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Population structure and genetic diversity of false killer whales (*Pseudorca crassidens*) in New Zealand waters: preliminary results

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ABSTRACT

False killer whales (*Pseudorca crassidens*) are globally distributed cetaceans, often found in deep oceanic waters but occasionally near coastlines. Despite their broad distribution, information on their abundance, genetics, and ecology remains limited. In New Zealand waters, these whales occur year-round, with increased sightings during the warmer months due to the East Auckland Current. This study investigates the genetic diversity and population structure of New Zealand false killer whales using 17 samples collected from 2005 to 2018 in four locations, comparing them to global studies. New Zealand samples revealed four unique haplotypes with low genetic diversity ($h = 0.42 \pm 0.141$; $\pi = 0.29\% \pm 0.002$). No genetic differentiation was observed between South Pacific and New Zealand populations ($F_{ST} = 0.05$ $p = 0.1602$ $\Phi_{ST} = 0.058$ $p = 0.145$). These findings suggest low genetic diversity for New Zealand false killer whales, but within values expected for other cetaceans with matrilineal social structures. The presence of shared haplotypes suggests potential historical or ongoing connections with wider Pacific populations. However, further research is needed due to the short mtDNA-CR fragment analysed and small sample size, which may have resulted in an inability to capture the full extent of the genetic variation. This study contributes to our understanding of this species and its conservation within New Zealand.

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Introduction

False killer whales (*Pseudorca crassidens*) are globally distributed in deep oceanic tropical and temperate waters (Baird et al. 2008). However, they have also been sighted near coastlines, especially around offshore islands and sometimes in shallow shelf waters (Acevedo-

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Gutierrez et al. 1997; Baird et al. 2008; Zaeschmar et al. 2014; Crofts et al. 2019; Palmer et al. 2023). As apex predators, false killer whales are relatively uncommon (Baird 2018a). Notably, three distinct populations with overlapping ranges have been identified in Hawaiian waters (Baird et al. 2008; Martien et al. 2014; Martien et al. 2019). Among these populations, two are classified as resident: one is found in the main Hawaiian Islands (Baird et al. 2008), currently classified as endangered under the US Endangered Species Act, and the second is found in the northwestern Hawaiian Islands (Baird et al. 2013; Martien et al. 2014).

Globally, the status of false killer whales is classified as 'Near Threatened' (Baird 2018b). In many regions within their habitat, there is a lack of comprehensive information on its abundance, genetic structure, movements, social behaviour, dispersal patterns, and their ecology. Abundance estimates are limited to a few populations, but they indicate low numbers for the species, even in regions where it is deemed common. (Barlow and Rankin 2007; Bradford et al. 2014; Bradford et al. 2018; Sánchez-Robledo et al. 2020).

Despite their widespread distribution, false killer whales exhibit genetic differentiation at the ocean basins level, particularly in populations from the North Pacific, eastern North Pacific, and Hawaiian Islands (Martien et al. 2014). These populations display significant differentiation and relatively low mitochondrial genetic diversity (Martien et al. 2014). Populations associated with islands in the central and eastern North Pacific exhibit distinct phylogeography and limited gene flow among them (Martien et al. 2014). However, current genetic information is limited in other regions to establish meaningful comparisons. Recently, a resident population of false killer whales was identified in the coastal areas of northern Australia. In that study, Palmer et al. (2023) found a novel mitochondrial control region haplotype shared among all samples. This finding, combined with additional movement data, suggested that the false killer whales inhabiting northern Australia are genetically distinct from offshore populations.

In New Zealand, false killer whales can be observed year-round (Zaeschmar 2014). Previous photo-identification studies along the North-eastern North Island suggested long-term site fidelity, despite a pronounced seasonal peak in their occurrence. The occurrence of false killer whales in New Zealand aligns with the seasonal movement of the East Auckland current (EAUC), a warm body of water that reaches the northeastern coast of New Zealand from December to May bringing warm waters and prey species closer to shore (Zaeschmar 2014). These whales are known to follow the shoreward flow of the EAUC during summer, likely in pursuit of prey, as observed in other regions (Baird et al. 2008; Zaeschmar 2014; Zaeschmar et al. 2014).

A low encounter rate in New Zealand coastal areas suggests that the distribution of false killer whales is likely concentrated further offshore (Zaeschmar et al. 2014). An opportunistic photo-identification study conducted along the east coast of the North Island of New Zealand identified 61 animals over 7 years. Interestingly, 54 whales were resighted, with 43 (70.5%) observed on three or more occasions. Two individuals were spotted as many as eight times. Additionally, 52 (85%) were observed in multiple years, and at least two individuals were seen nearly seven years after their initial identification. The movement of eight individuals was documented to extend as far as 650 km (Zaeschmar 2014). All photo-identified individuals appear to be part of a single social network with two distinct clusters within this network, with documented instances of repeated associations between individuals (Zaeschmar et al. 2014). This social structure is similar to what has been observed in the Hawaiian insular false killer whale population

(Baird et al. 2012) where an examination of associations spanning a 23-year period revealed that false killer whales residing near the main Hawaiian Islands exhibit a strongly modular and highly differentiated social structure. This structure comprises four distinct social clusters, with the majority of social interactions occurring within rather than between clusters. In addition, the four clusters have significant differences in association patterns, spatial use, and genetics (Mahaffy et al. 2023).

In this study, we explore the genetic diversity and population structure of false killer whales in New Zealand waters. We collected skin samples from remote biopsy sampling ($n = 9$) and strandings ($n = 10$), and analysed mitochondrial DNA control region sequences as well as five nuclear markers (microsatellites). To assess population structure across ocean basins, we compared the mitochondrial DNA sequences from New Zealand with previously published sequences from various regions worldwide (11 regions and 3 ocean basins overall).

Materials and methods

A total of 19 samples were collected between 2005 and 2018 in four different locations: offshore Hauraki Gulf ($n = 9$), Chatham Islands ($n = 8$), Gisborne (Anura Bay, $n = 1$) and Marlborough Sounds (Blenheim $n = 1$). All samples were preserved in 75% ethanol.

DNA was extracted from skin samples using the DNeasy Blood & Tissue kit (QIAGEN). The mitochondrial control region (mtDNA-CR) was amplified using the primers M13-Dlp1.5 (5′-TGTAAAACGACAGCCAGTTCACCCAAAGCTGRARTTCTA-3′; Dalebout et al. 1998) and Dlp5 (5′-CCATCGWGATGTCTTATTTAAGRGGAA-3′; 5′-CCATCGW-GATGTCTTATTTAAGRGGAA-3′; Baker et al. 1998) following the amplification protocol from Caballero et al. (2007). PCR products were visualised in 1.5% agarose gel red, purified using magnetic beads and sequenced in both directions using the Sanger sequencing method (Sanger and Coulson 1975). All sequences were manually edited and aligned using Geneious Prime 2019.1 (https://www.geneious.com).

NCBI-BLAST online software (https://blast.ncbi.nlm.nih.gov) was used for species confirmation. Samples were sexed following Gilson et al. (1998) amplifying male-specific SRY gene and ZFY/ZFX genes as positive controls (Aasen and Medrano 1990). We used previously reported haplotype sequences representing 223 control region sequences from two previously published studies: 203 sequences from Martien et al. (2014) and 20 sequences from Crofts et al. (2019). Locations included the main Hawaiian Islands (MHI), Northwestern Hawaiian Islands (NWHI), Central North Pacific (CNP), Eastern Tropical Pacific (ETP), West Pacific (WP), Indo-Pacific (IP), South Pacific (SP) Atlantic Ocean (AO, Martien et al. 2014), and Falkland Islands (Malvinas, Crofts et al. 2019). (GenBank access codes: EF601197 – EF601220, KJ567087- KJ567089, HQ438483- HQ438487).

MacClade software (Maddison and Maddison 2003) was utilised to define haplotypes for the purpose of conducting genetic diversity and population structure analyses. Estimates of mtDNA-CR haplotype and nucleotide diversity, as well as analyses of genetic structure using F_{ST}, and Φ_{ST}, validated through 10,000 permutation tests were performed using the software Arlequin 3.5.2.2 (Excoffier et al. 1992).

Twelve microsatellite loci were assayed: Ttr34, Ttr58, and Ttr63 (Rosel et al. 2005), MK8 (Krützen et al. 2001), KWM12 (Hoelzel A. R. 1998), Tur4_80, Tur4_141,

Tur4_105, Tur4_111 and Tur4_91 (Nater et al. 2009), D08 (Shinohara et al. 1997) and Dde66 (Coughlan et al. 2006). We followed the amplification protocol outlined in the aforementioned studies to individually amplify each microsatellite locus. To facilitate microsatellite analysis, all forward primers were tailed with a universal M13 sequence at 5′ to label each microsatellite with one of the four fluorescent dye-labels (NED, VIC, FAM or PET; Schuelke 2000). All microsatellites were genotyped employing Geneious Prime 2019.1 (https://www.geneious.com). Genotyping errors and the presence of null alleles were checked using MICRO-CHECKER. If null alleles were detected or the loci failed to amplify in >50% of the samples, it was discarded (Van Oosterhout et al. 2004).

Deviations from expectations of both linkage disequilibrium, Hardy-Weinberg proportions (HWE) and genetic diversity values, including expected (HE) and observed heterozygosity (HO) were obtained for those microsatellite loci that passed quality control using GENEPOP (https://genepop.curtin.edu.au/).

The genetic identification of individual dolphins was conducted by comparing microsatellite genotype profiles using the programme CERVUS 3.0 (Kalinowski et al. 2007) for five nuclear loci. Initial identification was based on matching at a minimum of four loci, allowing for mismatching at up to one locus. These 'fuzzy matches' were then reviewed for potential genotype errors. The probability of identity (PID) represents the average probability that two unrelated animals share the same genotype by chance, and was used to assure that duplicate samples were removed. PID was calculated following Paetkau and Strobeck (1994) as implemented in CERVUS 3.0 (Blouin 2003; Kalinowski et al. 2007).

Results

Out of the 19 samples in the New Zealand dataset, two samples did not successfully amplify DNA (one biopsy sample collected offshore in the Hauraki Gulf and one stranding sample from the Chatham Islands. Table 1, Figure 1), resulting in a total of 17 mtDNA-CR sequences available for analysis (Table 1). Overall, a total of 240 mtDNA-CR sequences were used for haplotype comparisons. To ensure comparability, the sequences were standardised to a consensus fragment of 478 bp in length. Analysis revealed the presence of 25 variable sites within this consensus fragment, defining a total of 22 distinct haplotypes worldwide (Table 2). No novel haplotypes were identified; all observed haplotypes corresponded to previously documented ones (Martien et al. 2014). Due to the difference in sequence lengths between the original haplotypes (947 bp) and the sequences analysed in this study (478 bp), only variable sites within

Table 1. New Zealand P. crassidens database including sample location, number of samples, year of collection, type of sample and haplotype identity ($n = 17$).

Location	Number of samples	Year of collection	Sample type	Haplotype
Offshore Hauraki Gulf	8	2017	Biopsy Sample	17 (8 samples)
Chatham Islands	7	2005	Stranding	17 (5 samples)
				30 (2 samples)
Gisborne (Anura Bay)	1	2000	Stranding	32 (1 sample)
Marlborough Sounds (Blenheim)	1	2017	Stranding	28 (1 sample)

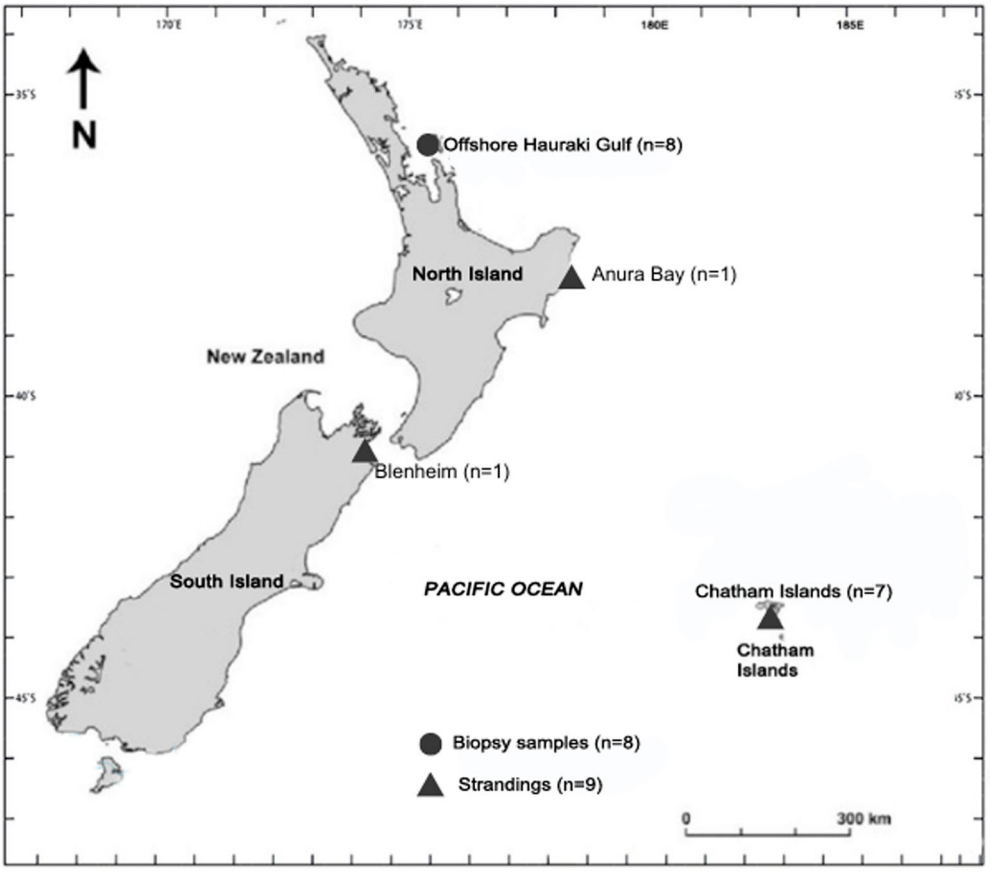

Figure 1. Map of New Zealand showing sampling locations and sample collection method (biopsy sampling $n = 8$, strandings $n = 9$).

this fragment could be determined. Consequently, we identified three pairs of identical sequences within the sample set (haplotypes 5 and 20, haplotypes 10 and 29, haplotypes 18 and 27). In order to uphold previously published sequence frequencies and haplotypes, we opted to remove haplotypes 20, 27, and 29, along with their associated frequencies, from our analysis. This action resulted in the exclusion of only three sequences. Additionally, haplotype 41 could not be distinguished from haplotype 17 in our shortened sequences. Notably, haplotype 41 is heteroplasmic (Crofts et al. 2019).

For the New Zealand samples, the sex of 7 of the 19 individuals could be identified, resulting in 5 females and 2 males.

For analyses of genetic structure and diversity, we excluded 9 sequences which included: all samples from the West Pacific (WP, n = 2), Indo-Pacific (IP, n = 3) Indian Ocean (IO, n = 2) and Atlantic Ocean (AO, n = 2) due to their very low haplotype frequencies, resulting in a total of 231 samples analysed (Tables 3 and 4).

Four unique haplotypes were documented from the 17 samples collected in New Zealand, haplotypes 17, 28, 30 and 32. Interestingly, haplotype 17, representing 13 samples in New Zealand, was shared with sequences from the South Pacific and Falkland

Table 2. Sample size ($n = 240$) and haplotype frequencies of *P. crassidens* across 11 geographic regions used in this study. Haplotype names and abbreviations following Martien et al. (2014). MHI: main Hawaiian Islands, NWHI: Northwestern Hawaiian Islands, CNP: Central North Pacific, ETP: Eastern Tropical Pacific, WP: the West Pacific, IP: the Indo-Pacific, IO: the Indian Ocean, AO: Atlantic Ocean, SP: the South Pacific, MV: Falkland Islands (Malvinas; Croffts et al. 2019) and NZ: New Zealand (this study).

	MHI	NWHI	CNP	ETP	WP	IP	IO	AO	SP	MV	NZ
Haplotype											
1	79	18									
2	27										
5	1					3					
6			1								
7			1								
9			14	14							
10				13							
11				2							
12				2							
16			1								
17									5	20	13
18					1						
19					1						
21							2				
23								1			
24								1			
25			2								
26			1						2		
28									2		1
30			4								2
31		1									
32			3						1		1
Total	107	19	27	31	2	3	2	2	10	20	17

Islands (Malvinas). Haplotype 28 with one sample in New Zealand was shared with the Falkland Islands (Malvinas). Haplotype 30, representing 2 samples in New Zealand, was shared with the Central North Pacific and haplotype 32 with one sample in New Zealand was shared among the South Pacific and Central North Pacific (Table 2).

We found relatively low levels of genetic diversity in New Zealand ($h = 0.42 \pm 0.141$; π (%) $= 0.29 \pm 0.002$) with 4 unique haplotypes identified in 17 samples. Significant differentiation was observed between New Zealand and all locations (Table 3) except with the South Pacific where no differentiation was found ($F_{ST} = 0.054$ $p = 0.16$; $\boldsymbol{\Phi}_{ST} = 0.058$ $p = 0.149$).

Table 3. Genetic structure (F_{ST} and Φ_{ST} values for the mitochondrial control region, 478 bp) of *P. crassidens* among New Zealand and six locations. Abbreviations: MHI = Main Hawaiian Islands, NWHI = Northwestern Hawaiian Islands, CN*P* = Central Pacific Ocean, ET*P* = Eastern Pacific Ocean, S*P* = South Pacific, MV = Falkland Islands (Malvinas; Crofts et al., 2019) and NZ = New Zealand (this study). Significant values are shown in bold.

Location	$\boldsymbol{F_{ST}}$	$\boldsymbol{F_{ST}}$ *P*- value	$\boldsymbol{\Phi_{ST}}$	$\boldsymbol{\Phi_{ST}}$ *P*-value
MHI	**0.59864**	**<0.00000**	**0.72609**	**<0.00000**
NWHI	**0.74494**	**<0.00000**	**0.78955**	**<0.00000**
CNP	**0.40399**	**<0.00000**	**0.41648**	**<0.00000**
ETP	**0.45789**	**<0.00000**	**0.57108**	**<0.00000**
SP	0.05420	0.16018	0.05768	0.14494
MV	**0.12606**	**0.03623**	**0.18014**	**0.03960**

Table 4. Estimates of genetic diversity of *P. crassidens* in New Zealand for five polymorphic microsatellite loci ($n = 13$). Abbreviations: Na = number of alleles, Ho = observed heterozygosity, He = expected heterozygosity.

Locus	Na	Ho	He
MK8	3	0.385	0.394
Dde66	5	0.417	0.580
Tur4_141	5	0.917	0.7890
Tur4_105	5	0.500	0.695
Ttr58	2	0.500	0.391
Mean	**4.000 ± 1.414**	**0.544 ± 0.25**	**0.570 ± 0.178**

Four microsatellite loci (Ttr34, KWM12, Tru4_91 and D08) and three samples failed to amplify. Overall, sixteen samples yielded successful PCR amplification for eight microsatellite loci (MK8, Tur4_80, Dde66, Ttr_63, Tur4_141, Tur4_105, Ttr_58, Tur4_111). However, two loci were monomorphic (Tur4_80 and Tur4_111) and one presented possible null alleles (Ttr_63) and were discarded. Three samples were omitted from the analysis due to incomplete data across three loci, resulting in a final set of 13 samples analysed for five loci (Table 4).

No instances of null alleles or scoring errors were detected across the five remaining microsatellite loci. Additionally, no significant linkage disequilibrium or deviations from Hardy-Weinberg equilibrium were observed for these loci.

The PID, indicating the likelihood of two unrelated animals sharing the same genotype by chance, ranged from 0 to 6.6^{-13} across pairwise comparisons, indicating the absence of duplicate samples in the database. There were no 'fuzzy matches'.

The observed and expected heterozygosity values were consistent across all microsatellite loci (Table 4).

Discussion

Collecting samples from cetacean species for population genetic studies has presented significant logistical difficulties. These studies typically require the sampling of a substantial number of individuals. Nevertheless, oceanic species are often dispersed across vast geographic regions and exhibit relatively low population densities, potentially leading to limited coverage of the population's genetic diversity (e.g. Baker et al. 1994; Dalebout et al. 1998; Dalebout et al. 2005; Amaral et al. 2012; Onoufriou et al. 2022).

Preliminary results from the genetic diversity analysis of false killer whales in New Zealand suggest that their mtDNA-CR genetic diversity is relatively low when compared to other delphinids inhabiting New Zealand waters. These include species like coastal bottlenose dolphins (mtDNA-CR $h = 0.91$, $\pi = 2.2\%$), killer whales ($h = 0.491$, $\pi = 0.18\%$), Hector's dolphin (mtDNA-CR $h = 0.85$, $\pi = 0.78\%$, Tezanos-Pinto et al. 2009; Hamner et al. 2012; Olavarria et al. 2014) and oceanic species such as common dolphins ($h = 0.99$, $\pi = 1.7\%$; Stockin et al. 2013). The only oceanic species in New Zealand that shows lower mtDNA-CR genetic diversity values than false killer whales are the long-finned pilot whales (*Globicephala melas*) that presented only 8 unique haplotypes from 358 samples and very low genetic diversity ($h = 0.30$, $\pi = 0.13\%$; Oremus et al. 2009).

Previous studies have similarly reported low levels of genetic diversity and pronounced patterns of phylogeography in false killer whales (Martien et al. 2014;

Martien et al. 2019; Palmer et al. 2023). Comparing the genetic diversity of New Zealand false killer whales ($h = 0.42$, $\pi = 0.29\%$) to other locations around the world also showed comparatively low values for New Zealand. Martien et al. (2014) reported two locations with lower values than New Zealand (NWHI: $h = 0.105$ and $\pi = 0.01\%$; n = 19 and MHI: $h = 0.395$ and $\pi = 0.09\%$; n = 107) whereas two other locations presented higher values (CNP: $h = 0.712$ $\pi = 0.3\%$; n = 27 and ETP: $h = 0.676$ $\pi = 0.22\%$; n = 33). However, it is important to note that our sample size is small in comparison to these other studies and our mtDNA-CR fragment is relatively short (478 bp).

Mean observed heterozygosity indicated that, on average 54.4% of individuals within the population possess two different alleles at the examined loci. This suggest that there is moderate genetic diversity among the individuals in the population at these specific genetic markers.

No population differentiation was found between New Zealand and the South Pacific. This result contrast with a recent study that found false killer whales are regular year-round residents in the coastal areas of northern Australia (Palmer et al. 2023). We analysed samples from Northern Australia from Palmer et al. (2023). However, given the length of our consensus sequence (478 bp) we needed to truncate Australian samples to 478 bp loosing significant variation and as a result, all Australian samples were designated as haplotype 30. There is a variable site at position 495 that differentiates haplotypes 30 and 45. Haplotype 45 is a novel mtDNA-CR sequence found only in Northern Australia (Palmer et al. 2023). This haplotype bears the closest resemblance to the two dominant haplotypes characterising the resident population(s) of the Hawaiian Islands, namely haplotypes 1 and 2 (Martien et al. 2014). Haplotype 1 is identified by a transversion (it has a C instead of a T) at position 295, setting it apart from other haplotypes. Similarly, haplotype 2 exhibits a transversion (T instead of C) at position 348, marking its distinction from other haplotypes. Additionally, haplotypes 30 and 45 are differentiated from each other by a transversion (haplotype 30 has a T instead of a C) at position 495. Given that our fragment is 478 bp, we could not capture the differentiation between haplotypes 30 and 45. For this reason, we excluded Australian samples from our analyses.

In northern Australia, the discovery that all samples shared a novel and unique haplotype, combined with additional movement data, suggested that false killer whales in this region are genetically distinct from oceanic populations, representing a resident coastal population. The limited sample size and the short length of our mtDNA-CR fragment hindered our ability to fully comprehend the population structure and potential connectivity or isolation of false killer whales in New Zealand. Subsequent investigations should integrate longer fragments of mtDNA-CR to encompass the entire range of variation and accurately delineate the true population structure of the species.

It is also possible that the absence of unique haplotypes within the New Zealand and lack of differentiation with the South Pacific suggests historic and likely continuous genetic interchange between South Pacific populations or the possibility that the New Zealand population is part of a broader oceanic population. This is further supported by the observation that all the haplotypes found in our New Zealand sample set were also present in the South Pacific population. The occurrence of shared haplotypes is consistent with successful female migration between these populations. However, we reiterate the limitations of our study using a relatively short fragment of mtDNA-CR (478 bp)

and small sample size that may have restricted our ability to capture the full extent of genetic diversity in the New Zealand's false killer whale population. Furthermore, since mtDNA primarily reflects female movements, the inclusion of more extensive genomic analyses and nuclear DNA could potentially yield additional insights and results.

The social structure of cetaceans can significantly influence genetic differentiation within populations (Hoelzel and Dover 1991; Gero et al. 2015; Mahaffy et al. 2023). Social behaviours, including mating patterns, dispersal, and group dynamics, can impact gene flow and genetic structure of populations (*e.g.* Hoelzel et al. 1998; Lyrholm and Gyllensten 1998; Whitehead 2003). For instance, species with strong matrilineal social structures, where males and females remain in natal groups, may exhibit higher levels of genetic differentiation between groups due to limited gene flow (Parsons et al. 2009; Alves et al. 2013; Esteban et al. 2016). This pattern is observed in species like killer whales (*Orcinus spp.*) and also recently, in false killer whales in the main Hawaiian Islands, where distinct matrilineal pods show significant genetic differentiation (Hoelzel et al. 1998a; Tavares et al. 2017; Mahaffy et al. 2023).

Mitochondrial DNA diversity (mtDNA) appears to be mostly influenced by the range and social structure of the species (Vachon et al. 2018). False killer whales are matrilineal in the sense that both males and females are generally closely grouped with their mothers while both are alive (Baird 2009; Mahaffy et al. 2023). Low mtDNA diversity has been observed in other matrilineal odontocetes, including killer whales (worldwide diversity $\pi = 0.52\%$; Hoelzel et al. 2002) and sperm whales (worldwide diversity $\pi = 0.09\%$; Morin et al. 2018). In contrast, cetaceans characterised by more flexible social structures, such as mysticetes and non-matrilineal odontocetes, typically exhibit significantly higher nucleotide diversity, a characteristic shared among these species (e.g. humpback whale nucleotide diversity worldwide $\pi = 0.88\%$; Baker et al. 1993). This phenomenon of reduced mtDNA diversity in certain cetaceans has been attributed to the concept of cultural hitchhiking, which is believed to influence their genetic patterns (Whitehead 2005; Whitehead et al. 2017).

False killer whales exhibit strong social structure, with most groups typically consisting of only one or two haplotypes (Martien et al. 2014; Martien et al. 2019). However, considering that our samples were obtained from one sighting and three stranding events spanning 13 years, the limited haplotypic diversity observed may not solely result from sampling a single social group. Only four samples presented different haplotypes (to haplotype 17): two samples collected on 13 February 2015, a mass stranding event in the Chatham Islands (haplotype 30; however other samples in this stranding all corresponded to haplotype 17) a third sample presented haplotype 28. This sample was collected on 10 January 2017 in Blenheim, Marlborough Sounds as a result from a stranding of one individual. It is noteworthy that haplotype 17 exhibited a high frequency among the New Zealand samples ($n = 13$). This particular haplotype has also been detected in 4 samples from American Samoa (Martien et al. 2014), 11 samples from the Falkland Islands (Malvinas, Crofts et al. 2019) and to our knowledge, it has not been identified in other regions outside of the southern hemisphere. A fourth sample was collected on 24 April 2000 in Anura Bay (Gisborne) and shared haplotypes with the Central North Pacific and South Pacific.

Our preliminary findings are consistent with previous studies that have reported reduced genetic diversity in matriarchal cetacean species, such as false killer whales (Whitehead 1998). Previous photo-identification studies along the North-eastern North Island of New Zealand suggested long-term site fidelity, low encounter rate and pronounced seasonal peak in their occurrence. These findings suggest that false killer whales are probably concentrated further offshore in their distribution.

The population size for the northeastern waters of New Zealand (from East Cape to North Cape) was estimated at 111 adult false killer whales (Zaeschmar et al. 2014). While this estimate is likely conservative, a small offshore population in New Zealand waters cannot be ruled out. The level of site fidelity observed off northeastern New Zealand is notably higher than expected for a transient species, with the vast majority of individuals repeatedly sighted over several years across various locations along approximately 650 kilometres of coastline (Zaeschmar 2014). This suggests the possibility of a small resident population of false killer whales in the region. False killer whales remain a high mass-stranding risk in New Zealand, second only to pilot whales, in terms of total numbers (Brabyn 1991). From 1970 to 2013, there have been 16 stranding events involving 322 false killer whales (Berkenbusch et al. 2013). Notably, one of these events constituted a mass stranding with approximately 300 whales involved (Brabyn 1991). The last mass-stranding event occurred on 24 January 2024 when a pod of 40 false killer whales and bottlenose dolphins stranded near Māhia, Hawke's Bay, in the North Island and had to be euthanised (Huston 2024). Despite the high number of animals stranded, there is a lack of substantial data or specimens collected from these incidents. Moreover, the available data from free-ranging individuals are scarce and part of an opportunistic photo-identification study (Zaeschmar et al. 2012; Zaeschmar 2014; Zaeschmar et al. 2014; Zaeschmar et al. 2020).

The false killer whale is considered problematic in its interactions with high sea fisheries, especially due to its frequent predation on long lines. This interaction is a major source of conflict, earning the false killer whale a reputation as a 'problem species,' particularly in low latitude regions. These interactions likely contribute to declining populations on a global scale. (Baird and Gorgone 2005; Gilman et al. 2006; Baird 2018a; Anderson et al. 2020; Fader et al. 2021). The problem is further confounded by misidentification or confusion of false killer whales with the considerably more common pilot whale (Baird 2010). In New Zealand, photo-identification studies revealed injuries consistent with line cuts from fishery interactions with only two individuals displaying such trauma over a period of 10 years (Zaeschmar 2014). As there are no reported cases of fisheries interactions in New Zealand waters, the extent of such interactions remains uncertain. However, based solely on scarring, fisheries interactions do not seem to be a prevalent cause of injury for the individuals identified. Given the species' resemblance to other globicephalids and the potential for misidentification (Baird 2010), improving the identification process for cetaceans interacting with fisheries in New Zealand waters is recommended.

False killer whales are currently listed as 'Naturally uncommon' by the New Zealand Threat Classification System (Baker et al. 2019). This classification was given considering that there is some evidence of fisheries interactions, but these are not thought to impact significantly on the total population. Nevertheless, the total population has never been assessed.

In summary, research from Hawaiian waters and Australian waters show that false killer whales display high site-fidelity in near-shore waters, present low abundance and high genetic isolation with low genetic diversity (Martien et al. 2014; Bradford et al. 2018; Martien et al. 2019; Mahaffy et al. 2023; Palmer et al. 2023), resulting in high vulnerability to local extinction (Frankham et al. 2002). Therefore, it is possible that a similar situation of a small, highly structured and isolated population of false killer whales is found in New Zealand waters. Further research is required to determine the genetic identity, population status and social structure of false killer whales in New Zealand waters.

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Disclosure statement

No potential conflict of interest was reported by the author(s).

Permits

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