Although introduced mammals are not known ever to have reached the islands, the introduction of weka (a native flightless rail, *Gallirallus australis*) from the South Island in the early 1900s is believed to have had an adverse impact on the flora and fauna of the islands (Stirling & Johns 1969; Burrows 1972; Craig Miller 1997, 1999).

The Open Bay Islands support several endemic species, including a terrestrial leech (*Hirudobdella antipodum*; Craig Miller 1997, 1999) and an undescribed gecko species (aff. *Hoplodactylus granulatus*, Hitchmough 1997; Whitaker & Lyall 2004; Hitchmough et al. 2007). Skinks were not observed on the Open Bay Islands until 1988, when researchers discovered them under roofing iron placed next to a hut on Taumaka (Patterson 2002; Fig. 3A). Morphological examination of one specimen suggested that it closely resembled the speckled skink, *O. infrapunctatum* (Patterson 2002; Whitaker & Lyall 2004), but preliminary allozyme data indicated that it was a distinct taxon, closely related to the scree skink, *O. waimatense* (Clare Miller 1999). Subsequent

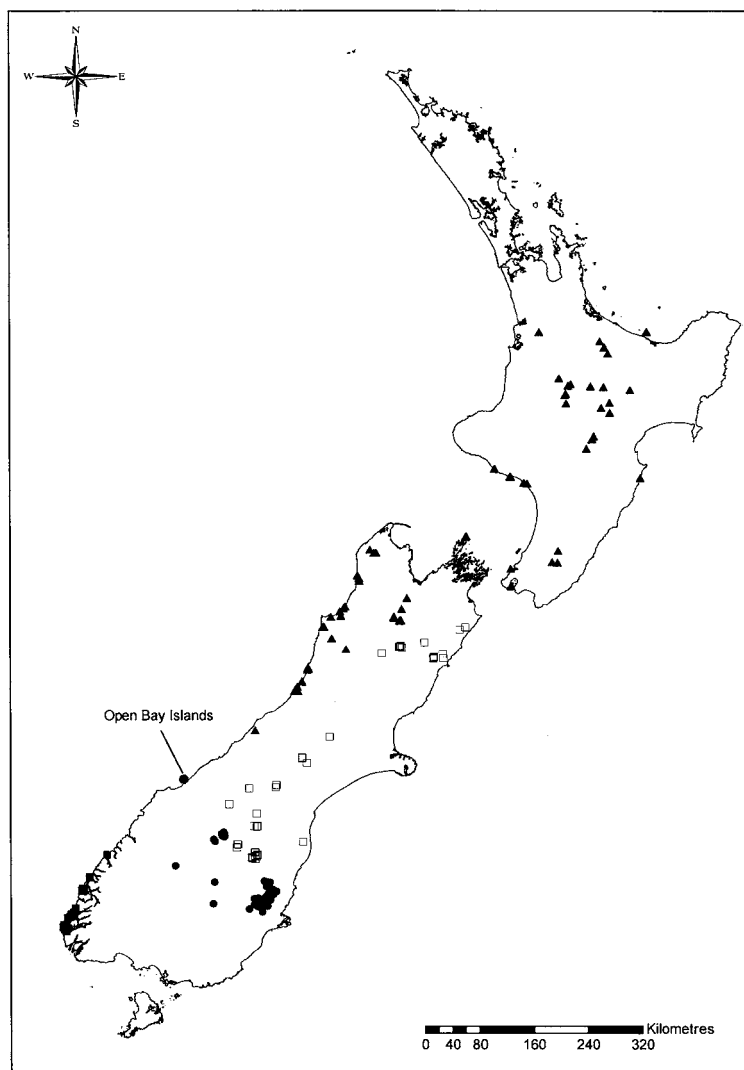
morphological analysis identified several characters distinguishing the specimen from *O. infrapunctatum*. Thus, although both the morphological and allozyme data provide strong evidence for its specific status, its exact phylogenetic affinities are unknown. Whitaker & Lyall (2004) listed description of this taxon as a research priority, along with determination of its phylogenetic affinities. Here, we formally describe the Open Bay Islands skink on the basis of morphological characteristics and mitochondrial sequence data (ND2, ND4) and provide evidence of its taxonomic affinities. Formal description will provide a framework for future research on the biology and ecology of this species, facilitating improved conservation management.

## MATERIALS AND METHODS

### Morphological analyses

The species description is based on two specimens of the Open Bay Islands skink from Taumaka Island, Open Bay Islands (Appendix 1). This species appears to be extremely rare on Taumaka Island (Whitaker & Lyall 2004), and these two specimens are believed to be the only animals ever collected from the island.

**Fig. 2** Map of New Zealand indicating the distribution of the species most closely related to the Open Bay Island skink: the Fiordland skink (*Oligosoma acrinasum*; solid black squares), the speckled skink (*O. infrapunctatum*; solid black triangles), the Otago skink (*O. otagense*; solid black circles) and the scree skink (*O. waimatense*; hollow squares) (data from the Department of Conservation's BioWeb Herpetofauna Database 2006). The location of the Open Bay Islands is indicated.



Morphological comparisons were made with the closely related species *O. otagense* (23 specimens; data from Patterson 1997), *O. waimatense* (21 specimens; data from Patterson 1997), *O. infrapunctatum* (10 specimens; this study, and additional data from Hardy 1977) and *O. acrinasum* (11 specimens; data from Hardy 1977) (Appendix 1).

Descriptions of morphology follow the techniques described in Patterson & Daugherty (1990, 1994, 1995). Midbody scale rows were counted at the midpoint between the fore- and hind legs. Ventral scales were counted in a line from the mental scale to the vent (including the mental and one preanal

scale). The subdigital lamellae were counted on the fourth hind toe of the right foot. Diagnostic head scales were counted (see Patterson & Daugherty 1990). The following nine measurements (mm) were made on all specimens: axilla to groin (AG), snout to axilla (SF), snout to ear (S-E), ear to axilla (EF), head length (HL) from the posterior part of the interparietal to the tip of the snout, head width (HW) between the lateral edges of the left and right parietals, intact tail length, fourth hind toe length from base of toe to tip excluding nail (FTL), and snout-vent length (SVL) (Patterson & Daugherty 1990, 1994).

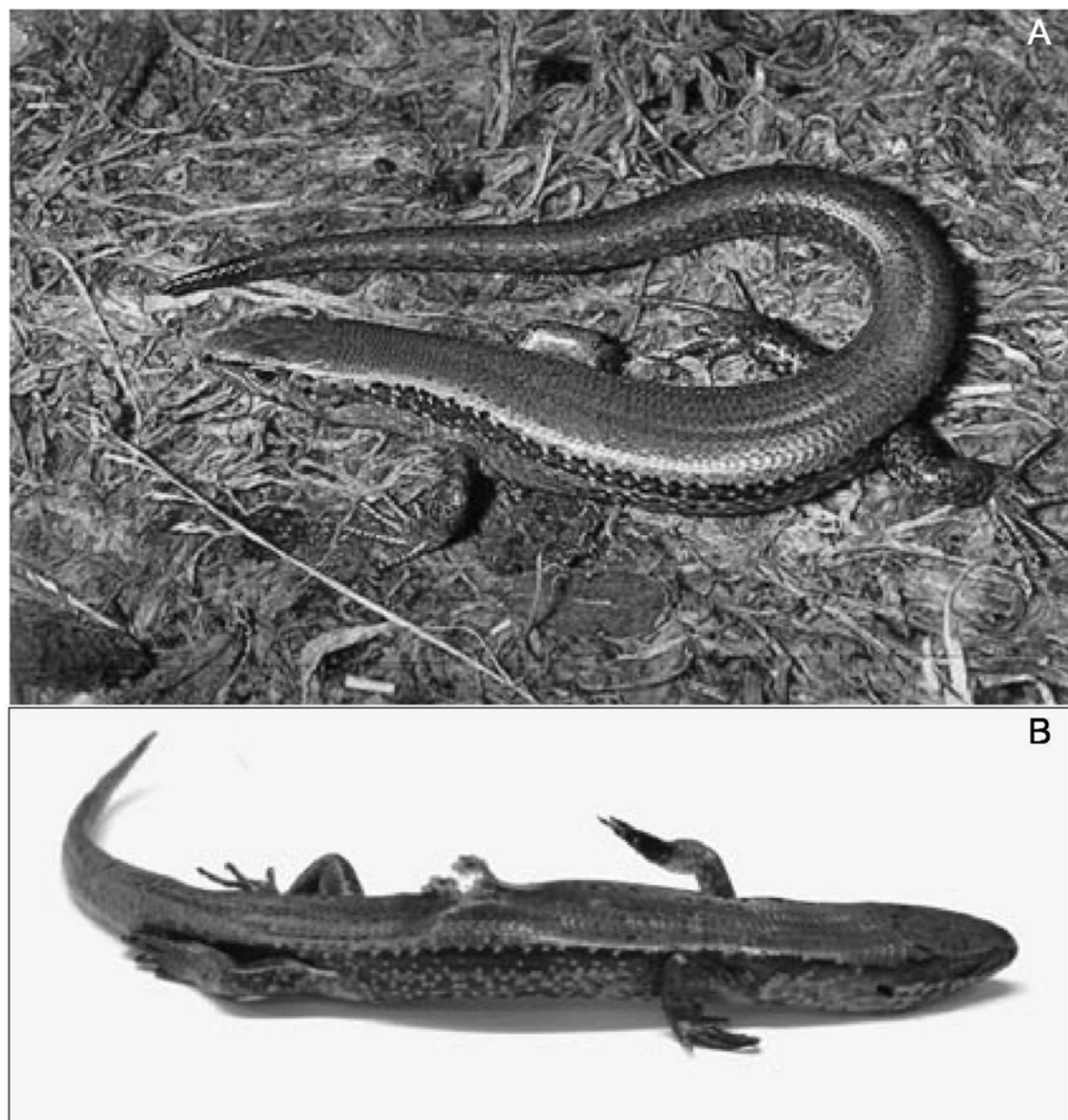


Fig. 3 A, Photo of *Oligosoma taumakae* in life. B, *Oligosoma taumakae* holotype (RE5237).

### Mitochondrial DNA analyses

#### Taxonomic sampling

Tissue samples were obtained from the same two specimens of the Open Bay Islands skink used for the morphological analyses (Table 1; Fig. 1, 2). Based on the results of a broader phylogenetic study of the relationships among all members of the New Zealand skink radiation (D. G. Chapple,

P. A. Ritchie & C. H. Daugherty unpubl. data), we included samples from all described species (*O. acrinasum*, *O. infrapunctatum*, *O. otagense* and *O. waimatense*) in the same subclade as the Open Bay Islands skink (Table 1; Fig. 2). Several other *Oligosoma* (*O. nigriplantare polychroma*, *O. smithi* and *O. zelandicum*) and *Cyclodina* (*C. oliveri*) species were included as outgroups in the study (Table 1). Samples were obtained from the National Frozen

Tissue Collection (NFTC, Victoria University of Wellington, New Zealand) and an ethanol preserved specimen housed at Te Papa (National Museum of New Zealand, Wellington).

#### *DNA extraction, amplification and sequencing*

Total genomic DNA was extracted from liver, toe or tail samples using a modified phenol-chloroform extraction protocol (Sambrook et al. 1989). For each sample we targeted portions of the mitochondrial genes ND2 (c. 600 bp) and ND4 (c. 850 bp, incorporating most of the flanking 3'tRNA cluster, including the histidine and serine tRNA genes). These regions were targeted because work at comparable taxonomic levels in other squamate reptile groups has indicated useful levels of variability (Chapple & Keogh 2004; Chapple et al. 2004, 2005; Keogh et al. 2005).

Several primers were used to amplify and sequence ND2 (L4437, Macey et al. 1997; ND2r102, Sadlier et al. 2004) ND4 (ND4I, tRNA-Leu, Forstner et al. 1995; ND4R-NZ, 5'CCAAGRGTGTTTGGTGCCTAAGACC3', Greaves et al. 2007). PCR and sequencing were conducted as outlined in Greaves et al. (2007).

Sequence data were edited using ContigExpress version 9.1.0 (Invitrogen), and aligned using the default parameters of Clustal X (Thompson et al. 1997). The aligned sequences were translated into

amino acid sequences using the vertebrate mitochondrial code to check whether the sequences were truly mitochondrial in origin. As no premature stop codons were observed (apart from within the tRNAs flanking the ND4 sequence) and no indels were present, we conclude that all sequences obtained are true mitochondrial copies. GenBank accession numbers for all sequences are provided in Table 1.

#### *Phylogenetic analyses*

We completed a partition homogeneity test in PAUP\* version 4.0b10 (Swofford 2002) to confirm that the phylogenetic signal from ND2 and ND4 was concordant (100 replicates,  $P = 0.55$ ) prior to concatenating the sequences for each sample into a single dataset. A maximum parsimony (MP) tree was generated in PAUP\* using the heuristic search option. ModelTest 3.7 (Posada & Crandall 1998) was used to determine the most appropriate model of evolution for our dataset, generating log-likelihood scores for the dataset in PAUP\* and conducting a hierarchical likelihood ratio test (hRLT). Base frequencies, substitution rates, gamma distribution (G), the proportion of invariant sites (I) and the among-site substitution rate variation were estimated in ModelTest, with these values implemented in PAUP\* to generate a maximum likelihood (ML) tree.

Bayesian analyses were completed using the computer program MrBayes 3.1.2 (Huelsenbeck &

**Table 1** Locality information and GenBank accession numbers for samples used in this study. 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, National Museum of New Zealand, Wellington.

Species	Tissue code	Museum code	Locality	GenBank accession no.	
				ND2	ND4
<i>Oligosoma taumakae</i>	OBI2	RE5237	Taumaka Island, Open Bay Islands	EF033048	EF033062
<i>Oligosoma taumakae</i>	OBI3	FT311	Taumaka Island, Open Bay Islands	EF033049	EF033063
<i>Oligosoma acrinasum</i>	OAC1	CD826	Fiordland	EF033046	EF033060
<i>Oligosoma acrinasum</i>	OAC3	RE1839	Five Fingers Peninsula, Resolution Island	EF033047	EF033061
<i>Oligosoma infrapunctatum</i>	OIF1	CD545	Stephens Island	EF033050	EF033058
<i>Oligosoma infrapunctatum</i>	OIF2	FT3749	Cobden Beach	EF033051	EF033059
<i>Oligosoma otagense</i>	OOT1	CD1053	Central Otago	EF033053	EF033064
<i>Oligosoma otagense</i>	OOT2	CD349	Macraes Flat	EF033054	EF033065
<i>Oligosoma waimatense</i>	OWA2	CD1209	Wairau River, Marlborough	EF033056	EF033066
<i>Oligosoma smithi</i>	OSM1	FT166	Middle Island, Mercury Islands	EF033055	EF033067
<i>Oligosoma zelandicum</i>	OZE3	FT3814	Mokihinui River Mouth	EF033057	EF033070
<i>Oligosoma nigriplantare polychroma</i>	ONP1	FT5252	Pukerua Bay	EF033052	EF033068
<i>Cyclodina oliveri</i>	COL1	CD1034	Aorangi Island, Poor Knights Islands	EF033045	EF033069

Ronquist 2001). We used the default value of four Markov chains per run, and ran the analysis for 1 million generations. The analysis was completed using a single partition using the model selected by ModelTest with the default priors. The chain was sampled every 100 generations in order to obtain 10 000 sampled trees. The program Tracer 1.3 (Rambaut & Drummond 2003) was used to check for chain convergence. The first 2500 sampled trees were discarded as the burn-in phase, with the last 7500 trees used to estimate the Bayesian posterior probabilities. We used both bootstrap values and Bayesian posterior probabilities to assess branch support. Parsimony bootstraps (1000 replicates) were generated in PAUP\*. We consider branches supported by bootstrap values greater than or equal to 70% (Hillis & Bull 1993), and posterior probability values greater than or equal to 95% (Wilcox et al. 2002) to be significantly supported by our data. Pairwise HKY corrected genetic distances were calculated in PAUP\*.

## RESULTS

### Species description

Genus *Oligosoma* Girard, 1857

*Oligosoma taumakae* sp. nov.

HOLOTYPE: Taumaka Island, Open Bay Islands (43°52'S, 168°53'E), RE5237 (collected by P. A. Van Klink in December 1998) (Fig. 3B).

PARATYPE: Taumaka Island, Open Bay Islands (43°52'S, 168°53'E), FT311 (collected by P. Carey in March 1988).

DESCRIPTION: Body elongate, oval in cross-section; limbs well-developed, pentadactyl. Lower eyelid with a transparent palpebral disc, bordered on sides

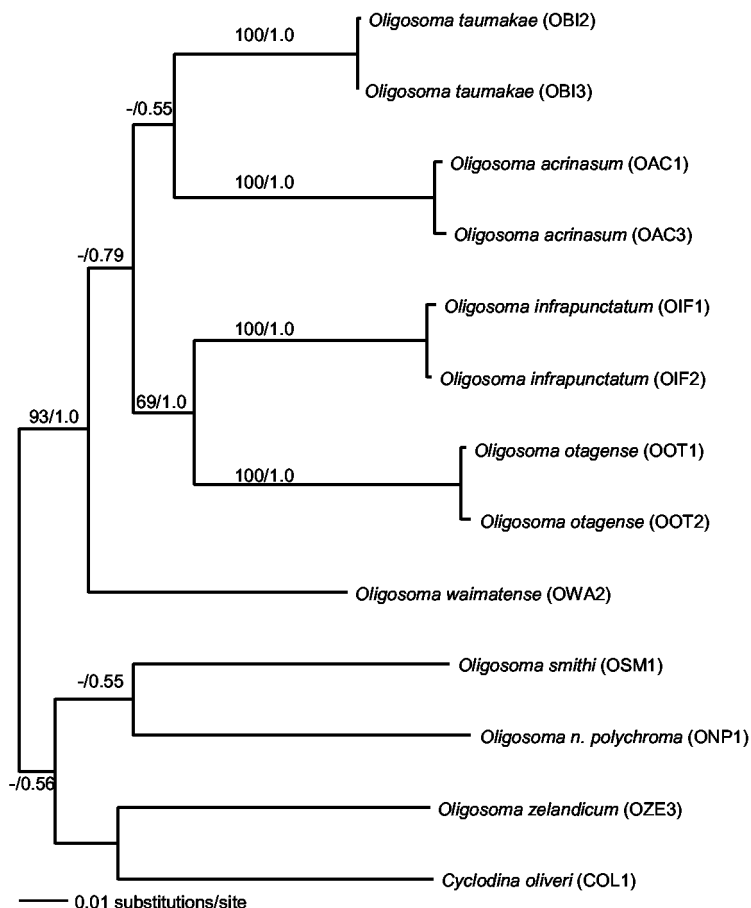
and below by small, oblong granules. Snout moderately blunt. Nostril centred just below middle of nasal, pointing up and back. Supranasals absent. Rostral broader than deep. Frontonasal broader than long, not separated from frontal by prefrontals meeting in midline. Frontal longer than broad, similar length to frontoparietal and interparietal together, in contact with one or two anteriormost supraoculars. Supraoculars 3 or 4, the first or second largest. Frontoparietals distinct, larger than interparietal. A pair of parietals meeting behind interparietal and bordered posteriorly by a pair each of nuchals and temporals, also in contact with interparietal, frontoparietal, third or fourth supraocular and two postoculars. Loreals 2, of similar sizes; anterior loreal in contact with first or second supralabial, posterior loreal, prefrontal, frontonasal and nasal; posterior loreal in contact with second, or second and third supralabial, first subocular, upper and lower preocular, prefrontal and anterior loreal. Supralabials 7, the sixth or seventh largest. Infralabials 6 or 7, several of them equal in size; fifth supralabial below centre of eye. Postmental similar to mental. Chinshields 3 pairs. One primary temporal. Dorsal scales largest, weakly striate. Ventral scales smooth. Subdigital lamellae smooth. Upper ciliaries 6–7; lower ciliaries 9–12; nuchals 3–4 pairs; midbody scale rows 32–34; ventral scale rows 72–76; subdigital lamellae 21 ( $n = 2$ ); supraciliaries 5; suboculars 7. Maximum SVL 78.9 mm (shrinkage about 5% based on original records).

Ratios for morphological measurements (RE5327 then FT311) (actual measurements in mm provided in parentheses): AG/SF 1.2 (27/22.6), 1.3 (37.9/28.6); S-E/EF 1.1 (11.5/11), 0.9 (14.2/15.3); HL/HW 1.6 (9.6/6), 1.45 (10.7/7.4); FTL 6.8, 9.3 (Table 2). Neither specimen had an intact tail. Ear opening round, moderately large, with one or more projecting granules on anterior margin. Forelimbs shorter than

**Table 2** Morphological comparison of *Oligosoma taumakae* with its closest relatives: *O. infrapunctatum*, *O. acrinusum*, *O. ottagense* and *O. waimatense*. Data from Patterson (1997) for *O. ottagense* and *O. waimatense*. Data from Hardy (1977) for *O. acrinusum*. AG = axilla to groin length; SF = snout to axilla length; S-E = snout to ear length; EF = ear to axilla length.

Character	<i>O. taumakae</i> ( $n = 2$ )	<i>O. infrapunctatum</i> ( $n = 10$ )	<i>O. acrinusum</i> ( $n = 11$ )	<i>O. ottagense</i> ( $n = 23$ )	<i>O. waimatense</i> ( $n = 21$ )
Midbody scale rows	32–34	29–37	37–38	46–72	50–68
Ventral scale rows	72–76	70–89	90–100	92–126	97–122
Subdigital lamellae	21	18–28	16–19	23–30	25–33
Supraciliaries	5	6–9	7–8	6–9	6–11
AG/SF	1.26	1.6	1.62	1.33	1.30
S-E/EF	0.99	1.16	1.24	1.16	1.16

**Fig. 4** Maximum likelihood (ML) tree for *Oligosoma taumakae* and the closely related species *O. acrinasum*, *O. infrapunctatum*, *O. otagense* and *O. waimatense* based on the combined ND2 and ND4 mitochondrial data (1324 bp). The topology of the maximum parsimony and Bayesian trees were identical to the ML tree shown. Two measures of branch support are indicated, with parsimony bootstraps shown on the left and Bayesian posterior probabilities on the right (only values over 50 and 0.5, respectively, are shown).



hind limbs. Adpressed limbs barely meeting in adult. Digits moderately long, subcylindrical. Third front digit as long as the fourth or shorter.

Dorsal surface grey brown. Median dorsal stripe absent. Dorsal colour pattern an irregular arrangement of brown and black speckles. Dorsolateral line indistinct, notched on both margins. Lateral stripe dark brown extending from nostril above limb insertions to base of tail and beyond, flecked with light scales. Below this strip an indistinct pale lateral stripe, toothed on both margins, extending from behind ear to base of tail. Underside pale yellow, slightly speckled with dark brown. Outer surface of forelimbs grey-brown with dark brown speckling. Juvenile coloration unknown.

**DIAGNOSIS:** *Oligosoma taumakae* is recognised using both the phylogenetic (Fig. 4) and genotypic cluster species concepts (see Coyne & Orr 2004). Since *O. taumakae* is allopatric from its congeners,

the biological species concept is not applicable. The new species can be distinguished from its closest relatives (*O. acrinasum*, *O. infrapunctatum*, *O. otagense*, *O. waimatense*; see "Mitochondrial DNA analyses") on the basis of several characteristics. Its coloration differs from *O. acrinasum*, *O. otagense* and *O. waimatense*, which do not have brown coloration. Although coloration is very similar in both *O. taumakae* and *O. infrapunctatum*, a lower pale stripe is usually more distinct in *O. infrapunctatum*, and there is less flecking on the brown dorsolateral stripe compared to *O. taumakae*.

*Oligosoma taumakae* is superficially similar in appearance to some specimens of *O. infrapunctatum*. However, foot size clearly distinguishes these two species, with FTL approximately 25% greater in *O. taumakae* compared to *O. infrapunctatum* of similar SVL (SVL/FTL: *O. taumakae* 8.27 [ $n = 2$ ], *O. infrapunctatum* SVL/FTL 10.24 [ $n = 10$ ]). There is

also no overlap in supraciliary count, with 5 in *O. taumakae* compared with 6–9 in *O. infrapunctatum* (Hardy 1977; this study). Another feature of *O. taumakae* is an enlargement of several upper ciliary scales to form a flap overhanging the eye, which is more pronounced than in *O. infrapunctatum*. Several body ratios also appear to differ between *O. taumakae* and its closest relatives (see Table 2), although the small number of available *O. taumakae* specimens precludes statistical analyses.

The midbody scale count of *O. taumakae* (32–34) has no overlap with *O. acrinasum* (37–38), *O. waimatense* (50–68), or *O. otagense* (46–72) (Table 2). Since the geographic ranges of *O. acrinasum*, *O. waimatense* and *O. otagense* do not overlap with *O. taumakae* (Fig. 2), and *O. taumakae* is the only skink species present on the Open Bay Islands, identification of this new species should prove relatively straightforward.

**ETYMOLOGY:** From Taumaka Island, the type locality. Common name is the Open Bay Islands skink.

**DISTRIBUTION AND ECOLOGY:** *Oligosoma taumakae* is known only from the island of Taumaka in the Open Bay Islands off the south Westland coast of Haast (Whitaker & Lyall 2004). The biology, ecology and life history of this species is poorly known, although it is believed to have a low population density (Whitaker & Lyall 2004). Surveys over the past two decades have reported limited sightings of *O. taumakae* (<10 individuals per survey), with skinks predominantly observed in locations that are inaccessible to weka (Miskelly 1993). The skinks are most commonly sighted in a pile of wood and corrugated iron near the hut on the island, within the wall linings of the hut, and on a rock face just below the hut (Miskelly 1993). However, two individuals have been found halfway down the island on a slab of limestone covered in a cloak of the creeping vine, *Muehlenbeckia australis* (Peter Carey pers. comm.). It is a diurnal species that inhabits coastal forest, shrubland and supralittoral vegetation (sedge, tussocks and ferns) (Patterson 2002; Whitaker & Lyall 2004). *Oligosoma taumakae* is believed to be viviparous. The largest individual caught had a SVL of 92 mm and a mass of c. 20 g (Miskelly 1993; Whitaker & Lyall 2004). Although most skinks have been observed under cover, one individual has been observed actively basking (A. H. Whitaker pers. obs.).

**REMARKS:** *Oligosoma taumakae* is currently listed in New Zealand as Nationally Critical (Data Poor, One Location; Hitchmough et al. 2007). Its conservation

status is based primarily on it being restricted to a single island locality (20 ha). The formal description of *O. taumakae* will act to consolidate its conservation status in New Zealand and provide the basis for future research on this poorly known species.

### Mitochondrial DNA analyses

Following concatenation, the edited alignment comprised 1324 characters (550 bp ND2, 774 bp ND4), of which 404 (31%) were variable and 290 (22%) were parsimony-informative. For the ingroup only, the alignment contained 270 (20%) variable characters of which 225 (17%) were parsimony-informative. Base frequencies were unequal (A = 0.331, T = 0.245, C = 0.292, G = 0.132), but a  $\chi^2$  test confirmed the homogeneity of base frequencies among sequences (d.f. = 36,  $P$  = 0.328).

The hRLT from ModelTest supported the HKY + I + G substitution model as the most appropriate for our dataset ( $-\ln L$  = 4964.0957). Parameters estimated under this model were: relative substitution rates (A↔C = 4.13, A↔G = 36.22, A↔T = 2.86, C↔G = 2.90, C↔T = 31.93, G↔T = 1.00), gamma shape parameter (1.5991) and proportion of invariable sites (0.5784). The topology of the MP, ML and Bayesian trees was identical. Figure 4 shows the optimal ML tree ( $-\ln L$  = 5292.577), with bootstrap values and posterior probabilities indicating branch support. *Oligosoma taumakae* forms an extremely well-supported clade within the phylogeny (bootstrap 100, posterior probability 1.0), although its closest relative is not resolved. The mean genetic distance between *O. taumakae* and the most closely related described species range between 0.0924 and 0.1036 (Table 3), which is comparable to the mean genetic distance between other recognised species within the same clade (range 0.1056–0.1187).

**Table 3** HKY corrected genetic distances between *Oligosoma taumakae* and the closely related species *O. acrinasum*, *O. infrapunctatum*, *O. otagense* and *O. waimatense*.

Species	Mean genetic distance	Range
<i>O. acrinasum</i>	0.0924	0.0911–0.0937
<i>O. infrapunctatum</i>	0.0927	0.0922–0.0932
<i>O. otagense</i>	0.1013	0.0999–0.1026
<i>O. waimatense</i>	0.1036	0.1031–0.1040

## DISCUSSION

The formal description of *Oligosoma taumakae* is an essential step in enhancing the conservation management of this rare endemic species on the Open Bay Islands. Although the Open Bay Islands have no history of permanent human inhabitation (Burrows 1972), the introduction of weka sometime between 1905–12 may have had a significant impact on the fauna of the islands (Stirling & Johns 1969; Skeel 1974; Craig Miller 1997, 1999). Weka have flourished on the islands since their introduction and are now widespread on Taumaka (Burrows 1972). Soil disturbance as they search, scratch and dig for food is believed to have inhibited regeneration of the island's shrubby vegetation, even on relatively inaccessible cliff ledges (Burrows 1972). The low density of ground dwelling invertebrates on the islands (Stirling & Johns 1969; but see Skeel 1974) and the restricted abundance and distribution of the endemic Open Bay Islands leech (Craig Miller 1997, 1999) have been attributed to weka predation.

On the other hand, the only direct evidence for the adverse influence of weka on the fauna of the islands comes from an observation of weka destroying eggs from a spotted shag's (parekareka, *Stictocorbo punctatus*) nest (Stirling & Johns 1969). The potential impact of weka on *O. taumakae* requires further investigation, since the skink's terrestrial and diurnal habits must make it highly accessible to weak predation (Whitaker & Lyall 2004). Weka have been suggested to be "voracious lizard predators" in other regions of New Zealand (reviewed in Whitaker & Lyall 2004). The fact that most *O. taumakae* on Taumaka have been found in areas inaccessible to weka (e.g., under corrugated iron) suggests that weka are having an adverse impact on this skink (Craig Miller 1997). Accordingly, the New Zealand Department of Conservation has recommended the control and/or eradication of weka from the Open Bay Islands (Whitaker & Lyall 2004).

The Open Bay Islands support at least three endemic species, a leech (Craig Miller 1997, 1999), an undescribed gecko (Hitchmough 1997; Whitaker & Lyall 2004; Hitchmough et al. 2007) and a skink (this study). However, the reason why there are endemic species on these islands has yet to be examined in detail. The Open Bay Islands are located 5 km off the west coast of the South Island, separated by a maximum water depth (at present) of about 45 m (Burrows 1972). The islands were repeatedly connected to the South Island mainland during Pleistocene glacial cycles, including within

the last 10 kyr (Cockayne 1904; Burrows 1972). Taumaka has geological characteristics (e.g., outcrops of Landon limestone and glacial deposits) similar to those found at Jacksons Bay and near Martins Bay on the adjacent coast of the South Island (Cockayne 1904; Mutch & McKellar 1964; Burrows 1972). The endemic fauna might therefore represent remnant populations of species that were once more widely distributed on the mainland South Island. Indeed, Whitaker & Lyall (2004) suggested that *O. taumakae* might not represent a primary endemic, and could exist in undiscovered populations on nearby islands (e.g., Popotai Island, Barn Islands, Cascade Island, Browne Island and Gorge Island) and/or coastal and lowland habitats between Paringa River and the Cascade River on the adjacent mainland. This possibility warrants future research and surveys in these areas. It is clear that further study is needed to improve our knowledge of the distribution, biology and ecology of *O. taumakae* in order to conserve this rare species.

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**Appendix 1** Specimens examined. Abbreviations used: RE (Te Papa, National Museum of New Zealand, Wellington; S codes refer to specimens from the former Ecology Division collection, now housed at Te Papa; CD and FT codes refer to specimens from the Charles Daugherty, Victoria University of Wellington collection, now housed at Te Papa); CM (Canterbury Museum, Christchurch, New Zealand); OM (Otago Museum, Dunedin, New Zealand); MCZ (Museum of Comparative Zoology, Harvard, USA); BMNH (British Museum of Natural History).

*Oligosoma taumakae*—Taumaka Island, Open Bay Islands, FT 311 and RE5237.

*Oligosoma acrinasum*—Specimens examined by Hardy (1977): westernmost island in Gilbert Islands Group, Breaksea Sound, RE4452 (S810), RE4461 (S819), RE4462 (S820), RE4463 (S821), RE4464 (S822) (NOTE: a total of 11 specimens were examined. In some instances, the same accession number relates to multiple specimens).

*Oligosoma infrapunctatum*—Ngongataha (Rotorua), CD2531; Taumaranui, CD2532 and CD2533; Locality unknown, FT333; St Arnaud, FT3003; Westport, FT3004; Whale (Moutohora) Island, FT3023, FT3024; Granity, FT3395; Kaniere, Hokitika, FT3476. Additional specimens examined by Hardy (1977).

*Oligosoma ottagense*—Specimens examined by Patterson (1997): Foulden Hills, Middlemarch, RE1835; Macraes Flat, RE2101, RE5147 (S1512), RE 5148 (S1513); Sutton, RE1595, RE1909, RE5146 (S1509), RE5155 (S1520), RE5156 (S1521), RE5157 (S1522), RE5158 (S1523); Nenthorn, CD1053, CD1054; Central Otago, OM A75.10–12; Middlemarch, RE4063 (S421), RE4455 (S813), RE2419 (S839); Otago, CM Rep 566; no locality data, RE2159, MCZ R112264, OMA03.29.

*Oligosoma waimatense*—Specimens examined by Patterson (1997): Rag and Famish Stream, Wairau River, RE1827–RE1833; Molesworth Station, Marlborough, RE1911; Mt Ida, CD1207–CD1208; Little Mt Ida, CD1214; Wairau River, Marlborough, CD1209; Waimate, CM Rep 210, RE92; Mt Tarndale, Upper Wairau River, RE5167 (S1532), RE5168 (S1533); Lake Coleridge, BMNH 1905.11.30.5; south Canterbury, BMNH 1927.8.23.10; no locality data, RE2362, CM Rep 502, OMA98.82.