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Genetic data confirm that *Diomedea platei* Reichenow, 1898, is the correct name for the population of Buller's albatross *Thalassarche bulleri* breeding at the Chatham Islands, New Zealand

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Abstract: Buller's albatross *Thalassarche bulleri* is generally considered to comprise two subspecies: *T. b. bulleri*, which breeds on islands south of the South Island, New Zealand; and *T. b. platei*, which nests on the Three Kings Islands, off the northern tip of of the North Island, and on outlying islets of the Chatham Islands east of New Zealand. Although the name *platei* has been widely applied to the latter population, some authors have suggested that its type specimen is in fact a juvenile *T. b. bulleri*. As a result, those birds breeding in the Chatham and Three Kings groups have sometimes been considered to represent an unnamed subspecies, or even species, given recent evidence of their genetic differentiation. Because our own morphological examination of the specimen was inconclusive as to which population the type of *platei* belongs, we subjected the individual to molecular testing. From this, we can confirm that the name *platei* has been correctly applied to the northern population of Buller's albatross.

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INTRODUCTION

Buller's albatross *Thalassarche bulleri* has traditionally been considered to comprise two subspecies, both confined as breeding birds to the New Zealand region (Jouanin & Mougin 1979), albeit with quite different phenologies (Sagar & Warham 1998), which led to the suggestion that they might be better treated as two species (Robertson & Nunn 1998). *Thalassarche b. bulleri* (Rothschild, 1893) (southern Buller's albatross) nests on the Solander Islands and the Snares Islands, whilst *T. b. platei* (Reichenow, 1898) (northern Buller's albatross) breeds on the Chatham Islands (on the Sisters/Rangitatahi and Forty-Fours/Motuhara), with a very small colony on Rosemary Rock, in the Three Kings Islands, northwest of New Zealand's North Island (Wright 1984; Taylor 2000). Both subspecies are apparently much more widely distributed at sea, especially during the off-season and as pre-breeders, regularly reaching the Humboldt Current off Chile and southern Peru, especially between 30 and 40°S (Spear *et al*. 2003; Brooke 2004; Shirihai 2007). However, *T. b. bulleri* can occur as far north as 12°25'S, 105°06'W based on data from an individual banded as a chick on the Snares Islands (Warham 1982). Wold *et al*. (2021) cautioned that, especially during the off-season, the at-sea range of northern Buller's albatrosses is 'unknown'. Nevertheless, in offshore waters of southern Peru, among 41 Buller´s albatrosses, Quiñones *et al*. (2023) identified 40 as the 'northern taxon' and one as the 'southern taxon'. Data from tracked birds confirms that both taxa reach the Humboldt Current (Fischer *et al*. 2023) at different times reflecting their asynchronous breeding periods

Differentiating the taxa away from their colonies is especially difficult because adults overlap in some features, and younger individuals even more so. A comprehensive and critical assessment of characters to permit identification is yet to be published (see McCallum *et al*. 1985; Marchant & Higgins 1990; Shirihai 2007; del Hoyo & Collar 2014; Wold *et al*. 2021).

The names attributed to these taxa have attracted a degree of controversy, ever since Murphy (1930, 1936: 524) stated that *Diomedea platei* Reichenow, 1898 is a synonym of *Diomedea bulleri* Rothschild, 1893, going on to mention that the type of the former

Figure 1. Labels attached to the holotype of *Diomedea platei* (= *Thalassarche bulleri platei*) at the Museum für Naturkunde, Berlin (ZMB 47.77); the lower one is annotated "Typical young of bulleri R C Murphy", see main text (Carola Radke, © Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin)

Figure 2. The holotype of *Thalassarche bulleri platei* at the Museum für Naturkunde, Berlin (ZMB 47.77) (Carola Radke, © Museum für Naturkunde, Leibniz Institute for Evolution and Biodiversity Science, Berlin)

name "proves to be a young specimen of *bulleri*, entirely comparable with others of like age in our American Museum Collection" (Murphy 1930: 6; Murphy 1936: 526). The reverse side of one of the labels attached to the holotype is annotated in Murphy's hand "Typical young of bulleri", presumably written in 1926 when he is known to have visited the Berlin Museum (https://digitallibrary.amnh.org/handle/2246/6241). Mathews (1927: 907) had already suggested that *platei* is a junior name for *bulleri*, albeit without explanation. Peters (1931), Mathews (1934), and Hellmayr & Conover (1948) implicitly followed Murphy (1930) in not recognising any subspecies. The realisation that two taxa (perhaps even species) were involved was accepted only in the late 1970s and 1980s (Jouanin & Mougin 1979; C.J.R. Robertson *in* Reader's Digest 1985; Turbott 1990; Marchant & Higgins 1990). During a surge of interest in the systematics of the albatrosses in the 1990s, Robertson & Nunn (1998) postulated that "the Chatham population is actually an undescribed taxon and *T. platei* should be reduced to a synonym, being just a juvenile plumage phase of *T. bulleri* (Murphy 1936; C. Robertson pers. obs.)". It bears mention, however, that Murphy (1930: 6; Murphy 1936: 525) was evidently choosing not to recognise subspecific recognition within *bulleri*, despite by then having to hand ample material from the Chatham Island group (around the Forty-Fours Islets and Round Rock = Rangituka, southwest of Pitt Island) collected in March 1926 during the Whitney South Sea Expedition (1920–41). He was not necessarily implying that the holotype of *platei* was not from the Chatham population. As noted by Gill *et al*. (2010), who continued to use the name *platei* in reference to the latter subspecies, Robertson & Nunn's claim lacked evidence for their assertion. Nevertheless, authors such as Shirihai (2007) and Onley & Scofield (2007) referred to the possibility of the Chatham birds representing an undescribed taxon, and Dickinson & Remsen (2013: 173, footnote 9) considered the issue to be unresolved.

The holotype of *platei* is held at the Museum für Naturkunde Berlin (ZMB 47.77) and is an immature (unsexed) individual collected at Cavancha, just south of Iquique (20°14'S, 70°10'W), Tarapacá Region, in northern Chile, on 18 July 1893 (Figs. 1–3). Because of the extreme difficulty of

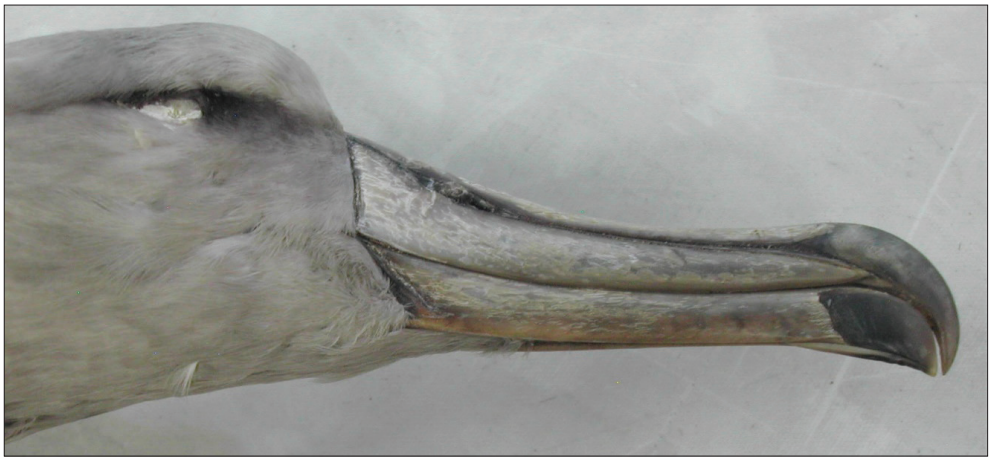

Figure 3. Detail of the right side of the bill of the holotype of *Thalassarche bulleri platei* at the Museum für Naturkunde, Berlin (ZMB 47.77) (Guy M. Kirwan)

identifying the holotype to taxon/population using either plumage or biometrics (see Results, notwithstanding the assertion of Robertson & Nunn 1998 to the contrary), and because both taxa could occur at the collection locality, we elected to subject the holotype of *platei* to genetic screening, and thereby hopefully resolve the issue of its identity.

MATERIAL & METHODS

Molecular analysis

A partial fragment of the mitochondrial control region of the holotype of Diomedea platei ZMB 47.77 was sequenced for comparison with sequences published in Wold *et al*. (2018). DNA from a piece of skin from the belly fissure was extracted using the QIAamp DNA Micro Kit (Qiagan) with an adapted digestion protocol that ensures high quantities of DNA (Lutgen & Burri 2020). A digestion time of 40 hours was applied and additional 20 µl of Proteinase and 180 µl buffer ATL were added after the first six hours of digestion. The primers SPECF1 and GLUR7 from Wold et al. (2018) were used and PCR reaction volumes were 25 µl containing 12.5 µl GoTaq Hot Start Green Master Mix (Promega), 2 µl genomic DNA, 2 µl of each primer with a concentration of 10 µM and 6.5 µl ddH2O using a standard reaction protocol (Schweizer & Shirihai 2013) with annealing temperature of 55°C. PCR was performed on a SensoQuest thermal cycler and sequencing was performed in both directions with the primers used for PCR with LGC Genomics (Berlin).

All sequences of *T. bulleri* from Wold *et al*. (2018), which were obtained on the breeding grounds (26 of *T. b. platei* from the Forty-Fours/Motuhara and the Sisters/Rangitatahi, and 47 of *T. b. bulleri* from North East Island, in the Snares group, and Solander Island), were downloaded from GenBank.

As an independent check, a further five *Thalassarche bulleri* study skins of known provenance at the Museum of New Zealand Te Papa Tongarewa (NMNZ), Wellington, NZ, were sequenced: *T. b. platei*: NMNZ OR.18634; NMNZ OR.18635; NMNZ OR.18107 and *T. b. bulleri*: NMNZ OR.030176; NMNZ OR.18633. A sliver of footpad was removed from each specimen with a sterile scalpel blade. DNA extraction of the footpad tissue, PCR amplification, purification and sequencing followed Shepherd *et al*. (2022), except that the primers used were SPECF1 and GLUR7 (Wold *et al*. 2018) and the PCR annealing temperature was 60°C. Bidirectional sequencing with the same primers was performed by Macrogen (Seoul, South Korea). Sequence alignment was performed using the MAFFT algorithm *7.450* (Katoh *et al*. 2002; Katoh & Standley 2013) implemented as a plug-in in Geneious 2022.0.2 (https://www.geneious.com) with default settings. To visualise genetic variation, a median-joining haplotype network (Bandelt *et al*. 1999) was constructed using PopART 1.7 (Leigh & Bryant 2015) with default settings (epsilon = 0).

Morphology

We examined the holotype of *Diomedea platei* at the Museum für Naturkunde Berlin (ZMB 47.77) on a total of three different occasions (GMK and HS, separately and together). We assessed the following characters: biometrics, bill colour, and plumage colouration.

Measurements were collected by a single person (HS), including of the *platei* holotype, and otherwise restricted to sexed specimens collected on, or near, breeding islands and thus of known population. All available specimens held at the Museum of New Zealand Te Papa Tongarewa (NMNZ), Wellington, NZ, and at the American Museum of Natural History (AMNH), New York, USA, were measured. In total 34 adult and full-grown juveniles of the two populations were available (Table 1, Appendix 1).

Parameters measured included wing length (flattened), tail, tarsus, culmen to feathers, bill width (at the junction of the latericorn and ramicorn), bill depth (at the feathers), bill depth at unguis (maximum height/apex), mandibular unguis length (measured along the base), height of the orange line along the mandibular ramicorn at its mid/highest point, and the height of the uncoloured area at its mid/highest point. Additionally, HS scored the grey of the head (1: pale, 2: medium, 3: dark); how well delineated the paler cap is at its rear (1: diffuse, 2: medium, 3: sharp), and the extent of the pale cap (1: to just behind the eye, 2: to rear crown, 3: to nape), as well as the shape of the upper end of the culminicorn (1: round; 2: intermediate; 3: flat). HS also attempted to assess the size of the dark loral patch measured from the front of the eye to the distal end of the patch. Univariate and multivariate statistics (Principal Component Analysis, PCA, correlation matrix on scaled variables) were then performed on the biometric data from all birds using package Factormine on R (colouration variables were not included in the PCA since they were not continuous).

RESULTS

Molecular analyses

The final control region sequence alignment was 221 base pairs in length. The resulting median-joining haplotype network was consistent with the results presented in Wold *et al*. (2018) and clearly separated the populations of *T. b. bulleri (*including the two newly sequenced samples from the Snares Islands) from those of *T. b. platei* (including two of the three newly sequenced samples from Rangitatahi). However, three samples of *T. b. platei* were located between the two clusters (one of the three newly

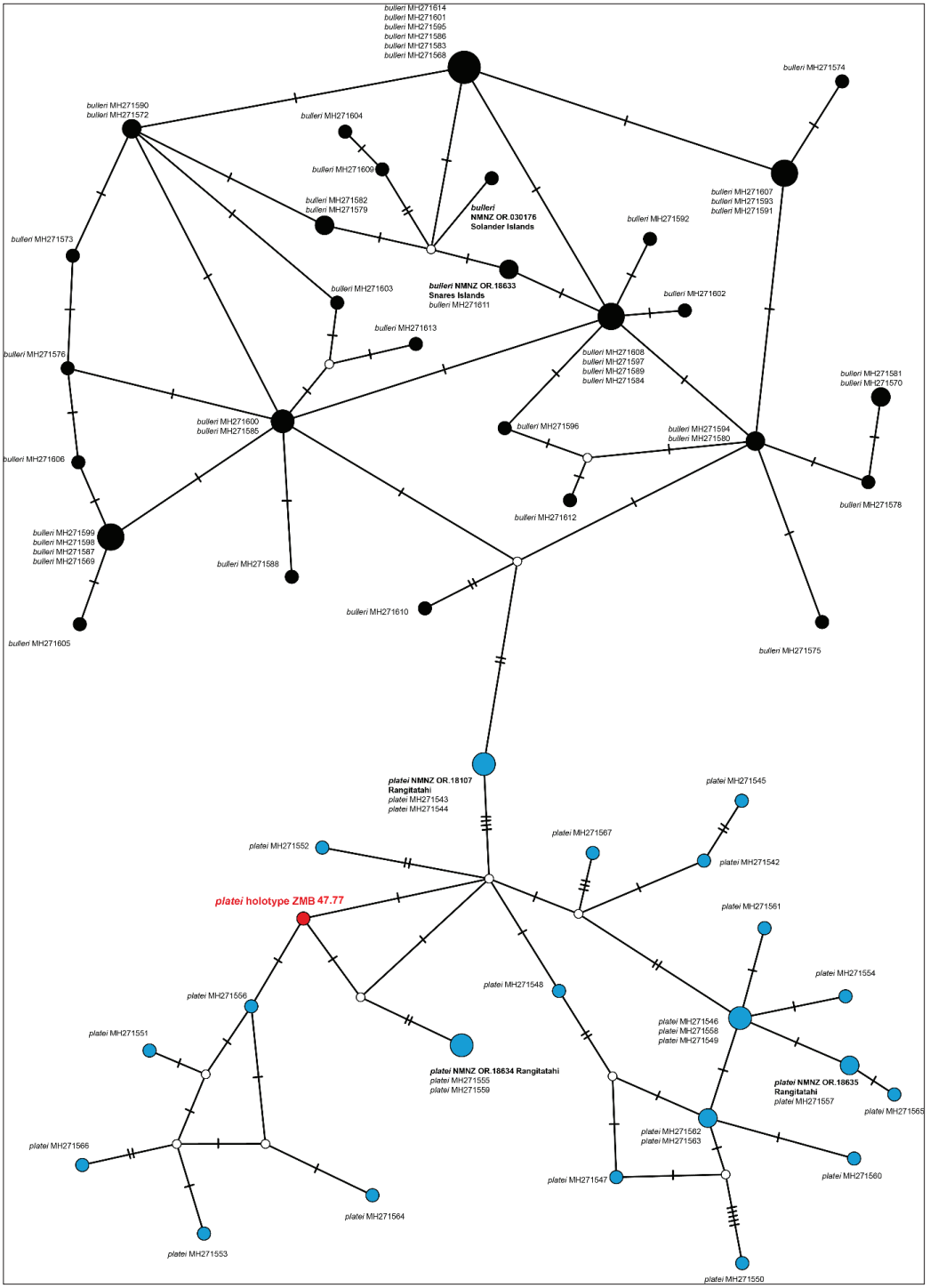

Figure 4. Haplotype network based on 221 base pairs of the mitochondrial control region of 26 individuals of *Thalassarche bulleri platei* and 47 of *Thalassarche b. bulleri* from Wold *et al*. (2018), two *T. b. bulleri* and three *T. b. platei* of known provenance from NMNZ, Wellington, NZ (highlighted in bold), and the holotype of *T. b. platei* ZMB 47.77, (highlighted in red). The latter clusters with samples of *T. b. platei*.

sequenced samples from Rangitatahi and two from Motuhara derived from Wold *et al.* 2018) (Fig. 4). The holotype of *Diomedea platei* ZMB 47.77 clearly clustered with all other samples of *T. b. platei* in Fig. 4.

Morphology

Table 1 summarises biometrics of the analysed specimens of *T. b. bulleri* and *T. b. platei* for juveniles and adult males and females separately, as well as for the type of *T. b. platei*. The holotype of *platei* shows comparatively extreme measurements in bill depth and bill width. In general, its bill is rather narrow, elongated, not so broad and consequently more closely matches the overall shape of *T. b. bulleri* than *T. b. platei*. The height of the orange line along the mandibular ramicorn measured 4.5 mm in the *platei* holotype and is thus close only to female *T. b. platei*. In contrast, the height of the uncoloured area in the *platei* holotype was much closer to *T. b. bulleri*. The scored character states of the *platei* holotype overlapped with both *T. b. bulleri* and *T. b. platei*.

In general, *T. b. platei* differs from *T. b. bulleri* by its darker grey head and neck, more restricted and better delimited white cap, and it has a broader bill profile but with a rounder upper end to the culminicorn, as well as a narrower orange line along the mandibular ramicorn.

The first two axes of the PCA of all biometric measurements explained 44.23% and 18.76% of the total variance (Fig. 5). There was a tendency for a separation between taxa in both adults and juveniles, but even more pronounced between adults and juveniles within both taxa. The *platei* holotype clustered more closely with *T. b. bulleri* juveniles rather than with *T. b. platei* but sample sizes for juveniles were very low. In addition, it has to be taken into account that three of the measured juveniles of *T. b. platei* were taken from the nest and were probably not yet fully grown.

In plumage colouration, the scores of the *platei* holotype were within the range of all other taxa and age classes except in the darkness of the head compared to adult *T. b. bulleri* (Table 1).

DISCUSSION

Our results based on a single mitochondrial genetic marker indicate that at least the mother of ZMB 47.77, the holotype of *Diomedea platei*, belonged to the northern population of Buller's albatross, based on the comparative data available in Wold *et al*. (2018), as well as our independent check of specimens from known populations at NMNZ. Given that there is a lack of inferred gene flow based on genome-wide data between northern and southern populations of Buller's albatross (Wold *et al*. 2021), we consider it highly unlikely that the holotype of *platei* is

Table 1. Mean measurements, by subspecies and age, for all the museum skins included in this study. The measurements of the *platei* holotype specimen are presented in the 'Type' column. Ad = Adult, Juv = Juvenile, F = Female, M = Male. The first 11 parameters were measured in millimetres, and the colour of the last three were scored between 1 and 3 (see Methods). Mean values and standard deviations are given.

	T. b. bulleri			*T. b. platei*			Type
	Ad		Juv	Ad		Juv	
	F (n=6)	M (n=5)	(n=4)	F (n=8)	M (n=7)	(n=4)	
Wing	501.3±9.3	507.2±4.7	498.3±8.7	492.8±10.5	502.1±12.0	497.3±8.1	499
Tail	189.5±4.7	191.0±7.6	177.3±7.5	188.4±1.6	189.5±5.9	173.5±4.5	175
Culmen	116.8±2.3	122.2±4.5	111.7±4.8	118.0±4.2	122.6±1.5	116.2±2.6	115.6
Bill depth (base)	42.3±1.6	45.5±0.8	41.2±1.5	45.9±3.0	47.6±1.4	41.2±1.5	38
Bill depth (unguis)	24.8±1.0	25.4±1.1	22.3±0.5	25.8±0.7	27.2±0.5	23.9±0.9	23
Bill width	26.9±1.0	27.3±0.7	26.6±1.8	29.5±1.8	29.2±1.2	27.3±1.1	23.4
Tarsus	79.3±3.5	82.5±2.6	78.7±2.9	79.5±2.4	82.5±1.9	78.3±1.2	81.5
Mandible	16.7±0.8	17.5±1.3	15.5±1.2	17.8±1.3	18.0±1.1	17.5±0.7	17.9
Height orange line	5.82±0.8	6.7±0.7	6.9±0.8	5.06±0.6	5.76±0.6	5.8±0.2	4.5
Height remaining	3.7±0.6	3.6±1.0	3.5±1.0	5.14±0.7	4.8±0.7	5.1±0.7	4
Loral patch length	18.1±2.7	18.1±2.7	15.4±3.1	15.4±3.4	17.0±3.9	16.8±2.7	17.9
Head colour	1.8±0.4	1.6±0.6	2.0±0.8	2.5±0.5	2.43±0.5	1.75±0.5	1
Rear cap colour	1.0±0.0	1.4±0.6	1.8±0.5	2.3±0.7	2.3±0.5	2.0±0.8	1
Cap colour	2.5±0.6	2.4±0.9	2.5±0.6	1.9±0.3	1.9±0.4	1.0±0.0	1

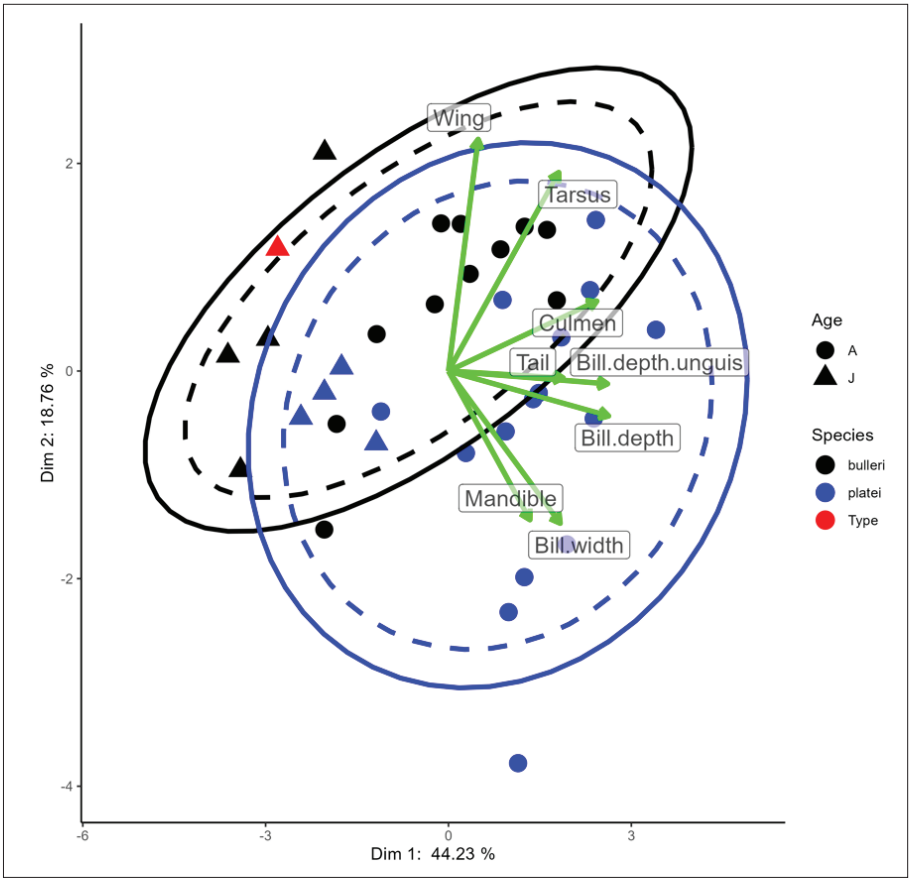

Figure 5. Results of Principal Component Analysis (PCA) on the 35 measured specimens. Symbols represent individuals in multivariate space (here, the first plan with PC axes 1 and 2), according to subspecies (colour) and age (symbol). The holotype of *Thalassarche bulleri platei* is denoted by the red triangle. Biometric variable components are overlaid on the same graph (in green).

of hybrid origin. We can thus be confident that the name *platei* has been correctly applied to the northern population of Buller's albatross.

Morphometric analyses tended to suggest that the *platei* holotype may be slightly morphologically closer to *T. b. bulleri* rather than to *T. b. platei*, in contrast to the genetic results. However, the *platei* type is an unsexed young immature bird and its morphometrics, bill colour and plumage characteristics could be compared only with adults and fully grown juveniles of *T. b. bulleri*. The data provided in Table 1 suggest that the *platei* holotype apparently has atypical measurements for bill depth and width.

In general, phenotypic differences between the two subspecies must be considered as minor; the lack of characters to separate non-adult *T. b. platei* and *T. b. bulleri* was outlined by Shirihai (2007).

The identity of ZMB 47.77 has been the subject of much debate over the years, especially in the first three decades after Reichenow's description. Murphy (1930: 6) noted that *Diomedea platei* had been synonymised with shy albatross *Thalassarche cauta* by several authors, e.g. Ogilvie-Grant (1905: 559), although Godman (1908: 346) refuted this hypothesis and upheld Reichenow's (1898, 1899) original diagnosis. Some authors even regarded *platei* as a subspecies of *T. cauta* (Mathews & Iredale 1921: 54; Dabbene 1926: 324); however, Mathews (1927: 907) subsequently treated the specimen as a synonym of *bulleri*, as did Murphy (1930, 1936). Loomis (1918) considered *platei* to be a young specimen of black-browed albatross *T. melanophris*. Our results confirm that the application of the name *platei* to the northern population of Buller's albatross is correct.

There is growing interest in the taxonomy of *T. bulleri*, especially following the discovery of strong mtDNA genetic differentiation and lack of inferred gene flow between its northern and

southern populations, possibly because of their asynchronous breeding seasons (Wold *et al*. 2018, 2021). Speciation through allochrony, i.e. prezygotic isolation via temporal segregation of breeding populations, has been documented on several occasions in Procellariiformes (Friesen *et al*. 2017; Taylor *et al*. 2018, 2019) and other bird groups (e.g. Gómez-Bahamón *et al*. 2020; Tang *et al*. 2022), and may also be occurring in Buller's albatross. As already proposed by Wold *et al*. (2021), this, in combination with minor morphological differences described above for adults (see also Shirihai 2007), might justify the treatment of *bulleri* and *platei* as species level taxa applying an integrative approach towards species delimitation (e.g. Schweizer *et al.* 2023). However, as explained here, identification of the two taxa at sea is not straightforward and is probably impossible for many immatures.

The estimated annual breeding population of both subspecies combined is 32,134 pairs, with 8,704 pairs on the Snares Islands (*bulleri*), 5,280 pairs on the Solander Islands (*bulleri*), 16,000 pairs on the Forty-Fours (*platei*), 2,130 pairs on the Sisters (*platei*) and 20 pairs on Rosemary Rock (*platei*) (BirdLife International 2024), and the species is assessed as Near Threatened (BirdLife International 2024). Clearly, the conservation status of both taxa, especially nominate *bulleri* with its overall smaller population, would require careful reassessment against IUCN Red List criteria should they be treated as separate species, as well as perhaps enhanced measures to protect their relatively small populations.

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Appendix 1. Measurements and morphology scores of museum specimens included in analyses. AMNH = American Museum of Natural History, NMNZ = Museum of New Zealand Te Papa Tongarewa, ZMB = Museum für Naturkunde Berlin. All measurements in millimetres apart from the final four columns, which were scored on a scale of 1 to 3 as explained in footnotes.

Taxon	Museum number	Age and sex	Wing	Tail	Tarsus	Culmen	Bill width	Bill depth	Bill depth at unguis
T. b. bulleri	NMNZ OR.018631	Ad. male	501	193	83.6	124.3	26.4	46.5	23.5
T. b. bulleri	NMNZ OR.016630	Ad. male	504	189	84.4	123.5	28.3	46.0	25.5
T. b. bulleri	NMNZ OR.005579	Ad. male	508	201	78.0	114.4	27.2	44.6	25.6
T. b. bulleri	AMNH 27374	Ad. male	511	180	83.2	126.1	27.6	44.9	25.8
T. b. bulleri	AMNH 526942	Male	512	192	83.4	122.5	27.0	45.3	26.4
T. b. bulleri	NMNZ OR.016631	Ad. female	505	198	81.0	119.6	27.7	44.0	24.8
T. b. bulleri	NMNZ OR.005582	Ad. female	506	186	83.2	117.8	26.8	43.5	26.3
T. b. bulleri	NMNZ OR.018632	Ad. female	507	187	83.0	117.6	28.5	43.0	25.0
T. b. bulleri	NMNZ OR.018633	Ad. female	494	188	77.1	113.8	26.1	39.7	24.9
T. b. bulleri	NMNZ OR.030176	Ad. female	486	186	75.6	114.0	26.2	42.7	23.3
T. b. bulleri	NMNZ 526943	Female	510	192	76.0	117.8	26.4	41.1	24.4
T. b. bulleri	AMNH 8771	Juv. male	496	186	78.3	110.2	25.5	40.3	22.9
T. b. bulleri	AMNH 18195	Juv. male	506	168	77.5	109.6	28.7	40.1	21.6
T. b. bulleri	AMNH 18194	Juv. male	504	176	82.8	118.8	27.5	41.2	22.3
T. b. bulleri	NMNZ OR012303	Juv. female	487	179	76.1	108.3	24.7	43.3	22.4
T. b. platei holotype	ZMB 47/77	Immature	499	175	81.5	115.6	23.4	38.0	23.0
T. b. platei	NMNZ OR.018107	Ad. male	507	188	85.3	124.1	29.4	45.9	28.1
T. b. platei	NMNZ OR.018634	Ad. male	504.5	188.5	83.8	122.6	27.8	48.8	27.4
T. b. platei	NMNZ OR.018479	Ad. male	498	180	83.6	125.1	27.8	46.7	27.1
T. b. platei	AMNH 211396	Male	480	188	82.1	121.0	29.5	48.2	26.9
T. b. platei	AMNH 211395	Male	520	200	82.3	121.9	29.5	48.8	27.4
T. b. platei	AMNH 211394	Male	505	191	81.0	121.1	31.2	48.8	26.8
T. b. platei	AMNH 211397	Male	500	191	79.7	122.6	29.3	45.9	26.5
T. b. platei	NMNZ OR.018635	Ad. female	508	186	79.7	120.3	29.8	49.9	25.4
T. b. platei	NMNZ OR.018106	Ad. female	508	186	78.1	109.6	28.4	39.8	26.3
T. b. platei	NMNZ OR.018478	Ad. female	495	188	84.0	122.6	27.2	45.4	25.1
T. b. platei	AMNH 211401	Female	480	189	75.6	121.5	33.0	44.7	25.3
T. b. platei	AMNH 211403	Female	486	189	79.8	115.9	30.6	47.9	26.5
T. b. platei	AMNH 211405	Female	493	190	79.4	115.2	28.0	46.7	25.9
T. b. platei	AMNH 211400	Female	485	190	81.0	118.6	28.8	47.4	26.9
T. b. platei	AMNH 211404	Female	487	189	78.1	120.3	30.3	45.7	25.2
T. b. platei	NMNZ OR.019251	Juv. male	487	176	79.4	116.4	27.8	42.9	25.1
T. b. platei	NMNZ OR.019252	Juv. female	498	177	78.2	116.9	25.6	41.9	24.2
T. b. platei	NMNZ OR.019253	Juv. female	507	167	76.6	118.8	27.7	40.7	23.3
T. b. platei	AMNH 18699	Juv. female	497	174	79.0	112.7	27.9	39.4	23.2

Details of measurements and scoring systems: Culmen = bill length to base of feathers; Bill width = width at the junction of the latericorn and ramicorn; Bill depth where culmen meets feather bases; Bill depth at unguis measured at maximum height/apex; Unguis length = mandibular unguis length (measured along the base); Orange line height = Height of the orange line along the mandibular ramicorn at its mid/highest point; Uncoloured line height = height of the uncoloured area of the mandibular ramicorn at its mid/highest point; Loral patch length = front of eye to front edge of dark loral patch; Grey of head scored as 1: pale, 2: medium, 3: dark; Cap delineation = how well delineated the pale cap is at its rear (1: diffuse, 2: medium, 3: sharp); Cap extent = extent of pale cap, scored as 1: to just behind the eye, 2: to rear crown, 3: to nape; Culminicorn base shape, scored as 1: round; 2: intermediate; 3: flat.

Museum number	Unguis length	Orange line height	Uncoloured line height	Loral patch length	Grey of head	Cap delineation	Cap extent	Culminicorn base shape
NMNZ OR.018631	17.4	6.4	3.4	17.1	2	2	2	3
NMNZ OR.016630	18.6	6.6	3.6	21.8	2	1	3	1
NMNZ OR.005579	15.4	7.5	2.7	17.7	1	1	3	1
AMNH 27374	18.0	5.8	3.0	14.5	2	2	1	1
AMNH 526942	18.2	7.2	5.2	19.5	1	1	3	1
NMNZ OR.016631	16.1	5.5	3.9	19.0	2	1	2	3
NMNZ OR.005582	16.5	6.8	2.8	18.5	2	1	3	2
NMNZ OR.018632	15.5	5.3	4.4	20.8	2	1	3	3
NMNZ OR.018633	17.2	5.8	3.4	18.2	2	1	2	2
NMNZ OR.030176	17.7	6.7	3.7	12.9	2	1	2	2
NMNZ 526943	17.1	4.8	4.0	18.9	1	1	3	3
AMNH 8771	15.7	5.9	2.9	12.1	2	2	3	3
AMNH 18195	15.7	7.8	2.7	16.2	2	2	2	3
AMNH 18194	13.9	6.9	4.9	14.0	3	2	2	1
NMNZ OR012303	16.7	7.3	3.3	19.1	1	1	3	1
ZMB 47/77	17.9	4.5	4.0	17.9	1	1	1	2
NMNZ OR.018107	16.4	6.5	4.9	24.0	3	2	1	3
NMNZ OR.018634	17.8	6.1	4.2	18.0	3	2	2	3
NMNZ OR.018479	18.5	4.7	4.5	17.5	2	2	2	2
AMNH 211396	18.5	5.5	3.7	18.0	2	3	2	3
AMNH 211395	19.9	5.7	5.7	13.2	2	2	2	1
AMNH 211394	17.7	6.3	5.4	16.8	3	3	2	2
AMNH 211397	17.2	5.5	5.2	11.8	2	2	2	1
NMNZ OR.018635	17.6	4.8	5.1	19.5	3	3	2	2
NMNZ OR.018106	18.0	4.3	4.2	16.9	3	2	2	3
NMNZ OR.018478	17.3	4.9	4.9	16.1	2	2	2	2
AMNH 211401	19.6	5.1	4.4	17.2	3	3	1	3
AMNH 211403	18.0	4.8	5.1	16.6	2	1	2	2
AMNH 211405	17.2	5.3	5.5	10.5	2	3	2	3
AMNH 211400	15.6	4.9	6.0	16.2	2	2	2	2
AMNH 211404	19.4	6.4	5.9	9.9	3	2	2	2
NMNZ OR.019251	16.6	6.1	5.0	18.8	2	2	1	1
NMNZ OR.019252	17.5	5.6	5.6	18.4	2	2	1	3
NMNZ OR.019253	18.2	5.8	4.1	17.2	2	3	1	2
AMNH 18699	17.6	5.8	5.6	13.0	1	1	1	2