Phylogeography of the common New Zealand wrasse species, *Notolabrus celidotus*, and the phylogenetics of the pseudolabrine tribe



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"Species such as sea otter can have effects that cascade down through lower trophic levels and can reduce abundance of prey species and modify communities...The same role has been suggested for wrasses." (Shepherd and Clarkson 2001)

Abstract

The New Zealand coastline and marine environment is a diverse place and presents plenty of dispersal obstacles to many of the organisms that live there. This thesis investigates the phylogeography of one of the most common fish species around the coast of New Zealand, the endemic wrasse Notolabrus celidotus, using the mitochondrial DNA control region and compares genetic variability to another common New Zealand wrasse, Notolabrus fucicola in a local setting. These species are part of a tribe of temperate fish, the pseudolabrines, which can be found throughout the South and North-West Pacific. The phylogeny of this tribe was also analysed using the mitochondrial 16S gene to investigate the relationships among the New Zealand pseudolabrines and to those species elsewhere. The results suggest that pseudolabrines from mainland New Zealand are closely related and are likely to have originated from southern Australia while species from the Kermadec Islands and other northern islands are more closely related to the species of eastern Australia. The Notolabrus and Pseudolabrus genera should be reviewed to remedy paraphyly of Pseudolabrus. Furthermore, N. celidotus shows no population structuring throughout its range and appears to be rapidly expanding. Genetic variability was similar for both N. celidotus and N. fucicola. The results suggest that the pseudolabrine tribe has made multiple migrations to New Zealand where Notolabrus celidotus was able to spread around the three main islands and, likely facilitated by a long planktonic larval duration, was able to maintain high gene flow among populations.

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Permits

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Contents

- ii. Abstract
- iii. Acknowledgements
- v. Table of Contents
- viii. List of Figures
- ix. List of Tables

Chapter One: General Introduction

New Zealand pseudolabrine species (family: Labridae) and their phlogeography and	
phylogeny	2
1.1 Phylogeography in the marine environment	2
1.2 Phylogeography and population structure in New Zealand	5
1.3 Population genetic markers	8
1.3.1 Mitochondrial DNA	9
1.4 Labridae	.11
1.5 Aims of this study	.13

Chapter Two

Phylogeography of the coastal fish species Notolabrus celidotus shows New Zeala	and
wide genetic homogeneity	14
2.1 Abstract	14
2.2 Introduction	14
2.3 Materials and Methods	19
2.3.1 Sampling and collection	19

Contents

2.3.2 DNA extraction and sequencing	21
2.3.3 Statistical analysis	22
2.4 Results.	24
2.4.1 Variability within the mtDNA control region	24
2.4.2 Phylogeography and population structure	24
2.5 Discussion	28
2.5.1 Genetic variability and Ne	28
2.5.2 Gene flow	

Chapter Three

Phylogeny of the pseudolabrine tribe (family: Labridae) reveals paraphyly w	ithin the
Notolabrus and Pseudolabrus genera	32
3.1 Abstract	32
3.2 Introduction	
3.3 Materials and Methods	37
3.3.1 Sampling and collection	37
3.3.2 DNA extraction and sequencing	
3.3.3 Statistical analysis	
3.4 Results	41
3.5 Discussion	45

Chapter Four

Comparison of variation between two species of <i>Notolabrus</i> fish in New Zealand	50
4.1 Abstract	50
4.2 Introduction	50

Contents

4.3 Materials and Methods53
4.3.1 Sampling and collection
4.3.2 DNA extraction and sequencing
4.3.3 Statistical analysis55
4.4 Results
4.4.1 Variability within the mtDNA control region
4.4.2 Haplotype and nucleotide diversity in control region of marine fish60
4.4.3 Population structure
4.5 Discussion
4.5.1 Variability within the mtDNA control region
4.5.2 Population structure

Chapter Five: General Discussion

Phylogeography and phylogeny in New Zealand's coastal marine fish: Insights from	
Notolabrus celidotus	5
5.1 Phylogeography of New Zealand's coastal marine fish65)
5.2 Phylogeny	7
5.3 Future directions	}
References)
Appendix	3

List of figures

Figure 2.1	Major current systems of the New Zealand coast	15
Figure 2.2	Sampling locations of Notolabrus celidotus and population	
	boundaries	20
Figure 2.3	Gene map of Notolabrus celidotus control region	23
Figure 2.4	Mismatch distribution for <i>N. celidotus</i>	26
Figure 2.5	Neighbour-joining tree for <i>Notolabrus</i> celidotus	27
Figure 3.1	Distribution of <i>Pseudolabrus</i> species	34
Figure 3.2	Distribution of <i>Notolabrus</i> species	35
Figure 3.3	Most parsimonious tree of the pseudolabrine tribe	42
Figure 3.4	Bayesian phylogram of the pseudolabrine tribe	43
Figure 3.5	Phylogeny of pseudolabrines based on ontogeny	46
Figure 3.6	Phylogeny of pseudolabrine based on morphology	47
Figure 4.1	Phylogeny of N. celidotus and N. fucicola	61
Figure 4.2	Mismatch distribution for N. celidotus and N. fucicola	62

List of tables

Table 2.1	Sample size and control region variation for populations of				
	N. celidotus	.25			
Table 2.2	AMOVA for <i>N. celidotus</i>	.25			
Table 2.3	Pairwise F _{ST} values between <i>N. celidotus</i> populations	.26			
Table 3.1	List of studies used in pseudolabrine phylogeny and the sequence				
	origin	.40			
Table 4.1	Review of genetic variation within the control region of global fish				
	species	.56			

Chapter One: General Introduction

New Zealand pseudolabrine species (family: Labridae) and their phylogeography and phylogeny.

This chapter discusses the background and context of a study into the phylogeography of the New Zealand *Notolabrus celidotus*, the spotties, with comparisons to another common New Zealand pseudolabrine, *Notolabrus fucicola*, or the banded wrasse, and the placement of these species and their New Zealand relatives in a Pacific-wide pseudolabrine phylogeny.

1.1 Phylogeography in the marine environment

Phylogeography is the study of DNA sequence variation in populations using phylogenetic techniques to infer evolutionary patterns and the geographic distribution of DNA sequence variation (Avise 1994; Avise 2000). The term 'phylogeography' with respect to molecular techniques and species distribution was first coined by John Avise and his colleagues (Avise et al. 1987). Phylogeography created a means to study microevolutionary processes within species, such as genetic drift, mutation, natural selection and migration, to help explain macroevolutionary differences between species (Avise et al. 1987). The use of DNA sequences for constructing gene genealogies (intraspecific phylogenies) allows for analysis on an individual by individual basis, compared to the population basis of allele frequency data given by microsatellites and allozymes (Avise 1994; Avise 2000). This has lead to an increased popularity of

phylogeography and particularly the use of mitochondrial DNA in the field of population genetics (Avise 2000).

Phylogeographic patterns of DNA sequences can be separated into five categories (Avise 2000). Category One describes a situation where haplotypes are unique to a geographic location (population) and each population is separated by large genetic gaps as a result of separation for a long period of time. This is a common pattern and has been found in Smith's red rock rabbit, Pronolagus rupestris, in South Africa (Matthee and Robinson 1996) where a large number of mutational steps splits samples collected from the east and south of South Africa from those in the northwest. However, mutational steps within each of the populations are much fewer. Category Two shows panmixia over geographic locations, however, there are large genetic gaps between some haplotypes within a population. One species that shows a Category Two distribution is the snow goose, Chen caerulescen, which nests in the Arctic and shows no genetic differentiation between populations but the differentiation within a population is split into two major clades (Avise et al. 1992). The pattern found in Category Two can be a result of secondary admixture in populations that have evolved in isolation (Avise 2000). Category Three shows populations separated geographically are represented by different haplotypes with shallow genetic gaps between populations and is shown in beach mice, Peromyscus polionotus, in south-eastern USA (Avise et al. 1979). Geographic populations are isolated; however, divergence is low between populations. Category Four shows panmixia as in Category two, however, like Category Three, the gaps between haplotypes are shallow. Species in Category Four include the American eel, Anguilla rostrata, that show no genetic differentiation along the North American coastline (Avise et al. 1986). The lack of genetic differentiation could possibly be due to migration to a single site to spawn. This pattern was also found in red-winged blackbirds, *Agelaius phoeniceus*, where little genetic differentiation was found throughout North America (Ball et al. 1988). Finally, Category Five shows some haplotypes to be unique to a location while other haplotypes are spread between neighbouring geographic populations and likely represent ancestral haplotypes that were present before a genetic break occurred. This final result can be found in bowfin fish, *Amia calva*, in river drainages in south-eastern USA (Bermingham and Avise 1986). The most common haplotype was found in almost all drainages in the sample while other minor haplotypes were unique to a single drainage.

The dispersal ability and mobility of an organism and its physical environment plays a major role in an organism's distribution and the level of connectivity among populations (Edwards et al. 2008). While long distance dispersal in terrestrial animals is less common and occurs mostly in adults (Kinlan et al. 2005), the planktonic larvae of many marine organisms are much more capable of long distance dispersal. Plankton phases can last as long as several hours or be as extensive as a year or more, for example rock lobster (Ovenden et al. 1992) and eels (Avise 1994). However, the duration of the planktonic phase is not the only process affecting the distribution and gene flow of organisms as many previously thought (Ayre et al. 1997). Hydrographic features such as currents or upwellings can all work to limit or contribute to a marine organism's dispersal ability (Goldstien et al. 2006). Furthermore, not all marine organisms have a planktonic phase. Some species are direct developers whereby their eggs may be attached to the substrate as in some fish and elasmobranchs including the skate *Rioraja agassizii* (Estalles et al. 2009) or brooded in the mouth as in some fish species or a pouch (seahorses and pipefish). Alternatively, some species give birth to

live young as seen in marine mammals and many sharks including the tiger shark, Galeocerdo cuvier (Whitney and Crow 2007), and the smooth-hound shark, Mustelus mustelus (Saidi et al. 2008), however, these species often have more active adult phases. For the most part, reproduction by direct development would be expected to result in less dispersal than those with planktonic phases (Avise 1994). The complexity of incorporating all of the factors influencing dispersal and, hence, gene flow has meant that phylogeography has become an important method in the study of species distribution. Phylogeographic methods enable levels of gene flow to be determined with little prior knowledge of dispersal and has lead to some unexpected findings whereby species with high dispersal ability are found to have limited gene flow (Taylor and Hellberg 2003) or species of low dispersal ability are found to have gene flow over long distances (Sponer and Roy 2002; Derycke et al. 2005). Dispersal leads to gene flow if the dispersers become incorporated reproductively into the population to which they recruit. Overall, one would expect a highly dispersive species to show high levels of gene flow and general panmixia and poor dispersers to be found in genetically differentiated populations.

1.2 Phylogeography and population structure in New Zealand

Phylogeography and studies of population structure in New Zealand are still in their early days and have had a rather patchy coverage of species with at least 42 studies covering coastal invertebrates (Ross et al. 2009), but very few studies of algae and fish species. Studies have found a wide range of population structures and varying levels of gene flow around the coast.

A study of the green-lipped mussel (Perna canaliculus) using allozymes found a significant difference between populations in the North from Tauranga and Kaipara and those from the South Island and Castlepoint (Smith 1988). Later studies on P.canaliculus using mtDNA (Apte and Gardner 2002; Apte et al. 2003) and randomly amplified polymorphic DNA (RAPD) (Apte et al. 2003; Star et al. 2003) also found a genetic North-South divide of populations. However, the mussels of the Cook Strait region were found to be genetically closer to the North Island populations and the genetic disjunction between north and south was found to be around 42°S. Although not all studies of *P.canaliculus* have shown a North-South division (Gardner et al. 1996; Apte and Gardner 2001), several genetic studies in other invertebrates have reached similar conclusions. The North-South genetic break is now the most commonly reported pattern in New Zealand-wide phylogeographic studies (Ross et al. 2009). A separation has been recorded within the Greater Cook Strait region in the cushion star Patiriella regularis (Waters and Roy 2004; Ayers and Waters 2005), the brooding brittle star, Amphipholis squamata (Sponer and Roy 2002), three limpet species, Cellana ornata, C.radians and C.flava (Goldstien et al. 2006) and the sea-grass Zostera muelleri (Jones et al. 2008), and at East Cape in the amphipod, Paracorophium excavatum (Stevens and Hogg 2004), and the tuatua, Paphies subtriangulata (Smith et al. 1989). Many of the studies with a conclusion of a genetic break around East Cape have had large sampling gaps between sites and, hence, the actual site of the break is little more than an educated guess. Meanwhile, greater sampling intensity has been used to pinpoint a divide at 42°S (e.g. (Apte and Gardner 2002). Many have suggested the presence of upwelling on the East and West Coasts acting as a barrier to larval dispersal by transporting coastal larvae offshore (Apte and Gardner 2002; Star et al. 2003; Waters and Roy 2004; Ayers and Waters 2005). However, it has been suggested that the upwelling hypothesis may be flawed due to an error in the calculating of the divergence date and molecular divergence was likely earlier than can be explained by upwelling (Goldstien et al. 2006). Additionally, due to high variability in weather patterns in New Zealand, upwellings can be very temporally irregular (Blanchette et al. 2009). Evidence suggests that planktonic behaviour and extended planktonic larval durations (PLD) can mean that upwellings are less of a barrier to gene flow than once thought (Lett et al. 2007; Johansson et al. 2008), making it seem unlikely that upwellings alone are creating this divergence (Ross et al. 2009). On the East Coast, it has been suggested that the cessation of southerly flow at 42°S by the East Cape Current could cause the genetic division (Ross et al. 2009). At its Southern bound, the East Coast Current divides into two with part of it travelling out over the Chatham Rise along the subtropical convergence while the other part heads north-east where it is incorporated into the Wairarapa Eddy. This means that coastal larvae from the north are likely to be either transported offshore or retained in the Wairarapa Eddy, though retention has been postulated to be for an extensive period of time (Chiswell and Roemmich 1998).

Despite the majority of studies showing a pattern of genetic division between the North and South, other patterns have also been found through genetic analysis. A few studies have shown an East-West division sometimes in addition to the North-South division. The East-West division has been found in the amphipod *Paracorophium lucasi* (Stevens and Hogg 2004) and the sea-grass *Zostera muelleri* (Jones et al. 2008). Other papers have concluded that an isolation-by-distance pattern fits their species best, as was the case with the green-lipped mussel, *Perna canaliculus* (Gardner et al. 1996). Not all coastal marine species have been shown to have genetic structure around New Zealand. A wide variety of invertebrates have been shown to be panmictic throughout New Zealand including two species of rock lobster, *Jasus edwardsii* (Smith et al. 1980; Ovenden et al. 1992) and *Jasus verreauxi* (Brasher et al. 1992), the mussel *P. canaliculis* (Apte and Gardner 2001) in contradiction to many previous studies as reported above, the sea-star *Coscinasterias muricata* (Waters and Roy 2003) and the gastropods, *Austrolittorina antipodum* and *Scutus breviculus* (Waters et al. 2007).

Only three papers have studied the New Zealand-wide population structure of coastal fish. A study of snapper found differentiation in allozymes between east coast populations and west coast populations (Smith et al. 1978). A later study using microsatellites and the mitochondrial DNA found no genetic structure within the mtDNA but a similar pattern of microsatellite differentiation to the earlier allozyme work (Bernal-Ramirez et al. 2003). Microsatellites were also able to identify an isolated population of snapper within Tasman Bay. More recently a mitochondrial study of eight species of triplefin found a negative relationship between depth and population differentiation whereby triplefin species found at the shallowest depth were much more genetically structured than the deeper water species that showed very little or no genetic structuring (Hickey et al. 2009).

1.3 Population genetic markers

There is a growing number of genetic markers available (Feral 2002; Ray 2007) each offering different levels of resolution which can be used to detect different levels of evolutionary divergence. The application of these range from pedigree studies through to population structure and intraspecific gene flow to phylogenetic studies and historical

biogeography (Feral 2002). All genetic markers have there own advantages and drawbacks some of which will be discussed in this chapter. Allozyme electrophoresis was the first marker type to be used to make inferences about the levels of genetic diversity and genetic structure of populations (Hubby and Lewontin 1966). Later, methods that directly sampled the mitochondrial DNA (mtDNA) and nuclear DNA were developed and used to estimate gene genealogies (Avise et al. 1979). In the 1980's, variable numbers of tandem repeats (VNTRs) in the form of minisatallites or microsatellites were found to be hypervariable and could thus give higher resolution genetic structure results than previous methods. More recently even higher resolution techniques have been described including amplified fragment length polymorphisms (AFLPs) for use in closely related within species variation such as DNA fingerprinting (Vos et al. 1995). In the last decade whole genomes can now be used in population studies and this has been helped by the recent leaps in high-throughput sequencing technology (Meyer et al. 2008).

1.3.1 Mitochondrial DNA

The mtDNA of animals is a circular molecule (Jobling et al. 2004) and, in most fish, is around 16,000 nucleotides long. It contains 12 protein coding genes, two ribosomal RNA genes, 22 transfer ribose nucleic acids (tRNAs) (Mabuchi et al. 2007) and the control region (or dloop), a non-coding region that contains the elements necessary for the initiation of transcription and replication (Copeland 2002; Wallace 2002).

MtDNA has been widely used to construct phylogenies and determine phylogeographic patterns. It has been used in more than half of all published phylogeographic studies (Avise 2000). There are several reasons for its popularity. Firstly, mtDNA is thought to

have fewer mechanisms for DNA repair when compared with nuclear DNA and this results in a high mutation rate (Wallace 2002). A high mutation rate is particularly useful in intraspecific studies where variation is generally low (Avise 2000). Secondly, while a cell only contains one copy of the nuclear DNA, it contains multiple copies of mtDNA (Zink and Barrowclough 2008) which makes DNA extraction a lot easier. Furthermore, the inheritance of mtDNA from the mother only in the form of a virtual clone with no recombination means that tracing relationships of individuals to their ancestors and other individuals is much more direct (Curole and Kocher 1999). Finally, the popularity of mtDNA itself can be a reason to use it, as records from databases such as Genbank can be used for comparison or to supplement studies as outgroups.

However, there are also some limitations to the use of mtDNA in population genetic studies. While matrilineal inheritance and absence of recombination have their advantages they can also limit the data that can be extrapolated from mtDNA. The absence of genetic data on male members of the population means that estimates of effective population size (N_e) from mtDNA will only comprise females that are reproductively active. Matrilineal inheritance can also limit conclusions that can be made particularly about gene flow as a researcher only has information on the female half of the population and any differences in male behaviour and gene flow will not be observed. This can be a problem in species where migration only occurs in one gender while the other remains fairly stationary or exhibits homing behaviour. However, the use of additional nuclear loci can help to eliminate these issues. The high mutation rate coupled with a lack of recombination can also result in DNA reaching saturation much more quickly than nuclear DNA (Zink and Barrowclough 2008) which creates problems

for developing genealogies as transitions may have returned to their original state and parsimony is no longer as likely.

1.4 Labridae

The teleost family, Labridae, commonly known as the wrasse, are an ideal group for studies of taxonomy and distribution due to the high level of diversity and number of species within the family. Since the incorporation of the parrotfish (Scaridae) and the Odacidae to the labrids (Kaufman and Liem 1982) the family has grown to 559 described species (Choat et al. 2006) and is the second largest family of marine fishes in the world (Westneat and Alfaro 2005; de Mitcheson and Liu 2008). Although most labrids are tropical reef fish, the diversity within the family is extremely high particularly in the areas of feeding morphology and behaviour (Pitkin 2001).

The current morphological classification places the labrids in the suborder labroidei within the order Percomorpha (Kaufman and Liem 1982). This clade also contains the cichlids (Cichlidae), surfperchs (Embiotocidae) and the damselfishes (Pomacentridae) which, all together, account for up to 10-15% of all living fish species (Stiassny and Jensen 1987; Streelman and Karl 1997). The labroidei are classified solely on the pharyngeal jaw apparatus (PJA) (Liem and Greenwood 1981) which shows seven important morphological features, of which three are considered major, that were suggested as the means by which the labrids and cichlids had been able to diversify so greatly (Stiassny and Jensen 1987; Mabuchi et al. 2007). While, the labroids are the only perciformes to possess all such morphological features of the PJA, none of the modifications are unique to them (Stiassny and Jensen 1987; Johnson 1993; Streelman

and Karl 1997) and there is a lack of morphological similarities outside the pharynx that cast doubt on the clade (Stiassny and Jensen 1987; Rosen and Patterson 1990; Johnson 1993). More recently, molecular studies have shown that the molecular data suggests multiple origins of the PJA (Streelman and Karl 1997; Sparks and Smith 2004; Azuma et al. 2008). The largest and most comprehensive of these studies was undertaken by Mabuchi et al. (2007) who analysed the whole mitochondrial genome for 76 percomorph species and found the labrids to be unrelated to the cichlid/embiotocid/pomacentrid clade. They suggested that labrids had evolved the PJA independently and were more closely related to the anglerfish (Lophiiformes), the Tetraodontiformes including the pufferfish, porcupinefish, sunfish and filefish, and parts of the Zeiformes (boarfishes) and Percoidei (sea breams).

The labrids are well-represented in all tropical oceans and the temperate Indo-Pacific, the latter consisting of a large number of endemic species (more than 20) (Mooi and Gill 2002). However, despite the obvious significance of this family on global oceans and marine ecosystems, the labrids are mostly taxonomically classified by morphology which can lead to difficulties such as cryptic species and parallel evolution (Byrkjedal et al. 2007). There have been few phylogenetic studies of the labrids and, of those published, most have looked at large scale molecular relatedness while within genera phylogeny has remained, for the most part, untested (Read et al. 2006).

In New Zealand, an endemic species from the labrid family, *Notolabrus celidotus*, or the spotty, is one of the most common coastal fish species. Therefore, it makes an ideal species for studying the phylogeography.

Aims

The present study has three main aims:

- First, to determine the phylogeographic structure of *Notolabrus celidotus* using mitochondrial DNA control region sequences and determine the levels of gene flow among coastal locations. (Chapter Two)
- Second, to conduct a phylogenetic analysis of New Zealand members of *Notolabrus* and *Pseudolabrus*. The analysis of the two genera will be used to assess monophyly of the species and compared to an analysis of morphological features. (Chapter Three)
- Finally, to compare genetic variation within the control region of two *Notolabrus* species, *N. celidotus* and *N. fucicola*, to compare levels of haplotype and nucleotide diversities among similar species. (Chapter Four)

Chapter Two:

Phylogeography of the coastal fish species *Notolabrus celidotus* shows New Zealand wide genetic homogeneity.

2.1 Abstract

Notolabrus celidotus (spotty) is an endemic fish species of New Zealand, and it is very common and widely distributed around the coastline. The DNA sequence from the mitochondrial control region of 190 *N. celidotus* samples from throughout their range was determined and analysed. *N. celidotus* showed a homogeneous pattern of genetic diversity and no significant genetic differentiation was detected among the sampled locations. High haplotype diversity paired with low nucleotide diversity was found. A mismatch distribution analysis of pairwise differences suggested that *N. celidotus* has recently experienced population expansion.

2.2 Introduction

New Zealand is a long, thin landmass which passes through nearly 25 degrees of latitude from the Kermadec Islands in the subtropical north to Campbell Islands in the sub-Antarctic south (Francis 1996; Ross et al. 2009). The separation of the country into distant islands and the strong currents that can be found in the Cook Strait between the North and South Islands and the Foveaux Strait between the South Island and Stewart Island (Fig 2.1) would lead many to conclude that coastal species with a widespread



Fig 2.1. Map of New Zealand showing the hydrographic features of its coasts. Adapted from Ross *et al.*, 2009. Arrows show direction of prevailing currents. Circles show major eddies.

distribution might have very little gene flow between populations. However, many of the species studied thus far have had surprising amounts of homogeneity. There have been only a few studies that have shown extreme population structure and local retention and these have often studied unique environments such as Fiordland where local retention and differentiation between and within fiords is documented in the stylasterid hydrocoral, *Errina novaezelandiae* (Miller et al. 2004) and the seastar, *Coscinasterias muricata* (Perrin et al. 2004).

Very few studies have been conducted on the phylogeography of New Zealand's coastal fish though the studies that have been reported show huge variation among species. An allozyme study of New Zealand snapper found two genetically distinct populations demonstrating an east west division (Smith et al. 1978). This was later backed up by microsatellite data (Bernal-Ramirez et al. 2003) with the addition of a genetically isolated population at Tasman Bay. Mitochondrial DNA from the same paper showed no genetic differentiation. In 2009, a study by Anthony Hickey and associates found that phylogeographical patterns varied among species of triplefin. Unusually among fish species they found that population structure among species decreased with habitat depth. Six species (Grahamina capito, G. nigripenne, Bellapiscis medius, B.lesleyae, Forsterygion lapillum and F.varium) show population structure with each indicating between two and four divergent populations. While no triplefin species showed the strong North-South divide found in invertebrates, G.capito did show divergence between two populations, one occurring around the southern and eastern coasts of the South Island and the other covering the entire North Island coast and the west coast of the South Island. Most species show the south and east of the South Island to be distinct from other regions (G. capito, G. nigripenne, B. medius, B. leslevae and F. lapillum

with Wellington included). However, unlike the majority of invertebrate studies, many of the triplefins were found to have genetic divergence amongst North Island populations. *Grahamina gymnota* and *Ruanoho whero* showed no population structure (Hickey et al. 2009).

Notolabrus celidotus, commonly known as the spotty, is a temperate coastal labrid found only in New Zealand where it is widespread and common (Choat 1962; Choat and Ayling 1987; Francis 1996). *N. celidotus* was one of the first fish species to be collected from New Zealand by Europeans (Parrott 1957) and was described in 1801 by Bloch & Schneider. Though originally described as being present in both New Zealand and Australia, only two Australian samples of *N. celidotus* have ever been collected (Choat 1968) and as further specimens have never been found and both were collected on trips that also went to New Zealand, it is suggested that these were labelling errors and the species is restricted to New Zealand (Choat 1968).

N. celidotus is a relatively small fish (Russell 1988), growing up to 27cm long (Paul and Moreland 1993). They are voracious predators and while mostly feeding on molluscs such as bivalves, limpets, chitons and other gastropods, they also eat urchins, brittle stars and crustaceans such as crabs (Choat 1962; Jones 1984b; Denny 2005). Juvenile recruitment has been found to be positively correlated to areas of rocky reef particularly amongst stands of the brown algae, *Ecklonia radiata* (Jones 1984a). However, many studies have found greater densities of adult *N. celidotus* within urchin barren or broken rocky habitats, though adults can still be found in kelp stands (Jones 1984b; Hickford and Schiel 1995; Anderson and Millar 2004; Williams et al. 2008). It seems likely that while juveniles are quite specific about their kelp habitat due to their need for shelter

and a place to hide from predators, adults are able to move around more freely in search of a wider variety of foods (Choat 1962).

A closely related species, the banded wrasse, N. fucicola covers a similar niche (Choat 1962; Denny and Schiel 2002) and there is a good chance that competitive exclusion occurs to some extent. This appears to be supported by observations of much higher N. fucicola densities in areas where N. celidotus is absent (Hardy 1986). While N. celidotus are mostly confined to sheltered parts of the coast (Denny 2005), N. fucicola can often be found at a greater range of exposures (Hardy 1986; Denny 2005). This is backed up by reports of low or no abundance of N. celidotus on the more exposed west coasts of both the North and South Islands of New Zealand and greater densities in the sheltered east coast harbours (Francis 1996; Francis et al. 2005). Despite their widespread distribution status, N. celidotus is absent from many offshore islands including the Three Kings Islands (Hardy 1986; Choat and Ayling 1987; Francis 1996) and the sub-Antarctic Islands including the Snares Islands (Hardy 1986; Francis 1996) and rare on others including the Poor Knights Islands (Choat and Ayling 1987; Doak 1991). Early reports found no evidence of N. celidotus at the Chatham Islands, however, more recently they have become abundant there which has lead to suggestions that they may have colonised recently possibly with indirect assistance from humans (Andrew Stewart, personal correspondence).

The affiliation of spotties with kelp and sheltered regions means they often live around the kelp covered pillars of wharves (Parrott 1957; Choat 1962; Paul and Moreland 1993) where they can be caught by amateur fisherman and, particularly, children. However, their small size, the difficulty with which the bones are removed from the flesh (Parrott 1957) and their territorial nature (Jones 1981; Paulin 1998) have not lent them to commercial fishing. Subsequently, *N. celidotus* is the most well studied New Zealand wrasse (Denny and Schiel 2001), however, much of this work has covered feeding and habitat preferences (Jones 1984a; Jones 1984b; Denny 2005; Francis et al. 2005; Williams et al. 2008) and no genetic data has been collected for this species.

The aim of this chapter is to determine the phylogeographic structure of *Notolabrus celidotus* using samples collected from around New Zealand. Ecological similarities between *N. celidotus* and the triplefin species suggest that it is likely that *N. celidotus* will have similar phylogeographic patterns.

2.3 Materials and Methods

2.3.1 Sampling and collection

Tissue samples were collected from 461 individuals of *Notolabrus celidotus* (see Appendix). Most samples collected north of Auckland were obtained from frozen whole specimens stored at the National Institute of Water and Atmospheric Research (NIWA) which were subsampled mostly by taking a fin clip but some by muscle tissue sample. All samples were collected from coastal areas mostly with the use of a bait catcher net box. Most individuals were fin clipped by taking a small section (about 10mm²) of the caudal fin and then returned to the sea alive. Fin clips were preserved in 70% ethanol until needed for DNA extraction. Samples were labelled with a geographical code and a number (see Appendix)



Fig 2.2. Map of New Zealand and inset of Hauraki Gulf indicating the location of *Notolabrus celidotus* samples that were successfully sequenced for this study. The limits of populations used in analysis were adapted from (Shears et al. 2008) and are shown with population names and number of sequences of *N.celidtous* in each population. Populations in gray were not sampled or sequencing was unsuccessful.

Samples were taken from the caudal fin for several reasons. Firstly, the caudal fins were easily accessible and large enough to sample unlike the dorsal and anal fins which were often small and held against the body by the fish upon capture. Secondly, labrids mostly use their pectoral fins for thrust during swimming, a style known as "wrasse stroke" (Choat 1962; Doak 1991; Denny 2005), so these fins were left intact due to a perceived risk to swimming ability due to sampling. Finally, caudal fins were observed to have tears and become ragged naturally in larger fish with no apparent swimming disadvantage to the fish.

2.3.2 DNA extraction and sequencing

Fin tissue used for DNA extraction was generated using a fin punch to acquire a circular section of tissue of around 1mm diameter. For tissue samples, a small piece of tissue of comparable size was taken using a scalpel. The fins and muscle tissue were digested using Proteinase Κ SDS followed extraction and and by using Phenol:Chloroform:Isoamyl (25:24:1) (Sambrook et al. 1989). PCR primers for the control region were designed using the complete mitochondrial DNA sequence of Pseudolabrus sieboldii from Genbank (Oh et al. 2008). The primers used were 5'-TAGAGCTGACAGCAAAGTCAGG-3' the 12S from rRNA and 5'-TYTAACTCCCACCCCTAACTCC-3' from tRNA-Pro. This allowed a 940bp fragment of DNA incorporating the control region to be amplified and sequenced (Fig 2.2). Four samples of *N. celidotus* and one sample of *Notolabrus fucicola* (the banded wrasse) were sequenced. The sequences were aligned and used to design a pair of species-specific primers for N. celidotus control region. The new primers were 5'-AATTAAGCTACGCGAGCAGTTG-3' from tRNA-Phe 5'and TYTAACTCCCACCCCTAACTCC-3' from tRNA-Pro. The polymerase chain reaction (PCR) was carried out in 15µL volumes containing buffer, 6µg bovine serum albumin (BSA), 800µM dNTPs (consisting of 200µM each of dATP, dTTP, dCTP and dGTP), 0.4µM each of forward and reverse primers, 1.5mM MgCl₂, double-distilled water (ddH₂O) and 0.6U DNA polymerase. Thermal cycling conditions were an initial denaturation of 30 seconds at 94°C, followed by 40 cycles of 94°C for 30 seconds, 50°C for 45 seconds and 72°C for 45 seconds, then a final extension stage for three minutes at 72°C. Amplified products were treated with ExoSAP-IT and then sequenced on an ABI3730 at the Massey University Genome Service in Palmerston North.

2.3.3 Statistical analysis

Chromatograms were edited using FinchTV Version 1.4.0 (Geospiza_Inc 2006) and sequences were aligned in MEGA 4.0 (Tamura et al. 2007). Due to the low number of observed insertions and deletions the sequences were easily aligned by eye. Tajima's D statistic and Fu F_s tests of neutrality were carried out in Arlequin (Excoffier et al. 2005). *N. celidotus* sequences were separated into six populations (Fig 2.2) based on an analysis of biogeographic regions in New Zealand (Shears et al. 2008). Nucleotide and haplotype diversities and mismatch distributions were generated for these populations and the total population by DnaSP (Librado and Rozas 2009). An AMOVA was used to generate φ_{ST} to measure genetic divergence within and among populations and pairwise F_{ST} values were calculated using Arlequin ver. 3.5.1.2 (Excoffier et al. 2005) . The formula $\theta=2N_{e(f)}\mu$ (where θ is the expected level of diversity and μ is the mutation rate per site per generation) was used to estimate effective female population size. Mutation rate (4-8% per million years) was taken from a estimate rate for the control region of *Pagrus pagrus* a species from the Percoidei a sister family to the labridae (Ball et al. 2007). Generation time was estimated based on lifespan and growth and maturation



rates (Jones 1984b) to be around 2 years. Thus, μ is estimated to be 12 x 10⁻⁶. The mean θ value was calculated from three theta values calculated in DnaSP (Librado and Rozas 2009). These were based on the nucleotide diversity, the number of segregating sites and the total number of mutations and all gave similar results.

2.4 Results

2.4.1 Variability within the mtDNA control region

The DNA sequence of 786 base pair section of the mitochondrial control region was determined for a total of 190 *Notolabrus celidotus* specimens collected from around New Zealand (Fig 2.2.). The average frequency for the sequences was 29.3% thymine, 17.3% cytosine, 27.4% adenine and 26.0% guanine. There were 126 variable sites in total (114 transitions, 20 transversions and two indels) of which 85 were parsimony informative. There were 170 haplotypes detected which gave an overall haplotype diversity of 0.9985 \pm 0.0008 and a nucleotide diversity of 0.0101 (see Table 2.1). There was little difference in haplotype and nucleotide diversities among populations (Table 2.1). The majority of the few shared haplotypes found in this dataset were not restricted within regions or the populations set out in Fig 2.2.

2.4.2 Phylogeography and population structure

A neighbour-joining tree showed no clear phylogeographic pattern between haplotypes and location (Fig 2.5). There was low nucleotide diversity among haplotypes which reduced the level of resolution, signified by low branch support given by bootstrap values. There was a clear separation of the outgroup *N. fucicola* sequences from the *N. celidotus* sequences. A Fu's F_s value of -8.68159 (P=0.1055) was found. A negative

Location	N	h	Hd S K		K	π
Raglan	7	7	1.0000	27	9.3333	0.0119
Northeastern	37	35	0.9955	68	7.8318	0.0096
Portland	13	13	1.0000	41	8.8462	0.0113
Abel	73	70	0.9989	91	8.3128	0.0103
Cook	18	17	0.9935	52	8.50327	0.0109
SSI	42	40	0.9977	66	7.4750	0.0094
Total	190	170	0.9985	126	8.1078	0.0101

Table 2.1. Number of samples per *Notolabrus celidotus* population (N) and the corresponding number of observed haplotypes (*h*), haplotype diversity (H*d*), segregating sites (S), mean number of polymorphisms (K) and nucleotide diversity (π)

Table 2.2. Analysis of molecular analysis (AMOVA) for Notolabrus celidotus.

Source of variation	d.f.	Percentage of variation	F-statistics	P-values
Among groups	5	-0.47	F _{CT} =-0.00474	0.67351
Among populations within groups	8	0.61	F _{SC} =0.00610	0.23069
Within populations	176	99.86	F _{ST} =0.00138	0.36559

	Raglan	Northeastern	Portland	Abel	Cook	Stewart Is
Raglan	_	0.28829	0.70270	0.34234	0.63063	0.45946
Northeastern	0.01217	—	0.29730	0.24324	0.25225	0.62162
Portland	-0.01893	0.00311	—	0.58559	0.87387	0.38739
Abel	0.00210	0.00343	-0.00551	—	0.20721	0.44144
Cook	-0.03031	0.00745	-0.01712	0.00598	—	0.19820
Stewart Is	-0.00435	-0.00247	0.00493	-0.00033	0.00765	—

Table 2.3. Pairwise FST values (below diagonal) and adjoining p-value (above diagonal) for six *N. celidotus* populations



Fig 2.4. Mismatch distribution for entire New Zealand population of *Notolabrus celidotus*.

value means that a large amount of recent mutations have taken place based on an excess of rare alleles (Fu 1997). However, the p-value shows that the statistic is not significant and, thus, we can accept the null hypothesis of neutral evolution. Likewise, the Tajima D statistic was -1.16225 (P=0.21264). An AMOVA showed that almost all variation was found within populations (99.86%) and none of the F-stats were significant (Table 2.2).



Fig 2.5. Neighbour joining (NJ) phylogenetic tree based on the mitochondrial DNA control region showing the relationship within *Notolabrus celidotus*. Tree is rooted with samples of *Notolabrus fucicola*. Purple square=Raglan; red circles=Northeastern; green triangles=Portland; blue triangles=Abel and Cook and yellow diamonds=Stewart Island, Open circles=*N.fucicola* outgroup.
Additionally, all pairwise F_{ST} values were not significant (Table 2.3). As there was a high number of haplotypes and the low nucleotide diversity, a haplotype network constructed using TCS 1.21 (Clement et al. 2000) gave little resolution and the network was not informative (data not shown). The total mismatch distribution and those of the larger populations showed a bimodal graph (Fig 2.4) with a raggedness statistic of 0.0061. The effective female population size was calculated to be around 1000.

2.5 Discussion

2.5.1 Genetic variability and Ne

The data presented in this study suggests a genetically homogeneous population of *Notolabrus celidotus* along almost 1600km of New Zealand's length. The high haplotype diversity but low nucleotide diversity found within this study is a common occurrence among fish populations (von der Heyden et al. 2010). In comparison to other New Zealand coastal fish, *N. celidotus* shows particularly high levels of haplotype diversity (*h*=0.9985). Haplotype diversity in snapper was 0.764 (Bernal-Ramirez et al. 2003) and three of the eight studied species of triplefin showed haplotype diversities below 0.9 (Hickey et al. 2009). However, two species of triplefin , *Ruanoho whero* (*h*=0.981, π =0.016) and *Grahamina gymnota*, now *Forsterygion gymnota* (*h*=0.999, π =0.033) (Hickey et al. 2009) did possess similar haplotype and nucleotide diversities to those found for *N. celidotus* and both triplefin species showed no population structuring. While explanations for high haplotype diversity in other vertebrates have suggested either a high mitochondrial mutation rate, historical isolation, or a model of expansion and subsequent decline (Chiari et al. 2009), high haplotype diversity is often aided by the large population sizes found in many fish (von der Heyden et al. 2010) though

increasingly this pattern in marine fish is being linked to random recruitment, historic bottleneck and expansion events and natural selection (Grant and Bowen 1998).

Calculations of effective female population size resulted in an estimate of around 1000 reproductively active females. Based on my own sampling effort and visual count or catch data (Hickford and Schiel 1995; Anderson and Millar 2004; Francis et al. 2005), which shows as many as 950 fish caught per km towed, this is obviously a gross underestimate of true numbers. Additionally, monandric protygynous hermaphrodites like *N. celidotus* are often found to have a female biased sex ratio (Sadovy and Shapiro 1987). In *N. celidotus* the female/male sex ratio appears to vary with location but on average is around 4.1:1 (Jones 1980; Denny and Schiel 2002). A result of 1000 for the effective population size of reproductively active females in the population results in an estimate of around 250 reproductively active males using the 4.1:1 sex ratio. Such a low estimate of effective population size could indicate that expansion has occurred recently and rapidly from a much less diverse gene pool (Jobling et al. 2004).

2.5.2 Gene flow

The pattern of gene flow in *N. celidotus* most closely reflects that found in the two triplefin species *Forsterygion gymnota* and *Ruanoho whero* (Hickey et al. 2009). These two species are found in reef habitats similar to those inhabited by *N. celidotus* and at similar depths (Denny 2005; Hickey et al. 2009). The planktonic larvae of *R. whero* have been associated with drift algae which have been suggested to assist long-distance dispersion of fish species (Kingsford 1992). A similar association between drift algae and larval *N. celidotus* has also been suggested (Kingsford 1992; Kingsford 1993; Morrisey et al. 2006) though other studies of drift algae did not find *N. celidotus*

(Kingsford and Choat 1985). However, while *R. whero* is found on offshore islands such as the Three Kings Islands, *N. celidotus* is absent which seems to suggest that they are still somewhat more restricted in their dispersal ability than *R. whero*.

The extended planktonic larval duration estimated to be as long as five months in *N. celidotus* is also likely to aide increased gene flow in the species (Ovenden et al. 1992) particularly when overcoming biogeographic barriers suggested to restrict other species, such as the Wairarapa Eddy (Chiswell and Roemmich 1998). The mismatch distribution for the overall population has a very low raggedness statistic and one particularly large peak which indicates an expansion event in the past and this is supported by the negative Tajima D statistic (Jobling et al. 2004). However, the second smaller peak on the mismatch distribution is interesting. This is often observed when there are two populations either because there is a cryptic species within the data or that the populations have at some point been separated and diversified without any contact then have subsequently been brought back together before speciation has occurred. The former is unlikely as nucleotide diversity was so low and a comparison with a close relative, *N. fucicola*, showed sequences were much closer to each other than to the outgroup. Another possibility could be that a greater coverage of all population variation is required to smooth out the curve (Wu et al. 2006).

The pattern found in *N. celidotus* is consistent with the Category Four phylogeography discussed in Chapter One. Category Four shows no regional differentiation and shallow divergence between haplotypes (Avise 2000). This pattern is often found in species with a small to moderate effective population size and high gene flow, but, few persistent biogeographic barriers. This pattern is also common in species that have experienced

recent, rapid population expansions from a relatively small original population (Wu et al. 2006). A well-known example of a rapidly expanding population which fits this explanation is humans (Hawks et al. 2000; Jobling et al. 2004) but is being increasingly recognised in fish (Grant and Bowen 1998).

Phylogeny of the pseudolabrine tribe (family: Labridae) reveals paraphyly within the *Notolabrus* and *Pseudolabrus* genera.

3.1 Abstract

The pseudolabrine tribe consists of 25 species from six genera. Four of these genera are confined to Australia (*Pictilabrus, Austrolabrus, Dotolabrus* and *Eupetrichthys*) and *Notolabrus* is found in New Zealand and Australia. The *Pseudolabrus* genera however, is not restricted to the Southern Hemisphere and has an antitropical distribution whereby it can be found throughout Australia, New Zealand, many of the islands of the South Pacific as well as in Japan and Korea to the South China Sea. The six species of pseudolabrine found in New Zealand have been underrepresented in recent phylogenetic work on this tribe with only *Pseudolabrus miles* being sequenced. This has left uncertainty over results of paraphyly between the *Pseudolabrus* and the *Notolabrus*. The incorporation of a further three of the New Zealand species gives weight to the need for a revision of the *Notolabrus* and *Pseudolabrus* genera.

3.2 Introduction

There are 21 species of Labridae found in New Zealand waters (Denny and Schiel 2001). However, most of these are only found around the sub-tropical Kermadec Islands. The tropical nature of labrids means only a small number of labrid species are found around the New Zealand mainland. The members of *Notolabrus* and *Pseudolabrus* from the pseudolabrines tribe (Westneat and Alfaro 2005) are an exception.

The *Pseudolabrus* genus is unique among labrids and most marine fish, in that they are temperate species that follow an anti-tropical distribution (Mabuchi et al. 2004) Organisms with this distribution can be found in both the Northern and Southern Hemispheres in regions of the sub-tropics, temperate or even the poles. However, they do not occur in tropical regions around the equator which raises questions about dispersal and species origin. In the case of *Pseudolabrus*, a paper by Kohji Mabuchi and colleagues (2004) studied the phylogeny of members of the *Pseudolabrus* and *Notolabrus* to discover the origins of Northern Hemisphere *Pseudolabrus* species. *Pseudolabrus* are found distributed throughout Australia, New Zealand and the South Pacific Islands from Lord Howe Island in the west to Easter Island in the east as well as members in Japan, and along the coast of China to the South China Sea in the Northern Hemisphere (Fig 3.1). Their results suggested that, surprisingly, Northern Hemisphere species appeared most closely related to species of the south-east Pacific Islands.

Although *Notolabrus* are also temperate species they are unlike *Pseudolabrus* in that they are only found in the Southern Hemisphere with species distributed around southern and eastern Australia including Lord Howe and Norfolk Islands and throughout New Zealand including The Chatham and Kermadec Islands (Fig 3.2).

Further to the findings of the origin of Northern Hemisphere pseudolabrines, Mabuchi







et al. (2004) also raised questions on the monophyly of *Pseudolabrus* as addition of *Notolabrus* to the phylogeny showed nesting of the members of *Notolabrus* within a paraphyletic *Pseudolabrus*. The genus *Notolabrus* had previously been split from the remaining members of *Pseudolabrus* in a paper by Barry Russell (1988) based on morphological differences within the pectoral rays, dorsal and anal fins, vertebrae, jaws and the laterosensory canal tube.

To date, 12 species of *Pseudolabrus* and seven species of *Notolabrus* have been described. Two species of *Pseudolabrus (P. luculentus* and *P. miles)* and four species of *Notolabrus (N. celidotus, N. cinctus, N. fucicola* and *N. inscriptus)* can be found in the waters around New Zealand (fishbase.org). Of these, three species (*P. miles, N. celidotus* and *N. cinctus*) are endemic. While many of these fish are rare in New Zealand, *N. fucicola* and *N. celidotus* are common in shallow coastal waters around wharves and in kelp forests.

The aim of this chapter is to add DNA sequence data from the New Zealand *Notolabrus* and *Pseudolabrus* species to the phylogeny of the pseudolabrines. This data will be used to address the questions of whether *Notolabrus* and *Pseudolabrus* are distinct monophyletic genera as described by Russell (1988), or whether they are one monophyletic assemblage as suggested in Mabuchi *et al.* (2004) and the two genera should be merged.

3.3 Materials and Methods

3.3.1 Sampling and collection

Tissue samples were collected from three of the four *Notolabrus* species and one of the two *Pseudolabrus* species represented in New Zealand. Tissue samples of *N. inscriptus* from the Kermadec Islands were provided by the Museum of New Zealand, Te Papa Tongarewa. Samples of *N. celidotus, N. fucicola* and *P. miles* were caught with a baitcatcher net box as part of the collection of *Notolabrus celidotus* for a phylogeography and were obtained from right around the country. All individuals other than the *N. inscriptus* tissue samples were fin clipped by taking a small (about 10mm²) section of the caudal fin. All finclips and tissue samples were preserved in 70% ethanol until DNA extraction.

DNA sequences from the outgroup species and non New Zealand members of *Notolabrus* and *Pseudolabrus* were obtained from Genbank (Accession numbers: Table 3.1). Incorporation of non-New Zealand pseudolabrines resulted in the representation of six of the seven recognised species of the *Notolabrus* genus and eight of the 12 recognised species of *Pseudolabrus* (Table 3.1). Members from *Austrolabrus*, *Pictilabrus, Dotolabrus* and *Eupetrichthys* have been classified within the pseudolabrine tribe and are considered sister genera of *Notolabrus* and *Pseudolabrus*. Therefore, incorporation of the single species found within *Austrolabrus* and *Eupetrichthys* and one of the three species from *Pictilabrus* (Russell 1988; Mabuchi et al. 2004) was deemed important to give power to the results. No sequences of the two *Dotolabrus* species could be found and, therefore, it could not be incorporated into this study. A further seven outgroup genera were added to correctly root the tree (Table 3.1).

These were determined via reference to the phylogeny compiled by Westneat and Alfaro (2005) and availability on Genbank. Suezichthys gracilis, Ophthalmolepis lineolata and Halichoeres tenuispinnis are all considered part of the crown tribe julidine or the labrichtyines which have been found to be nested within the julidines (Westneat and Alfaro 2005). Pseudolabrines have been placed as the sister tribe to these tribes (Westneat and Alfaro 2005) and are considered to be closely related due to several key morphological features (Russell 1988). The Halichoeres genus has recently been found to be polyphyletic (Barber and Bellwood 2005; Westneat and Alfaro 2005). However, all 35 species sampled in these studies were still found to reside within the julidines and, thus, H. tenuispinnis was retained in this study. Cheilinus undulatus and Pteragogus *flagellifer* represent the cheiline and pseudocheiline tribes respectively and *Choerodon azurio* is a member of the hypsigenyines tribe which is considered to be the basal labrid tribe (Mabuchi et al. 2004; Westneat and Alfaro 2005). Additionally, Emmelichthys struhsakeri was placed as the non-labrid outgroup. While traditional taxonomy has placed the Labridae within the labroidei suborder with the Cichlidae, Pomacentridae and Embiotocidae, recent molecular studies have suggested labrids are much more closely related to a part of the Percoidei family of which E. struhsakeri is a member.

3.3.2 DNA extraction and Sequencing

A piece of tissue about 1mm in diameter was taken from the caudal fin using a fin punch or a similarly sized portion of tissue was subsampled in the case of the Te Papa samples. Digestion of the tissue was carried out by Proteinase K/SDS dissolution and then extraction using the Phenol:Chloroform:Isoamyl method (Sambrook et al. 1989). Two sets of primers with an overlapping region of around 100bp were used to amplify a mitochondrial sequence incorporating part of the 12S rRNA gene, tRNA-Val and part of the 16S rRNA gene. The primers were obtained from Mabuchi et al. (2004) and this allowed for direct comparison of the sequences obtained in this study with previously published data. The first pair of primer sequences were: L1083-12S 5'-ACAAACTGGGATTAGATAC-3' and H1903-16S 5'-GTAGCTYTAGTTTCGGG-3'. The second pair of primer sequences L1803-16S 5'were: AGTACCGCAAGGGAAAGCTGAAA-3' 5'and H2590-16S ACAAGTGATTGCGCTACCTT-3'. PCR was carried out in 15µL volumes containing buffer, 6µg bovine serum albumin (BSA), 800µM dNTPs (consisting of 200µM each of dATP, dTTP, dCTP and dGTP), 0.4µM each of forward and reverse primers, 1.5mM MgCl₂, double-distilled water (ddH₂O) and 0.6U DNA polymerase. Thermal cycling conditions were an initial denaturation of 30 seconds at 94°C followed by 40 cycles of 94°C for 30 seconds, 50°C for 45 seconds and 72°C for 45 seconds then a final extension stage for three minutes at 72°C. Amplified products were treated with ExoSAP-IT and then sequenced on an ABI3730 at the Massey University Genome Service in Palmerston North.

3.3.3 Statistical analysis

Chromatograms were edited using FinchTV Version 1.4.0 (Geospiza_Inc 2006) and sequences were then aligned in MEGA 4.0 (Tamura et al. 2007) for analysis. All sequences were aligned by eye. Sequences from seventeen other species were taken from a paper by Kohji Mabuchi and associates (2004) via Genbank. In their results they found that once the sequences were split into stem and loop regions, the loop regions indicated transition saturation and were, therefore, eliminated from the analysis (Mabuchi et al. 2004). However, in this study, bootstrapped neighbour-joining trees done with transitions and transversions and with transversions only showed no

Classification	Species	Reference	Accession Number
Order: Perciformes			
Family:Percoidei	Emmelichthys struhsakeri	Miya <i>et al.</i> , 2003	AP004446.1
Family: Labridae			
Tribe: Hypsigenyins	Choerodon azurio	Mabuchi <i>et al.</i> , 2004	AB121235.1
Tribe: Cheilines	Cheilinus undulatus	Yin <i>et al.</i> , 2009	NC_013842.1
Tribe Pseudocheilines	Pteragogus flagellifer	Jung <i>et al.</i> , 2007	NC_010205.2
Tribe: Julidines	Halichoeres tenuispinnis	Mabuchi <i>et al.</i> , 2004	AB121236.1
Tribe: Labrichthyines	Ophthalmolepis lineolata	Mabuchi <i>et al.</i> , 2004	AB121237.1
	Suezichthys gracilis	Mabuchi <i>et al.</i> , 2004	AB121238.1
Tribe: Pseudolabrines	Eupetrichthys angustipes	Mabuchi <i>et al.</i> , 2004	AB121250.1
	Austrolabrus maculatus	Mabuchi <i>et al.</i> , 2004	AB121249.1
	Pictilabrus laticlavius	Mabuchi <i>et al.</i> , 2004	AB121248.1
	Pseudolabrus sieboldi	Oh et al., 2008; Mabuchi et al., 2007; Mabuchi et al., 2004	EU560727,1/NC_009067.1/AB121247.1
	Pseudolabrus eoethinus	Oh e <i>t al.</i> , 2008; Mabuchi e <i>t al.</i> , 2004	EU560728.1/AB121243.1
	Pseudolabrus fuentesi	Mabuchi <i>et al.</i> , 2004	AB121244.1
	Pseudolabrus biserialis	Mabuchi <i>et al.</i> , 2004	AB121242.1
	Pseudolabrus guentheri	Mabuchi <i>et al.</i> , 2004	AB121245.1
	Pseudolabrus miles	Mabuchi <i>et al.</i> , 2004; Own collection	AB121246.1
	Notolabrus parilus	Mabuchi <i>et al.</i> , 2004	AB121240.1
	Notolabrus tetricus	Mabuchi <i>et al.</i> , 2004	AB121241.1
	Notolabrus gymnogenis	Mabuchi <i>et al.</i> , 2004	AB121239.1
	Notolabrus inscriptus	Te Papa collection	
	Notolabrus fucicola	Own collection	
	Notolabrus celidotus	Own collection	

Table 3.1. List of species used in this study, their relation to each other and source of fish samples.

differences to branch length or species relatedness and resulted in only minor changes (3% or less) to bootstrap values. Thus, all trees included both transitions and transversions for this study. Neighbour joining and maximum parsimony trees were both created and bootstrapping of all branches was performed using MEGA 4.0 (Tamura et al. 2007). JMODELTEST (Guindon and Gascuel 2003; Posada 2008) was used to determine the model of nucleotide substitution that reflected the data most closely. This model was then used to establish a phylogeny estimated by Bayesian analysis using MrBayes 3.1.2 (Ronquist and Huelsenbeck 2003; Huelsenbeck and Ronquist 2005). Monte Carlo Markov chains were run for 2000000 generations. Trees were sampled every 100th generation after a burnin of 25% resulting in 15000 trees which were used to calculate posterior probabilities for the phylogeny.

3.4 Results

A 1510bp long fragment of mitochondrial DNA comprising 452bp of the 12S rRNA gene, all 74bp of tRNA-Val and 984bp of the 16S rRNA was obtained for 29 samples from 24 species. Six samples from four species were collected and sequenced for this study and 23 samples from 20 species were obtained from Genbank. Three ingroup species had not previously been incorporated in the pseudolabrine phylogeny. An analysis of parsimony (MP) produced one most parsimonious tree (Fig 3.3). A bootstrapped neighbour-joining tree (NJ) was also carried out. Both trees gave a monophyletic pseudolabrine tribe with a bootstrap value of 94 (MP) and 96 (NJ). *Austrolabrus maculatus* and *Eupetrichthys angustipes* were sister clade to the rest of the pseudolabrines and *Pictilabrus laticlavius* was sister to the *Notolabrus* and



Fig 3.3. The most parsimonious trees with bootstrap values indicated at branch nodes.



Fig 3.4. Phylogeny based on Bayesian analysis. Numbers on branches are posterior probabilities from 15000 trees.

Pseudolabrus genera though with low bootstrap support (NJ=58, MP=60). Pseudolabrus is shown as paraphyletic with both P. miles and P. biserialis nested within the Notolabrus. Both trees show the rest of the Pseudolabrus genus forming a monophyletic assemblage. Bootstrap support for this separation into two clades was high (NJ=98, MP=92). Both trees show the New Zealand species N. fucicola, N. celidotus and P. miles forming a monophyletic assemblage with P. biserialis with N. *fucicola* as the sister clade to what is a trichotomy formed by the other three species in the NJ tree but shows P. miles as the sister to N. celidotus and P. biserialis in the MP tree. However, the assemblage of these four species only had bootstrap support of 78 in the NJ tree and 24 for the MP tree. N. inscriptus was grouped with the remaining Notolabrus species; N. gymnogenis, N. tetricus and N. parilus and with much higher bootstrap support (NJ=97, mp=96). Suezichthys gracilis was sister to the pseudolabrines and Ophthalmolepis lineolata and Halichoeres tenuispinis formed the sister clade to the pseudolabrines with S. gracilis (Bootstrap: 91 (NJ) and 96 (MP)). Although no full matching sequence of the most easterly pseudolabrine, Pseudolabrus gavi exists for this analysis, a smaller 409bp matching segment of 12S consistently placed P. gavi (Accession no. AY279639.1 (Westneat and Alfaro 2005)) with P. fuentesi and both of them as sister clade to the Japanese species, P. eoethinus and P. sieboldi. The NJ tree was unable to resolve the outgroup which resulted in the non-labrid outgroup, E. struhsakeri falling within the labrid outgroups. The MP trees were able to correctly place *E. struhsakeri*, however, they had little resolution between the labrid outgroups.

Analysis by jMODELTEST (Guindon and Gascuel 2003; Posada 2008) resulted in the best fit in a likelihood ratio test given by the model TIM2+I+G. The Bayesian analysis provided 20000 trees of which 25% were discarded as burnin leaving 15000 trees for

providing posterior analysis to a consensus tree (Fig 3.4). The tree is similar to the phylogeny shown by the parsimony tree. However, the former places *N. fucicola* as the sister to the other *Notolabrines* + *P. miles* and *P. biserialis* with strong support from the posterior probability score. As in the parsimony tree, the phylogram produced from Bayesian analysis showed low support for relations within the *Notolabrus* genus but high support for the inclusion of *P. biserialis* and *P. miles*. The remainder of the *Pseudolabrus* genus formed a well supported clade.

3.5 Discussion

This study supports a previous phylogenetic study on the pseudolabrine tribe that found the *Notolabrus* and *Pseudolabrus* genera to be non-monophyletic (Mabuchi et al. 2004). This is contrary to the osteological data which was used to originally separate the genera (Russell 1988) (Fig 3.5). Nor does it match with a morphological phylogeny based mainly on cheek scalation but incorporating further morphological data (Choat 1962) (Fig 3.6). However, as the paraphyletic result is created by only two species of *Pseudolabrus*, it may be possible to re-examine the morphology of these species and consider re-classifying the two genera with *P. miles* and *P. biserialis* incorporated into the *Notolabrus* genus.

Due to the large number of pseudolabrines in Australia and the restriction of many of the genera (*Dotolabrus, Eupetrichthys, Austrolabrus* and *Pictilabrus*) to the continent it is likely that Australia is the centre of radiation for the tribe. It is also likely from the distributions of other closely related labrids (*Suezichthys gracilis*) that the pseudolabrines originated from a tropical Indo-Pacific ancestor. The New Zealand



Fig 3.5. Pseudolabrine phylogeny based on osteological features from Russell 1988

species appear to have come to New Zealand from two Australian populations. *N. inscriptus* appears to have reached the Kermadec Islands from Eastern Australia as it can also be found along Australia'a east coast and Norfolk Island and its closest relative, *N. gymnogenis*, is found along that coast and other closely related species *N.parilus* and *N. tetricus* are from south and south-eastern Australia respectively. The mainland species, *N. celidotus* and *P. miles* are much more closely related to the southwest Australian species *P. biserialis*. It seems a somewhat unlikely distribution that this clade is found in New Zealand and southwest Australia but not southeast Australia or Tasmania. However, one of the south-eastern species, *P. psittaculus*, has yet to be sampled for this phylogeny and could turn up to be the missing link. This is likely from a morphological viewpoint as *P. psittaculus* was originally classified as *P. miles* (Choat 1968), however as the Japanese *P. sieboldi* was also once classified as *P. miles* (Mabuchi and Nakabo 1997) though the phylogeny shows them to be not closely related this does not give much certainty. This misclassification gave *P. miles* a New Zealand, Australia and Japan distribution that had many scientists confused (Choat 1962) until it



Fig 3.6. *Pseudolabrus* phylogeny from Choat (1962) based mainly on cheek scalation but incorporating several other morphological features. The original name is given with the current classification given in parentheses. The phylogeny is not intended to show direct progression but instead shows the structural type which gave rise to each species

was finally cleared up (Choat 1968; Mabuchi and Nakabo 1997).

The placement of *N. fucicola* varies among trees and it is unclear what other species this fish is most closely related to. It appears that it is either closely related to the other species found around the New Zealand mainland, a result found in the maximum parsimony and neighbour-joining trees and that fits well geographically, or that *N. fucicola* is the sister species to all *Notolabrus* species and *P. miles* and *P. biserialis* as indicated by the Bayesian analysis. The distribution of *N. fucicola* includes southwest Australia (Russell 1988) and it would be of interest for pseudolabrine taxonomy to gain

samples of the Australian *N. fucicola* for comparison to the New Zealand specimens to verify that these are, truly, one species and to establish migration and movement between these distant populations. Southwest Australia is the most likely point of radiation for the *Notolabrus* genus so it is plausible that *N. fucicola* branched off early and, subsequently, made its own way to New Zealand either much more recently or with some gene flow still maintained between the two populations.

The low bootstrap support and variation among phylogenetic trees makes it unclear whether the mainland New Zealand species minus *N. fucicola* arrived in New Zealand as one species and then subsequently speciated or whether they are the result of multiple species migrations. Their absence from the Australian fauna indicates that *N. celidotus* and *P. miles* evolved into separate species once in New Zealand but lack of resolution means we cannot rule out speciation and, subsequent extinction in Australia with multiple dispersal events to New Zealand.

As found by Mabuchi *et al.* (2004), Japanese species of *Pseudolabrus*, *P. sieboldi* and *P. eoethinus*, were shown to be genetically closer to those species from the southeast Pacific, *P. fuentesi* from Easter and Pitcairn Islands and the Austral Islands in French Polynesia and *P. gayi* from Islas Juan Fernandez and Islas San Felix off the coast of South America. There are two hypotheses that have been proposed for the occurrence of anti-tropical marine species (Randall 1981). The first is that cold water species are able to use deeper water channels where cooler water passes over the equator. However, in the case of shallow coastal species such as *Pseudolabrus* a more likely explanation is that during periods of cooling, like that of the Pleistocene, cool water species were able

to stretch across the equator until subsequent warming caused distributions to recede and populations to be separated by the warm waters of the tropics .

The anti-tropical pattern of *Pseudolabrus* is even more mystifying as the Northern Hemisphere species inhabiting the northwest Pacific Ocean appear most closely related to the *Pseudolabrus* species from the southeast Pacific which are also the most geographically distant species. Another group of labrid fish within the subgenus *Verreo* also have an antitropical distribution with species present in Australia, New Zealand, Easter Island and Japan with one species, *Bodianus bathycapros* found in Hawaii (Gomon 2006). Unlike the other temperate *Verreo* species which are found in shallow waters less than six metres depth, the warmer waters around Hawaii have meant *B. bathycapros* lives much deeper (Randall 1981). Though the phylogeny of this genus is yet to be studied the distribution of these species may give an indication of how *Pseudolabrus* has accomplished its current distribution. It is possible that the Hawaiian Islands were once inhabited by *Pseudolabrus* during a period of atmospheric cooling and used as a stepping stone between the islands of the East Pacific and Japan. When the world began to warm again, *Pseudolabrus* was unable to tolerate conditions around Hawaii and, as a result, became locally extinct.

Chapter Four:

Comparison of variation between two species of *Notolabrus* fish in New Zealand

4.1 Abstract

Analysis of haplotype and nucleotide diversities, pairwise differences and tests of neutrality can give an indication of demographic changes within populations. *Notolabrus celidotus* was found to have very high haplotype diversity paired with low nucleotide diversity, an indication of recent expansion from a much smaller population. A related species *Notolabrus fucicola* shares an almost identical niche and distribution and would, therefore, be expected to show a similar pattern of genetic diversity. Sequences of the mitochondrial control region were compared for samples of both species collected from Wellington, New Zealand. A study of the literature showed that most fish species share the pattern of high haplotype diversity and low nucleotide diversity. *N. celidotus* and *N. fucicola* both showed very high haplotype diversity, even for fish, and relatively low nucleotide diversity and indicated that both were going through an expansion. The reason for this expansion is unknown, but it has often been linked to climate warming after an ice age in other temperate species.

4.2 Introduction

Most populations of animal species are characterised by low haplotype and nucleotide diversities often with one or two prevalent haplotypes. This pattern is found in species

of mammals (Garcia-Rodriguez et al. 1998; Klaus et al. 2001; Larson et al. 2002), birds (Mila et al. 2000; Martinez-Cruz et al. 2004; Zhang et al. 2004; Roques and Negro 2005; Shephard et al. 2005; Cadahia et al. 2007; Hailer et al. 2007), reptiles (Berry and Gleeson 2005) and marine invertebrates (Apte and Gardner 2002; Goldstien et al. 2006). In contrast, low haplotype diversity is very rarely found in fish with most species displaying high haplotype diversity with many low frequency haplotypes (von der Heyden et al. 2010). There are several hypotheses that have been suggested as the cause of high haplotype diversities including the presence of cryptic species, the occurence of an isolating event followed by secondary contact or a high mitochondrial substitution rate (Chiari et al. 2009). The presence of a cryptic species is most likely to show itself on a haplotype network or phylogenetic tree as two sets of haplotypes that are more highly diverged (Chiari et al. 2009) and is more likely to correspond with fairly high nucleotide diversity between subsets of the data. Past demographic changes can be tested for using neutrality tests such as Fu's F_S or Tajima's D and by analysis of mismatch distributions. A negative result in a neutrality test is often an indication of a recent population expansion event (Fu 1997; Weber et al. 2004; Lancaster et al. 2010), but, can also be a sign of positive selection (Jobling et al. 2004; Zvuloni et al. 2008). A single large peak in mismatch distribution is also a sign of an expansion event and distance from the v axis is an indication of the time since such an event.

When viewed against pelagic fish species and terrestrial animals, the adults of shallow water coastal fish are often comparatively sessile. Dispersal during the planktonic larval stages can often be the primary mode of dispersal and a key factor in homogenising genetic diversity among populations. This could suggest that coastal species may have similar patterns of gene flow and diversity, particularly in closely related species (Dawson et al. 2002; Hickey et al. 2009).

Notolabrus celidotus and N. fucicola are closely related species that share a similar niche (Denny and Schiel 2002) and, thus, could be expected to have similar patterns of genetic dispersal and diversity. Both species are found throughout New Zealand in waters generally shallower than 15 metres deep (Paulin 1998; Denny 2005) and often in relation to temperate reef habitats (Denny and Schiel 2001) though have been recorded in most habitat types (Anderson and Millar 2004; Williams et al. 2008). However, while *N. celidotus* is not found around many offshore islands, including the Snares (Hardy 1986; Francis 1996) and Three Kings Islands (Hardy 1986; Choat and Ayling 1987; Francis 1996), N. fucicola is found on these islands and can be found in higher abundances in the absence of N. celidotus (Hardy 1986), which suggests competition could be an issue where populations co-occur. Competitive exclusion may also play a part in why N. fucicola is often found in areas of greater exposure to N. celidotus (Denny 2005) though access due to size may play a role in this as *N. fucicola* can reach lengths of 50cm (Paulin 1998) while the maximum length of N. celidotus is around 27cm (Paul and Moreland 1993). N. fucicola is also found in south-eastern Australia while N. celidotus is restricted to New Zealand (Russell 1988). As seen in the majority of labrid species, N. celidotus and N. fucicola are diurnal fish (Russell 1988) and will shelter at night often exuding a mucous like covering (Russell 1988) and sometimes burrowing themselves in the sand (Choat 1962). Both N. celidotus and N. fucicola have similar food preferences, eating a wide variety of small animals including bivalves and other molluses, crabs, shrimps and small fish (Jones 1984b; Paul and Moreland 1993; Denny and Schiel 2001). N. fucicola have also been found with quantities of kelp within their stomachs and are, thus, described as omnivorous (Parrott 1957) though algae may be indirectly consumed in obtaining other prey items (Denny and Schiel 2001). Spawning occurs in late winter and spring in both species (Jones 1980; Jones 1981; Denny and Schiel 2002). Males defend a territory during this time (Jones 1981; Paulin 1998; Denny and Schiel 2002) and may spawn with multiple females (Jones 1981) with eggs released into the water column (Russell 1988) to carry out a planktonic larval stage. Their similarities and matching spawning time has meant that hybridisation does sometimes occur, though rarely (Ayling 1980), creating fish with intermediate characters.

The aim of this chapter is to compare the control region DNA sequence variation of *Notolabrus celidotus* to that of *Notolabrus fucicola* collected from Wellington Harbour, and to other fish species reported in the literature from around the world. The results will be compared to the results reported in Chapter Two regarding population expansion and haplotype diversity in *N. celidotus*.

4.3 Materials and Methods

4.3.1 Sampling and collection

Tissue samples were collected from 94 individuals of *Notolabrus celidotus* and 61 individuals of *Notolabrus fucicola* from around Wellington Harbour. Most of these samples were collected with the use of a bait catcher net box and were fin clipped by taking a small (about 10mm²) section of the caudal fin allowing for the return of live fish to the sea. Fin clips were preserved in 70% ethanol until needed for DNA extraction.

4.3.2 DNA extraction and sequencing

Fin tissue used for DNA extraction was generated using a fin punch to acquire a circular section of tissue of around 1mm diameter. In some cases, a small piece of tissue of comparable size was also taken using a scalpel. Digestion was carried out by Proteinase K and SDS and followed by extraction using Phenol:Chloroform:Isoamyl (25:24:1) (Sambrook et al. 1989). PCR primers for the control region were designed using the complete mitochondrial DNA sequence of Pseudolabrus sieboldii from Genbank (Oh et al. 2008). The primers used were 5'-TAGAGCTGACAGCAAAGTCAGG-3' from the 12S rRNA and 5'-TYTAACTCCCACCCCTAACTCC-3' from tRNA-Pro. This allowed a 940bp fragment of DNA incorporating the control region to be amplified and sequenced. Four samples of N. celidotus and one sample of Notolabrus fucicola were sequenced. The sequences were aligned and used to design a pair of more accurate primers for the control region. The new primers were 5'-AATTAAGCTACGCGAGCAGTTG-3' from tRNA-Phe 5'and TYTAACTCCCACCCCTAACTCC-3' from tRNA-Pro. The polymerase chain reaction (PCR) was carried out in 15µL volumes containing buffer, 6µg bovine serum albumin (BSA), 800µM dNTPs (consisting of 200µM each of dATP, dTTP, dCTP and dGTP), 0.4µM each of forward and reverse primers, 1.5mM MgCl₂, double-distilled water (ddH₂O) and 0.6U DNA polymerase. Thermal cycling conditions were an initial denaturation of 30 seconds at 94°C followed by 40 cycles of denaturation for 30 seconds at 94°C, annealing for 45 seconds at 50°C and extension for 45 seconds at 72°C then a final extension stage for three minutes at 72°C. Amplified products were treated with ExoSAP-IT and then sequenced on an ABI3730 at the Massay University Genome Service in Palmerston North.

4.3.3 Statistical analysis

Chromatograms were edited using FinchTV Version 1.4.0 (Geospiza_Inc 2006) and sequences were aligned in MEGA 4.0 (Tamura et al. 2007). Due to the low numbers of insertions and deletions the sequences were easily aligned by eye. Nucleotide and haplotype diversities, mismatch distributions and Tajima D and Fu's F_s neutrality tests were calculated for both species by DnaSP (Librado and Rozas 2009). A neighbour-joining tree was created using Mega 4.0 (Tamura et al. 2007) to compare species expansion patterns.

4.4 Results

4.4.1 Variability within the mtDNA control region

Notolabrus celidotus

Sequences obtained from mitochondrial control region for 23 *Notolabrus celidotus* were between 709 and 788 base pairs long. The average sequence composition was 29.3% thymine, 17.3% cytosine, 27.4% adenine and 26.0% guanine. There were 59 variable sites (54 transitions and four transversions) of which 24 were parsimony informative. This resulted in 22 haplotypes with high haplotype diversity and low nucleotide diversity (see Table 4.1). Neutrality tests gave a Tajima D statistic of -1.9065 which was significant at the 5% level and a Fu's Fs statistic of -15.935.

N. fucicola

Sequences obtained from mitochondrial control region for 15 *N. fucicola* were between 514 and 788 base pairs long. The average sequence composition was 31.0% thymine,

Table 4.1. List of fish species distributions and haplotype (h) and nucleotide (π) diversities for the mitochondrial control region.

Class	Species	Sampled distribution	Full distribution	Locations	Sample size	Haplotypes	h	Ħ	Reference
Elasmobranchii	Carcharhinus limbatus	East Coast USA	Global tropical and subtropical	4	323	23	0.805	0.0021	Keeney et al., 2005
	Chacharhinus obscurus	Australia and Indonesia	Global	4	28	7	0.282-0.857	0.160-1.00	Ovenden et al., 2009
	Carcharhinus sorrah	Australia and Indonesia	Tropical Indo-West Pacific	7	49	12	0.25-0.782	0.067-0.535	Ovenden et al., 2009
	Negaprion acutidens	East Indo-West Pacific	Indo-West Pacific	5	58	4	0.280	0.0006	Schultz et al., 2008
	Negaprion brevirostris	Atlantic and East Pacific	Atlantic and East Pacific	4	80	÷	0.780	0.0059	Schultz et al., 2008
	Prionace glauca	Australia, Indonesia and central Pacific	Global	12	60	16	0.89-1.00	0.74-0.878	Ovenden et al., 2009
	Rhizoprionodon lalandii	Sao Paulo state, Brazil	West Atlantic - Panama to Argentina	ę	~94	16	0.824	0.0048	Mendonca et al., 2009
	Sphyma lewini	Australia and Indonesia	Global	8	47	80	0.5-0.738	0.204-1.00	Ovenden et al., 2009
	Sphyma lewini	Global	Global	15	271	24	0.800	0.0130	Duncan et al., 2006
	Galeorhinus galeus	Global	South and East Pacific and Atlantic	9	116	38	0.92	0.0071	Chabot and Allen, 2009
	Cetorhinus maximus	Global temperate	Global temperate	8	62	9	0.720	0.0013	Hoelzel et al., 2006
	Carcharias taurus	Global	Global except East Pacific	9	193	6	0.725	0.0040	Ahonen et al., 2009
	Carcharias faurus	Australia and South Africa	Global except East Pacific	12	61	5	0.00-0.717	0.00-0.0031	Stow et al., 2006
	Rhincodon typus	Global	Global tropical and warm temperate	9	69	44	0.970	0.0110	Castro et al., 2007
	Rhincodon typus	Gulf of California	Global tropical and warm temperate	ъ	36	14	0.900	0.0050	Ramirez-Macias et al., 2007
	Squatus mitsukuni	Hawaii	Tropical and temperate Pacific	9	112		0.541	0.0010	Daly-Engel et al., 2010
Actinoptergyii	Cololabis saira	North Pacific	North Pacific	5	141	18	0.418	0.1700	Chow et al., 2009
	Merluccius australis	Chile, Argentina and New Zealand	South Pacific and Southwest Atlantic	e	96	5-8	0.308-0.667	0.0012-0.0023	Machado-Schiaffino et al., 2009
	Mentuccius capensis	South Africa and Namibia	South Africa and Namibia	21	312	107	0.85-0.88	0.0053-0.006	Von der Heyden et al., 2007
	Merluccius paradoxus	South Africa and Namibia	South Africa and Namibia	22	333	8	0.44-0.57	0.0011-0.0015	Von der Heyden et al., 2007
	Merluccius paradoxus	South Africa and Namibia	South Africa and Namibia	5	1013	19	0.530	0.0014	Von der Heyden et al., 2010
	Lophius budegassa	Northeast Atlantic	Northeast Atlantic	7	134	39	0.788-0.964	0.007-0.01	Charrier et al., 2006
	Lophius piscatorius	Northeast Atlantic	Northeast Atlantic	16	382	56	0.598-0.954	0.006-0.009	Charrier et al., 2006
	Chelon haematocheilus	Japan, Korea and China	Japan, Korea and China	6	272	93	0.960	0.0187	Liu et al., 2007

Class	Species	Sampled distribution	Full distribution	Locations	Sample size	Haplotypes	Ч	Ħ	Reference
	Mugil cephalus	East and South China Seas	Global tropical and subtropical	7	126	105	0.933-1.00	0.005-0.147	Jamandre <i>et al.</i> , 2009
	Mugil cephalus	China	Global tropical and subtropical	7	117	77	0.974	0.1413	Liu <i>et al.</i> , 2009
	Naso vlamingii	Tropical Indo-Pacific	Tropical Indo-Pacific	8	113	113	1.000	0.1360	Klanten <i>et al.</i> , 2007
	Trachurus trachurus	Northeast Atlantic	Northeast Atlantic	6	359	143	0.950-0.974	0.0077-0.0093	Comesana et al., 2008
	Hyperoglyphe antarctica	Southeast Australia and New Zealand	Southern oceans	11	320	49	0.821-0.921	0.015-0.025	Robinson <i>et al.</i> , 2008
	Seriolella brama	Southeast Australia	Australia and New Zealand	5	138	84	0.929-0.967	0.017-0.021	Robinson et al., 2008
	Seriolella punctata	Southeast Australia	Southern oceans	З	~63		0.937-0.995	0.0240	Robinson et al., 2008
	Clinus cottoides	South Africa	South Africa	14	343	41	0.660	0.0026	Von der Heyden <i>et al.</i> , 2008
	Lepidocybium flavobrunneum	Atlantic and Pacific	Global tropical and temperate	7	225	145	0.982	0.0260	Brendtro et al., 2008
	Caffrogobius caffer	South Africa	South Africa	10	242	55	0.956	0.0100	Neethling et al., 2008
	Pomatoschistus marmoratus	Spain	Europe	5	196	11	0.942	0.0108	Vergara-Chen et al., 2010
	Kajikia audax	Pacific	Indo-Pacific	7	83	79	0.998	0.0440	McDowell and Graves, 2008
	Girella punctata	Japan	Hong Kong to Japan	6	249	88	0.805-0.968	0.0069-0.0102	Saito et al., 2008
	Girella punctata	Japan and South Korea	Tropical and subtropical West Pacific	12	128	50	0.910	0.0090	Umino <i>et al.</i> , 2009
	Larabicus quadrilineatus	North and East Red Sea	Red Sea and Gulf of Aden	5	237	16-32	0.8-0.95	0.38-0.82	Froukh and Kochzius, 2007
	Notolabrus celidotus	New Zealand	New Zealand	21	190	171	0.999	0.0101	This study
	Notolabrus celidotus	Wellington	New Zealand	-	23	22	0.996	0.0133	This study
	Notolabrus fucicola	Wellington	New Zealand and Southeast Australia	-	15	13	0.990	0.0113	This study
	Parargyrops edita	China	East Asia	unknown	27	26	0.997	0.0140	Xia <i>et al.</i> , 2007
	Scarus psittacus	Tropical Indo-Pacific	Tropical Indo-Pacific	12	164	11	0.83-0.99	0.52-0.88	Winters et al., 2010
	Latris lineata	Southern temperate	Southern temperate	6	104	96	0.997	0.0290	Tracey et al., 2007
	Lutjanus carponotatus	Great Barrier Reef, Australia	Indo-West Pacific	4	188	43	0.742	0.0110	Evan <i>et al.</i> , 2010
	Ocyurus chrysurus	Brazil	Tropical and subtropical West Atlantic	4	17	58	0.961	0.0185	Vasconcellos et al., 2008
	Pleuragramma antarcticum	Antarctica	Antarctica	9	256	110	0.896	0.0084	Zane et al., 2006

Table 4.1. continued

Tabl	le 4.1. continued								
Class	Species	Sampled distribution	Full distribution	Locations	Sample size	Haplotypes	ų	Ħ	Reference
	Centropyge acanthops	Kenya	Western Indian Ocean	-	9	9	1.000	0.0332	Bowen et al., 2006
	Centropyge argi	Caribbean	Caribbean	-	14	14	1.000	0.0199	Bowen <i>et al.</i> , 2006
	Centropyge aurantonotus	Brazil	Brazil and Southern Caribbean	-	17	17	1.000	0.0221	Bowen et al., 2006
	Centropyge resplendens	Ascension Island	Ascension Island	~	15	14	0.991	0.0160	Bowen et al., 2006
	Amphiprion ocellaris	Indo-Malay Archipelago	Indo-Malay Archipelago	25	421	385	1.000	0.0740	Timm and Kochzius, 2008
	Dascyllus albisella	Hawaiian Islands and Johnston Atoll	Hawaii and Johnston Atoll	11	102	55	0.939		Ramon et al., 2008
	Pomacentrus coelestis	Taiwan and Japan	Indo-Pacific	8	170	71	0.956	0.0100	Liu <i>et al.</i> , 2008
	Stegastes fasciolatus	Hawaiian Islands	Indo-Pacific	11	219	152	0.986		Ramon <i>et al.</i> , 2008
	Cynoscion acoupa	Brazil	West Atlantic: Panama to Argentina	Unknown	297	83	0.892	0.0029	Rodrigues et al., 2008
	Larimichthys polyactis	Yellow and northern East China Seas	Yellow and East China Seas	8	114	87	0.980	0.0150	Xiao et al., 2009
	Micropogonias furnieri	Uruguay and Northern Argentina	Central and Southwest Atlantic	3	87	36	0.455-0.986	0.0024-0.0078	Pereira <i>et al.</i> , 2009
	Nibea albiflora	East China	East China	ю	65	37	0.968	0.0081	Han <i>et al.</i> , 2008b
	Pennahia argentata	Northwest Pacific	Northwest Pacific	12	132	113	0.998	0.0260	Han <i>et al.</i> , 2008a
	Epinephelus akaara	China	South and East China Seas	7	87	47	0.72-1.00	0.006-0.017	Chen <i>et al.</i> , 2008
	Plectropomus maculatus	Great Barrier Reef, Australia	Indo-West Pacific	4	164	86	0.941	0.0140	Evans et al., 2010
	Acanthocybium solandri	East USA, Caribbean and Hawaii	Global tropical and warm temperate	7	231	208	0.999	0.0530	Garber et al., 2005
	Scomber scombrus	North Atlantic and adjacent seas	North Atlantic and adjacent seas	5	205	124	0.988	0.0290	Nesbo et al., 2010
	Scomberomorus niphonius	East China, Yellow and Bohai Seas	Northwest Pacific	8	134	112	0.996	0.0236	Shui <i>et al.</i> , 2009
	Thunnus thynnus	Gulf of Mexico, Mediterranean	North Atlantic and Mediterranean Sea	3	140	21-62	0.949-0.997	0.0120-0.0240	Carlsson <i>et al.</i> , 2007
	Thunnus obesus	Indian, East Atlantic and West Pacific	Cosmopolitan global	9	380	355	0.996-0.999	0.043-0.062	Chiang et al., 2008
	Thunnus obesus	Global	Cosmopolitan global	9	258	222	0.999	0.0540	Martinez <i>et al.</i> , 2006
	Acanthopagrus latus	China	Indo-West Pacific	80	169	111	0.884-0.995	0.013-0.026	Xia <i>et al.</i> , 2008
	Pagrus pagrus	Caribbean, Brazil and East Atlantic	Warm temperate Atlantic	6	371		0.968-0.998	0.0100-0.0140	Ball <i>et al.</i> , 2007
	Aphanopus carbo	North Atlantic	Temperate Atlantic	6	101	58	0.966	0.0106	Stefanni and Knutsen, 2007

Chapter Four: Genetic variation within two Notolabrus species

Table 4.1. continued

Class	Species	Sampled distribution	Full distribution	Locations	Sample size	Haplotypes	ų	Ħ	Reference
	Xiphias gladius	Indian, Pacific and Mediterranean	Global	16	175	142	0.997	0.0148	Lu et al., 2006
	Glyptocephalus stelleri	Japan	Japan and Eastern Russia	S	143	96	066.0	0.0140	Xiao et al., 2010
	Hippoglossus stenolepis	Alaska	North Pacific	9	95	18	0.8-0.8446	0.0064-0.0073	Nielsen et al., 2010
3	Hippocampus capensis	Southern South Africa	South Africa	11	138	15	0.46-0.84	0.0030-0.0046	Teske et al., 2003

16.7% cytosine, 28.2% adenine and 24.2% guanine. There were a total of 27 variable sites of which 11 were parsimony informative. There were 25 transitions and only two transversions. This variation resulted in 13 haplotypes and a similar pattern of haplotype and nucleotide diversities as seen in *N. celidotus* (see Table 4.1). Neutrality tests gave a non-significant Tajima's D statistic of -0.88692 and a Fu's Fs statistic of -5.561.

4.4.2 Haplotype and nucleotide diversity in control region of marine fish

Overall, most marine fish show high haplotype diversity with low nucleotide diversity (Table 4.1). Around 59% of fish species in this study show haplotype diversities greater than 0.9. However, only 19.7% and 17.1% of species had haplotype diversities greater or equal to those found in *N. fucicola* and *N. celidotus* respectively. Nearly 79% of studied species have a nucleotide diversity of 0.05 or less and around 44% of species had nucleotide diversities less than or equal to those of *N. fucicola* and *N. celidotus*.

4.4.3 Population structure

A neighbour joining tree showed the two species to be clearly defined (Fig 4.1). Both species showed little intra-specific resolution characterised by low bootstrap support. Mismatch distributions show that while both species have one major peak with one or two outlying minor peaks (Fig 4.2), *N. celidotus* has minor peaks with greater pairwise differences than the major peak while the minor peak for *N. fucicola* has less pairwise differences than the major peak. The raggedness statistics were 0.0132 for *N. celidotus* and 0.0441 for *N. fucicola* and show that *N. celidotus* has a much smoother curve while the *N. fucicola* shows a ragged mismatch distribution.



Fig 4.1. Neighbour joining (NJ) phylogenetic tree based on the mitochondrial DNA control region showing comparison of *Notolabrus celidotus* and *N.fucicola*. Green circles are *N. celidotus* and blue circles are *N.fucicola*.



Fig 4.2. Mismatch distributions for *Notolabrus celidotus* (above) and *Notolabrus fucicola* (below).

4.5 Discussion

4.5.1 Variability within the mtDNA control region

Both *Notolabrus celidotus* and *N. fucicola* show a pattern of high haplotype diversity paired with low nucleotide diversity within the mitochondrial control region. This

pattern is very common in the control region of marine fish worldwide (Table 4.1). Nucleotide diversity is a measure of the average differences between haplotypes and, thus, is only slightly affected by extreme haplotypes, while the haplotype diversity is greatly effected by rare haplotypes (Glenn et al. 1999). Therefore, while nucleotide diversity is often low within a species, haplotype diversity will be affected by population size changes as population growth (increasing rare haplotypes) will lead to a large haplotype diversity while population decline (loss of rare haplotypes) will result in low haplotype diversity. Subsequently high haplotype diversity with low nucleotide diversity is suggested to be the result of a low population size followed by a dramatic and sudden population expansion (Weber et al. 2004; Matthee et al. 2006). Many studies attribute these diversity patterns to recovery from ice ages and other climatic events (Grant and Bowen 1998; Hailer et al. 2007). Patterns are thought to vary with latitude so that higher latitudes, particularly temperate latitudes, show lower genetic diversity (Merila et al. 1997; Mila et al. 2000). The global distribution of this pattern in fish and the ability of fish populations to increase rapidly mean there is a chance that climatic cooling, which would reduce oceanic volume and habitat availability could have created bottlenecks for fish populations worldwide and subsequently, caused rapid population increase when the climate warmed. The Tajima's D statistic of N. celidotus is significant which could suggest positive selection (Jobling et al. 2004). However, this is unlikely as the control region of mtDNA is a neutral marker. Such a high negative statistic means that the N. celidotus population has a large number of singleton sites. This is also an indication of an expanding population but should be corroborated by a search for similar patterns at other loci which would indicate expansion (Jobling et al. 2004). However, due to the neutrality of the marker and the other data that point to population expansion it is safe to assume that this is the reasoning for the high Tajima's
D statistic. *N. fucicola* did not have significant statistics in the neutrality tests, however, the negative results still indicate an excess of low frequency variation which could signify population expansion.

4.5.2 Population structure

The raggedness statistics are 0.0132 for N. celidotus and 0.0441 for N. fucicola. A raggedness statistic of less than 0.03 is considered a smooth curve (Jobling et al. 2004). A smooth curve with one large peak is generally considered an expanding population. This is likely true for N. celidotus though the presence of the smaller peaks could potentially be the result of a separated population that has then been reunited before speciation could occur. However, without further information this cannot be verified. An extra peak may also be a result of the small sample sizes used in this study (Wu et al. 2006). N. fucicola shows a much higher raggedness statistic suggesting a more constant population. Both these population expansion theories are backed up by the neighbour joining tree which shows constricted branch length in earlier branches of N. celidotus but the branches leading to individuals are longer suggesting a recent large population expansion. Whereas the more consistent branch length of N. fucicola suggests that population size has remained more constant (Jobling et al. 2004). However, the large peak on the mismatch distribution of *N. fucicola* is contradictory to both the raggedness statistic and the phylogenetic tree as it would suggest a population expansion. It is likely a population expansion has or is effecting haplotypes in *N. fucicola* but possibly not to such a great extent as that being seen in *N. celidotus*.

Chapter Five: General Discussion

Phylogeography and phylogeny in New Zealand's coastal marine fish: Insights from *Notolabrus celidotus*

5.1 Phylogeography of New Zealand's coastal marine fish

Notolabrus celidotus showed no phylogeographic structure across its range. There was a large number of unique haplotypes. However, shared haplotypes showed no location affinity as some individuals were found to be sharing haplotypes with others caught as far apart as Auckland and Golden Bay, or Stewart Island and Napier. Statistical analysis of population structure all suggests that the current *N. celidotus* population has arisen from a small, potentially bottlenecked population and has expanded rapidly in the recent past (Jobling et al. 2004) (Chapter Two). Though a full phylogeography of *Notolabrus fucicola* was beyond the scope of this study, a similar pattern of high haplotype diversity and low nucleotide diversity (Chapter Four) and a shared haplotype from Wellington and Jackson Bay, suggests that this species may produce a similar homogeneous phylogeographic pattern.

There is little evidence to suggest the reasons behind a bottleneck in the *N. celidotus* population. One hypothesis is that the bottleneck occurred when *N. celidotus* first arrived in New Zealand. However, as *N. celidotus* is a New Zealand endemic it is most parsimonious to assume that *N. celidotus* speciated after reaching New Zealand rather than that it originally occurred in Australia before spreading to New Zealand and then

subsequently becoming extinct in Australia. If the former is the true dispersal of *N*. *celidotus* then it is unlikely that dispersal to New Zealand is the source of the bottleneck.

Another potential hypothesis for the source of a potential bottleneck within *N. celidotus* and potentially other New Zealand labrids is that a period of global atmospheric cooling, such as the last glacial maximum of around 20000 years ago, increased the land area of New Zealand (Fleming 1962) and, thus, reduced gene flow between increasingly distant coastal marine regions. Atmospheric cooling is also likely to have had major affects on the recruitment of New Zealand labrids. Recruitment of N. celidotus has been associated with the presence of *Ecklonia radiata* (Jones 1984a) a brown algae growing in temperate regions including New Zealand (Wernberg et al. 2003). Once N. celidotus juveniles have recruited to an area their growth and subsequent maturation is density dependent (Jones 1984b). Growth of E. radiata is known to be temperature dependent (Novaczek 1984), therefore, cool sea surface temperatures in the last glacial maximum, which may have been as much as 8°C lower than they are today around New Zealand (Barrows and Juggins 2005), could have reduced growth, abundance and the southern distribution of E. radiata which would, subsequently, affect the numbers of N. celidotus juveniles reaching maturity. This pattern may be present in temperate labrids and other coastal New Zealand fish species as many of these fish exhibit associations with algal stands (Jones 1992) and other organic habitats.

Ultimately, a comparative phylogeographic study of multiple New Zealand marine species is needed to fully understand the biogeographic patterns which appear in this study. This would allow us greater understanding, particularly of climatic and geological events, as these large scale processes are likely to have affects on many codistributed species at once and should, therefore, result in similar patterns within the genetic structure of these organisms (Bermingham and Avise 1986).

5.2 Phylogeny

Just as morphological features such as colour and pattern were found to be not fully indicative of a species one hundred and fifty years ago (Choat 1965), this study shows that morphology is not able to fully describe tribe relations within the pseudolabrines (Chapter Three).

The close relationship between some, or all, of the mainland New Zealand *Notolabrus* and *Pseudolabrus* species would suggest that New Zealand species may have migrated before speciation occurred. However, *N. fucicola* is also found in southeast Australia and could be the sister species to the other *Notolabrines* and *P. miles* and *P. biserialis* which would suggest either a re-colonisation back to Australia or that currents from southeast Australia facilitated multiple introductions to New Zealand and a similarity in habitat also allowed species survival. Currents between New Zealand and Australia move in an easterly direction from the coast of Australia to Northern New Zealand. The direction of currents and the long planktonic larval duration of *N. celidotus*, estimated from spawning times and settlement dates to be as long as five months and likely to be of similar length in other pseudolabrine species, would facilitate multiple introductions of pseudolabrines to New Zealand from Australia.

As in *N. fucicola,* the presence of *N. inscriptus* in Australia and the prevailing easterly direction of current systems mean it is likely that *N. inscriptus* evolved on the east coast of Australia and then spread to Norfolk Island and further east to the Kermadec Islands.

In order to understand the processes affecting population structure and gene flow it is necessary to analyse multiple organisms in search of common patterns (Hickey et al. 2009). Organismal relations are important to this end as only with a full understanding of the phylogeny and relationships between species can we make informed conclusions about species biology with regards to other species. Once we know the relationships between species, we are able to use this knowledge to make hypotheses against which we can test phylogeography of related or co-occurring species.

5.3 Future directions

This thesis will hopefully be just one step on the path to a much greater understanding of phylogeography in New Zealand's coastal marine fish populations. Though these species are rarely of any importance to commercial fisheries, many coastal marine fish play integral roles in the coastal ecosystem. A thorough study of population structure within a much greater range of these species can give us a better idea of the population dynamics and gene flow within New Zealand's marine ecosystem both for use in fisheries and in cementing New Zealand's place as a centre of biodiversity and scientific study.

Incorporation of the few missing pseudolabrines to complete a full phylogeny of the tribe would allow us to understand divergence and may reveal further details in this phylogeny. The missing species now only include two from New Zealand, *Notolabrus cinctus*, which lives at depths and, unfortunately, samples could not be found for this study and *Pseudolabrus luculentus* which is rare on the mainland and only common at the Kermadec Islands and New Zealand's other northern offshore islands. Globally,

samples of *Pseudolabrus psittaculus* from Australia, *P. torotai* from Rapa Island in French Polynesia and *P. semifasciatus* from Easter Island as well as *P. luculentus* and a larger sample from *P. gayi* are still needed. *N. cinctus* is now the only *Notolabrus* species missing from the phylogeny. A full phylogeny would also require the addition of the two species of *Dotolabrus* and the final two species of *Pictilabrus*. Furthermore, a phylogeography of *N. fucicola* with samples from both Australia and New Zealand may help to clear up the question of how this species came to be in both countries and whether gene flow still occurs across the Tasman Sea, or if, possibly, the Australian fish are actually cryptic species.

Finally, the addition of more *N. celidotus* samples to its phylogeography and the incorporation of multiple loci will hopefully give greater weight to conclusions found here and allow for more accurate statistical testing and effective population size calculations. This could include sampling enough *N. celidotus* to cover the majority of existing haplotypes and increasing the coverage of *N. celidotus* sampling distribution. A study into the presence of *N. celidotus* on the Chatham Islands would also be useful to this end as the species is rare on offshore islands and is believed to have reached the Chatham Islands in recent times, possibly even in the last 50 years (Andrew Stewart, personal correspondence). Recently, microsatellite markers have been developed for *N. celidotus* which will help to test and, hopefully, verify the findings within this thesis.

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Appendix

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
RAN01	Rangaunu	Northeastern	Notolabrus celidotus		NIWA collection	Yes
RAN02	Rangaunu	Northeastern	Notolabrus celidotus Notolabrus		NIWA collection	No
RAN03	Rangaunu	Northeastern	celidotus Notolabrus		NIWA collection	Yes
RAN04	Rangaunu	Northeastern	celidotus Notolabrus		NIWA collection	Yes
RAN05	Rangaunu	Northeastern	celidotus Notolabrus		NIWA collection Alejandro Perez-	No
WHA01	Whangarei	Northeastern	celidotus		Matus	Yes
MOK01	Mokohinau Island	Northeastern	Notolabrus celidotus	23/10/2008	NIWA collection	Yes
MOK02	Mokohinau Island	Northeastern	Notolabrus celidotus	23/10/2008	NIWA collection	Yes
MOK03	Mokohinau Island	Northeastern	Notolabrus celidotus	23/10/2008	NIWA collection	Yes
MOK04	Mokohinau Island	Northeastern	Notolabrus celidotus	23/10/2008	NIWA collection	Yes
MOK05	Mokohinau Island	Northeastern	Notolabrus celidotus	23/10/2008	NIWA collection	Yes
MOK06	Mokohinau Island	Northeastern	Notolabrus celidotus	23/10/2008	NIWA collection	Yes
MOK07	Mokohinau Island	Northeastern	Notolabrus celidotus	23/10/2008	NIWA collection	Yes
MOK08	Mokohinau Island	Northeastern	Notolabrus celidotus	23/10/2008	NIWA collection	Yes
MOK09	Mokohinau Island	Northeastern	Notolabrus celidotus	21/10/2008	NIWA collection	Yes
MOK10	Mokohinau Island	Northeastern	Notolabrus celidotus	22/10/2008	NIWA collection	No
MOK11	Mokohinau Island	Northeastern	Notolabrus celidotus	22/10/2008	NIWA collection	Yes
GBI02	Great Barrier Island	Northeastern	Notolabrus celidotus	10/03/2008	NIWA collection	Yes
GBI03	Great Barrier Island	Northeastern	Notolabrus celidotus	10/03/2008	NIWA collection	No
GBI04	Great Barrier Island	Northeastern	Notolabrus celidotus	10/03/2008	NIWA collection	Yes
GB105	Great Barrier Island	Northeastern	Notolabrus celidotus	10/03/2008	NIWA collection	No
GB106	Great Barrier Island	Northeastern	Notolabrus celidotus	10/03/2008	NIWA collection	No
GBI07	Great Barrier Island	Northeastern	Notolabrus celidotus Notolabrus	12/03/2008	NIWA collection	Yes
LEI01	Leigh	Northeastern	celidotus Notolabrus	11/02/2008	NIWA collection	Yes
LEI02	Leigh	Northeastern	celidotus Notolabrus		Matus Aleiandro Perez-	Yes
LEI03	Leigh	Northeastern	celidotus		Matus	Yes

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
LEI04	Leigh	Northeastern	Notolabrus celidotus		Alejandro Perez- Matus	Yes
LEI05	Leigh	Northeastern	Notolabrus celidotus		Alejandro Perez- Matus	Yes
KAI01	Kaipara Harbour	Raglan	Notolabrus celidotus		NIWA collection	Yes
KAI02	Kaipara Harbour	Raglan	celidotus		NIWA collection	Yes
KAI03	Kaipara Harbour	Raglan	celidotus		NIWA collection	Yes
KAI04	Kaipara Harbour	Raglan	celidotus		NIWA collection	Yes
KAI05	Kaipara Harbour	Raglan	celidotus		NIWA collection	Yes
TAW01	Tawharanui	Northeastern	celidotus	12/02/2008	NIWA collection	No
KAW01	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
KAW02	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
KAW03	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
KAW04	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
KAW05	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
KAW06	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	No
KAW07	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
KAW08	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
KAW09	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
KAW10	Kawau Island	Northeastern	celidotus	22/02/2007	NIWA collection	Yes
TIRI01	Tiritiri Matangi Island	Northeastern	Notolabrus celidotus	26/09/2008	NIWA collection	Yes
TIRI02	Tiritiri Matangi Island	Northeastern	Notolabrus celidotus	26/09/2008	NIWA collection	No
TIRI03	Tiritiri Matangi Island	Northeastern	Notolabrus celidotus	26/09/2008	NIWA collection	Yes
TIRI04	Tiritiri Matangi Island	Northeastern	Notolabrus celidotus	25/09/2008	NIWA collection	No
TIRI05	Tiritiri Matangi Island	Northeastern	Notolabrus celidotus	26/09/2008	NIWA collection	No
TIRI06	Tiritiri Matangi Island	Northeastern	Notolabrus celidotus Notolabrus	25/09/2008	NIWA collection	No
TOR01	Torbay	Northeastern	celidotus Notolabrus	25/09/2008	NIWA collection	No
TOR02	Torbay	Northeastern	celidotus	25/09/2008	NIWA collection	No
TOR03	Torbay	Northeastern	celidotus Notolabrus	25/09/2008	NIWA collection	No
TOR04	Torbay	Northeastern	celidotus Notolabrus	25/09/2008	NIWA collection	No
TOR05	Torbay	Northeastern	celidotus Notolabrus	25/09/2008	NIWA collection	Yes
TOR06	Torbay	Northeastern	celidotus Notolabrus	25/09/2008	NIWA collection	Yes
TOR07	Torbay	Northeastern	celidotus	25/09/2008	NIWA collection	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
TOR08	Torbay	Northeastern	Notolabrus celidotus	25/09/2008	NIWA collection	No
TOR09	Torbay	Northeastern	Notolabrus celidotus	25/09/2008	NIWA collection	No
TOR10	Torbay	Northeastern	Notolabrus celidotus	25/09/2008	NIWA collection	Yes
LNG01	Long Bay	Northeastern	celidotus	24/09/2008	NIWA collection	Yes
WCP01	Whangapoua Harbour, Coromandal Whangapoua	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP02	Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP03	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP04	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP05	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP06	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP07	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP08	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP09	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP10	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP11	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP12	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP13	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP14	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
WCP15	Whangapoua Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
	Whangapoua Harbour,		Notolabrus			
WCP16	Coromandal	Northeastern	celidotus		NIWA collection	No
	Harbour,		Notolabrus			
WCP17	Coromandal	Northeastern	celidotus		NIWA collection	No
	Whangapoua					
WCP18	Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
	Whangapoua					
	Harbour,	Nextbooks	Notolabrus			Nia
WCP19	Whangapoua	Northeastern	cellaotus		NIVVA collection	INO
	Harbour,	Northoastorn	Notolabrus		NII\A/A collection	No
WCF20	Coromanual	Nonneastern	Cendolus		NIWA COllection	NU
	Whangapoua Harbour		Notolabrus			
WCP21	Coromandal	Northeastern	celidotus		NIWA collection	No
	Whangapoua					
	Harbour,		Notolabrus			
WCP22	Coromandal	Northeastern	celidotus		NIWA collection	No
	Whangapoua					
WCP23	Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
	vvhangapoua Harbour,		Notolabrus			
WCP24	Coromandal	Northeastern	celidotus		NIWA collection	No
	Whangapoua					
WCD25	Harbour,	Northoastorn	Notolabrus		NIIWA collection	No
WGF 25	Coromanual	Nonneastern	cendolus		NIWA COllection	NO
	Whangapoua Harbour		Notolabrus			
WCP26	Coromandal	Northeastern	celidotus		NIWA collection	No
	Whangapoua					
	Harbour,		Notolabrus			
WCP27	Coromandal	Northeastern	celidotus		NIWA collection	No
	Whangapoua					
WCP28	Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIWA collection	No
	Harbour,		Notolabrus			
WCP29	Coromandal	Northeastern	celidotus		NIWA collection	No
	Whangapoua					
	Harbour, Coromandal	Northeastern	Notolabrus celidotus		NIIWA collection	No
	Coromanda	Nonneastern	cendolus		NIWA Collection	NO
	Whangapoua Harbour		Notolabrus			
WCP31	Coromandal	Northeastern	celidotus		NIWA collection	No
	Whangapoua					
MODAC	Harbour,	Northeastern	Notolabrus			Ne
WCP32	Coromandal	Northeastern	ceildotus Notolabrus		INIVVA COLLECTION	INO
KAWH01	Kawhia Harbour	Raglan	celidotus Notolabrus	2/05/2009	Surrey Scott	Yes
KAWH02	Kawhia Harbour	Raglan	celidotus	2/05/2009	Surrey Scott	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
•		1	1	•	•	<u> </u>
KAWH03	Kawhia Harbour	Raglan	Notolabrus celidotus Notolabrus	2/05/2009	Surrey Scott	Yes
NPM01	New Plymouth	Raglan	celidotus Notolabrus	3/05/2009	Surrey Scott	No
NPM02	New Plymouth	Raglan	celidotus	3/05/2009	Surrey Scott	No
NAP01	Napier	Portland	celidotus	23/03/2009	Surrey Scott	Yes
NAP02	Napier	Portland	celidotus Notolabrus	23/03/2009	Surrey Scott	Yes
NAP04	Napier	Portland	celidotus Notolabrus	23/03/2009	Surrey Scott	Yes
NAP06	Napier	Portland	celidotus Notolabrus	23/03/2009	Surrey Scott	Yes
NAP07	Napier	Portland	celidotus Notolabrus	23/03/2009	Surrey Scott	Yes
NAP08	Napier	Portland	celidotus Notolabrus	23/03/2009	Surrey Scott	Yes
NAP09	Napier	Portland	celidotus	23/03/2009	Surrey Scott	Yes
NAP10	Napier	Portland	celidotus	23/03/2009	Surrey Scott	Yes
NAP11	Napier	Portland	celidotus	23/03/2009	Surrey Scott	Yes
NAP12	Napier	Portland	celidotus	23/03/2009	Surrey Scott	No
NAP13	Napier	Portland	celidotus	23/03/2009	Surrey Scott	Yes
NAP14	Napier	Portland	celidotus	23/03/2009	Surrey Scott	No
NAP15	Napier	Portland	celidotus	23/03/2009	Surrey Scott	Yes
NAP16	Napier	Portland	celidotus	23/03/2009	Surrey Scott	Yes
NAP17	Napier	Portland	celidotus	23/03/2009	Surrey Scott	Yes
NAP18	Napier	Portland	celidotus	23/03/2009	Surrey Scott	No
NAP19	Napier	Portland	celidotus	23/03/2009	Surrey Scott	No
	Pauatahanui	Abol	Notolabrus	2008 0	Bronton Hodgson	Vos
FAUUT	Dauatabanui	Abei	Notolobrus	2000-9	Brenton nougson	165
PAU02	Inlet	Abel	celidotus	2008-9	Brenton Hodgson	Yes
	Pauatahanui	Abel	Notolabrus	1/07/2009	Surrey Scott	No
FA005	Dauatabanui	Abei	Notolobrus	1/0//2009	Surrey Scott	NO
PAU04	Inlet	Abel	celidotus	1/07/2009	Surrey Scott	Yes
PAU05	Pauatahanui Inlet	Abel	Notolabrus celidotus	1/07/2009	Surrey Scott	No
PAU06	Pauatahanui Inlet	Abel	Notolabrus celidotus	1/07/2009	Surrey Scott	Yes
PAU07	Pauatahanui Inlet	Abel	Notolabrus celidotus	1/07/2009	Surrey Scott	Yes
PAU08	Pauatahanui Inlet	Abel	Notolabrus celidotus	1/07/2009	Surrey Scott	Yes
WLG01	Wellington Harbour	Cook	Notolabrus celidotus	28/06/2008	Surrey Scott	No
WLG02	Wellington Harbour	Cook	Notolabrus celidotus	28/06/2008	Surrey Scott	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
WLG03	Wellington Harbour	Cook	Notolabrus celidotus	9/07/2008	Surrey Scott	Yes
WLG04	Wellington Harbour	Cook	Notolabrus celidotus	9/07/2008	Surrey Scott	No
WLG05	Wellington Harbour	Cook	Notolabrus celidotus	9/07/2008	Surrey Scott	Yes
WLG06	Wellington Harbour	Cook	Notolabrus celidotus	9/07/2008	Surrey Scott	No
WLG07	Wellington Harbour	Cook	Notolabrus celidotus	9/07/2008	Surrey Scott	Yes
WLG08	Wellington Harbour	Cook	Notolabrus celidotus	28/08/2008	Alejandro Perez- Matus & Surrey Scott	No
WLG09	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG10	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG11	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG12	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	Yes
WLG13	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	Yes
WLG15	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG16	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	Yes
WLG18	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	Yes
WLG19	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	Yes
WLG20	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG21	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG22	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG23	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG24	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG25	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG26	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG27	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
WLG28	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	Yes
WLG29	Wellington Harbour	Cook	Notolabrus celidotus	2008-9	Alejandro Perez- Matus	No
WLG30	Wellington Harbour	Cook	Notolabrus celidotus	18/04/2009	Surrey Scott	No
WLG31	Wellington Harbour	Cook	Notolabrus celidotus	18/04/2009	Surrey Scott	No
WLG32	Wellington Harbour	Cook	Notolabrus celidotus	18/04/2009	Surrey Scott	No
WLG33	Wellington Harbour	Cook	Notolabrus celidotus	18/04/2009	Surrey Scott	No
WLG34	Wellington Harbour	Cook	Notolabrus celidotus	18/04/2009	Surrey Scott	No
WLG35	Wellington Harbour	Cook	Notolabrus celidotus	18/04/2009	Surrey Scott	No
WLG36	Wellington Harbour	Cook	Notolabrus celidotus	18/04/2009	Surrey Scott	No
WLG37	Wellington Harbour	Cook	Notolabrus celidotus	18/04/2009	Surrey Scott	No
WLG38	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG40	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG41	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG42	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG43	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG44	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG45	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG52	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG54	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG56	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG59	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
WLG60	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
WLG61	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
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WLG64	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
WLG67	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
WLG68	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
WLG69	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
WLG70	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
WLG71	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	Yes
WLG73	Wellington Harbour	Cook	Notolabrus celidotus	20/01/2009	Alejandro Perez- Matus	No
WLG75	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG76	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG77	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG78	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG79	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG80	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG81	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG82	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG83	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG84	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG85	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG86	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG87	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG88	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG89	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG90	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
WLG91	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG92	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG93	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG94	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG95	Wellington Harbour	Cook	Notolabrus celidotus	23/02/2009	Alejandro Perez- Matus	No
WLG125	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG126	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG127	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG128	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG129	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG130	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG131	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG132	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG133	Wellington Harbour Wellington	Cook	Notolabrus celidotus Notolabrus	2/06/2009	Alejandro Perez- Matus Alejandro Perez-	No
WLG134	Harbour	Cook	celidotus	2/06/2009	Matus	No
WLG135	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG136	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG137	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG138	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG139	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG140	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	No
WLG141	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus	Yes
WLG142	Wellington Harbour	Cook	Notolabrus celidotus	2/06/2009	Alejandro Perez- Matus Alejandro Perez-	Yes
DUI01	D'Urville Island	Abel	Notolabrus celidotus	25/02/2009	Matus & Sebastian Hernandez	No

Sample ID	Location	Population	Species	Date	Samplers	Used in this study?
<u>eample ib</u>	Loodion	ropulation	opooloo	Gampieu	Alejandro Perez-	otady.
			Notolabrus		Matus & Sebastian	
DUI02	D'Urville Island	Abel	celidotus	25/02/2009	Hernandez	No
			Natalahrua		Alejandro Perez-	
	D'I Irville Island	Abel	relidotus	25/02/2009	Matus & Sebastian Hernandez	No
DOI00	D OI VIIIC ISIAIIU	Abei	cendolus	20/02/2000	Aleiandro Perez-	NO
			Notolabrus		Matus & Sebastian	
DUI04	D'Urville Island	Abel	celidotus	25/02/2009	Hernandez	No
DIOOA	D: (Notolabrus	04/00/0000	0 0 "	
PIC01	Picton	Abel	Celidotus	21/02/2009	Surrey Scott	NO
PIC02	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
			Notolabrus			
PIC03	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
			Notolabrus			
PIC04	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
	Dicton	Abol	Notolabrus	21/02/2000	Surroy Scott	No
FICUS	FIGION	Abei	Notolabrus	21/02/2009	Surrey Scoll	INO
PIC06	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
			Notolabrus		5	
PIC07	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
DIOOO	Distan	A I I	Notolabrus	04/00/0000	0	NI-
PIC08	Picton	Abei	Cellaotus	21/02/2009	Surrey Scott	NO
PIC09	Picton	Abel	celidotus	21/02/2009	Surrey Scott	Yes
			Notolabrus			
PIC10	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
			Notolabrus			
PIC11	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
	Picton	Abel	NOTOIADIUS	21/02/2000	Surrey Scott	Ves
11012	1 101011	Abei	Notolabrus	21/02/2003	ouncy ocon	103
PIC13	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
			Notolabrus			
PIC14	Picton	Abel	celidotus	21/02/2009	Surrey Scott	Yes
DIC15	Dictor	Abol	Notolabrus	21/02/2000	Surroy Scott	No
FICIS	FIGION	Abei	Notolabrus	21/02/2009	Surrey Scoll	INO
PIC16	Picton	Abel	celidotus	21/02/2009	Surrey Scott	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC17	Picton	Abel	celidotus	26/02/2009	Hernandez	No
			Notolabrus		Matus & Sebastian	
PIC18	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC19	Picton	Abel	celidotus	26/02/2009	Hernandez	Yes
			Notolabrus		Matus & Sebastian	
PIC20	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC21	Picton	Abel	celidotus	26/02/2009	Hernandez	Yes
			Notolabrus		Alejandro Perez- Matus & Sebastian	
PIC22	Picton	Abel	celidotus	26/02/2009	Hernandez	Yes
					Alejandro Perez-	
DIGGO	D . <i>i</i>		Notolabrus		Matus & Sebastian	
PIC23	Picton	Abel	celidotus	26/02/2009	Hernandez	Yes
			Notolahrus		Alejandro Perez- Matus & Sebastian	
PIC24	Picton	Abel	celidotus	26/02/2009	Hernandez	Yes
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC25	Picton	Abel	celidotus	26/02/2009	Hernandez	No
			Notolahrus		Alejanuro Perez- Matus & Sebestian	
PIC26	Picton	Abel	celidotus	26/02/2009	Hernandez	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
					Aleiandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC27	Picton	Ahel	celidotus	26/02/2009	Hernandez	Yes
11021		71001	00//40/40	20/02/2000	Aleiandro Perez-	100
			Notolabrus		Matus & Sebastian	
PIC28	Picton	۵hel	celidatus	26/02/2009	Hernandez	Ves
11020		Abei	centolius	20/02/2003	Aleiandro Perez-	103
			Notolabrus		Matus & Sobastian	
DIC 20	Dictor	Abol	nolidatus	26/02/2000	Hornondoz	No
PIC29	PICION	Abei	cendolus	20/02/2009		INO
			Matalahuus		Alejandro Perez-	
DICOO	Distan	Abal	NOLOIADIUS	00/00/0000		Nia
PIC30	Picton	Abei	cellaotus	26/02/2009	Aleiandre Derez	INO
			Matalahrua		Alejanulo Perez-	
DIGO	Distan	Abal	NOLOIADIUS	00/00/0000		Nia
PIC31	Picton	Abei	cellaotus	26/02/2009	Hernandez	INO
					Alejandro Perez-	
DIGGO	D: /		Notolabrus	00/00/0000	Matus & Sebastian	
PIC32	Picton	Abel	celidotus	26/02/2009	Hernandez	NO
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC33	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC34	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC35	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC36	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Aleiandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC37	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Aleiandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC38	Picton	Abel	celidotus	26/02/2009	Hernandez	No
		,			Aleiandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC39	Picton	Abel	celidotus	26/02/2009	Hernandez	No
11000		7.60	00//40/40	20,02,2000	Aleiandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC40	Picton	Ahel	celidotus	26/02/2009	Hernandez	No
11040		71001	00//40/40	20/02/2000	Aleiandro Perez-	110
			Notolabrus		Matus & Sebastian	
PIC41	Picton	۵hel	celidatus	26/02/2009	Hernandez	No
11041		71001	00//40/40	20/02/2000	Aleiandro Perez-	110
			Notolabrus		Matus & Sebastian	
PIC42	Picton	Abol	celidatus	26/02/2000	Hernandez	No
11042	T ICION	Abei	Centolus	20/02/2003	Aloiandro Poroz	NO
			Notolabrus		Matus & Sobastian	
	Dictor	Abol	nolidatus	26/02/2000	Hornondoz	No
FIC43	FICION	Abei	cendolus	20/02/2009	Aloiondro Doroz	INU
			Notolohrup		Matua & Sabastian	
	Distan	Abal	NOLOIADIUS	00/00/0000		Nia
PIC44	Picton	Abei	cellaotus	26/02/2009	Aleiandre Derez	INO
					Alejandro Perez-	
DIA / -	5. /		Notolabrus		Matus & Sebastian	
PIC45	Picton	Abel	celidotus	26/02/2009	Hernandez	NO
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC46	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC47	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC48	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC49	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC50	Picton	Abel	celidotus	26/02/2009	Hernandez	No

			a i	Date		Used in this
Sample IL	Location	Population	Species	sampled	Samplers	study?
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC51	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC52	Picton	Abel	celidotus	26/02/2009	Hernandez	Yes
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC53	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC54	Picton	Abel	celidotus	26/02/2009	Hernandez	Yes
					Aleiandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC55	Picton	Abel	celidotus	26/02/2009	Hernandez	Yes
11000		7.001	condotad	20,02,2000	Aleiandro Perez-	100
			Notolahrus		Matus & Sebastian	
DICES	Dictor	Abol	nolidatus	26/02/2000	Hornondoz	Voo
FIC50	FICIUII	Abei	cenuolus	20/02/2009	Aloiondro Doroz	res
			Matalahuun		Alejandro Perez-	
DI057			Notolabrus	00/00/0000	Matus & Sebastian	
PIC57	Picton	Abei	cellaotus	26/02/2009	Hernandez	Yes
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
PIC58	Picton	Abel	celidotus	26/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP01	Bay	Abel	celidotus	14/02/2009	Hernandez	No
	2				Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP02	Bay	Abel	celidotus	14/02/2009	Hernandez	No
	,				Aleiandro Perez-	
	Manua Tasman		Notolabrus		Matus & Sebastian	
MADO3	Bay	Abol	celidatus	11/02/2000	Hernandez	No
	Bay	Abei	Centolius	14/02/2003	Aloiandro Poroz	NO
	Manua Taaman		Natalahrua		Alejanulo Felez-	
	Mapua, Tasman	Abal	NOLOIADIUS	15/00/0000		Nia
MAP04	вау	Abei	cellaotus	15/02/2009	Hernandez	INO
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus	. =	Matus & Sebastian	
MAP05	Вау	Abel	celidotus	15/02/2009	Hernandez	Yes
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP06	Bay	Abel	celidotus	15/02/2009	Hernandez	Yes
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP07	Bay	Abel	celidotus	15/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP08	Bay	Abel	celidotus	15/02/2009	Hernandez	Yes
	2				Aleiandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP09	Bay	Abel	celidotus	15/02/2009	Hernandez	No
	20)	1.001			Aleiandro Perez-	
	Manua Tasman		Notolabrus		Matus & Sebastian	
MAP10	Bay	۵bel	celidotus	15/02/2009	Hernandez	Ves
	Bay	Abei	Centolius	15/02/2003	Aloiandro Poroz	163
	Manua Taaman		Natalahrua		Mature & Schootion	
	Napua, Tasman	Abol	NOLOIADIUS	15/02/2000	Malus & Sebasilan	No
MAPTI	вау	Abei	cellaotus	15/02/2009	Hernandez	INO
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP12	вау	Abel	celidotus	15/02/2009	Hernandez	NO
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP13	Bay	Abel	celidotus	15/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP14	Bay	Abel	celidotus	15/02/2009	Hernandez	No
	-				Alejandro Perez-	
	Mapua. Tasman		Notolabrus		Matus & Sebastian	
MAP15	Bay	Abel	celidotus	15/02/2009	Hernandez	No
	2		· · · · · · ·		Aleiandro Perez-	-
	Mapua Tasman		Notolabrus		Matus & Sebastian	
MAP16	Bay	Abel	celidotus	15/02/2009	Hernandez	No
	<u> </u>		00//00/00			

Querra la ID	l ti	Develotion		Date	Querralizat	Used in this
Sample ID	Location	Population	Species	sampled	Samplers	study?
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP17	Bay	Abel	celidotus	15/02/2009	Hernandez	Yes
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP18	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP19	Bay	Abel	celidotus	16/02/2009	Hernandez	No
	•				Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP20	Bav	Abel	celidotus	16/02/2009	Hernandez	No
					Aleiandro Perez-	
	Mapua Tasman		Notolabrus		Matus & Sebastian	
MAP21	Ray	Abel	celidotus	16/02/2009	Hernandez	No
	Day	Abei	cenaolas	10/02/2003	Aloiandro Doroz	
	Monuo Toomon		Notolohruo		Mature & Schootion	
	Napua, Tasiliali	Abal	NOLOIADIUS	40/00/0000		Nia
MAP22	вау	Abei	cellaotus	16/02/2009	Hernandez	NO
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP23	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP24	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Aleiandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP25	Bay	Abel	celidotus	16/02/2009	Hernandez	No
107 (1 20	Duy	7,001	00//00/00	10/02/2000	Aleiandro Perez-	
	Manua Tasman		Notolabrus		Matus & Sebastian	
MAD26	Boy	Abol	celidatus	16/02/2000	Hornandoz	Voc
MAFZO	Ddy	Abei	cenuolus	10/02/2009		res
	M				Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP27	Вау	Abel	celidotus	16/02/2009	Hernandez	Yes
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP28	Bay	Abel	celidotus	16/02/2009	Hernandez	Yes
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP29	Bay	Abel	celidotus	16/02/2009	Hernandez	Yes
					Aleiandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP30	Bay	Abel	celidotus	16/02/2009	Hernandez	Yes
111/1 00	Day	71001	oonaotao	10,02,2000	Aleiandro Perez-	100
	Manua Tasman		Notolahrus		Matus & Sebastian	
MAD31	Rov	Abol	celidatus	16/02/2000	Hernandez	No
	Day	Abei	cendolas	10/02/2003	Aloiandro Poroz	NO
	Manua Taaman		Notolohruo		Motuo 8 Sobostion	
	Napua, Tasiliali	Abal	NOLOIADIUS	40/00/0000		Nia
MAP32	вау	Abei	cellaotus	16/02/2009	Hernandez	NO
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP33	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP34	Bay	Abel	celidotus	16/02/2009	Hernandez	Yes
	-				Alejandro Perez-	
	Mapua. Tasman		Notolabrus		Matus & Sebastian	
MAP35	Bay	Abel	celidotus	16/02/2009	Hernandez	Yes
					Aleiandro Perez-	
	Manua Tasman		Notolabrus		Matus & Sebastian	
MAP36	Ray	Abel	celidotus	16/02/2009	Hernandez	No
	Day		condotas	10/02/2009	Alejandro Doroz	
	Manua Toomon		Notolobruo		Matus & Sobootion	
	Pov	Abel	adidatus	16/00/0000	Hornordoz	Vaa
WAP3/	Бау	Abei	cendotus	10/02/2009		res
	·· -				Alejandro Perez-	
	Mapua, Tasman		Notolabrus		iviatus & Sebastian	
MAP38	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP39	Bay	Abel	celidotus	16/02/2009	Hernandez	No
	-				Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP40	Bav	Abel	celidotus	16/02/2009	Hernandez	No
			001100100			

Sample ID	Location	Population	Species	Date	Samplers	Used in this study?
Campie ID	Location	ropulation	Opeoles	Sampica	Aloiandro Doroz	Study:
	Manua Taaman		Natalahrua		Alejanulo Perez-	
	Mapua, rasman	Abal	NOLOIADIUS	40/00/0000		Nia
MAP41	вау	Abei	cellaotus	16/02/2009	Hemandez	INO
	Manua Taaman		Matalahuun		Alejandro Perez-	
	Mapua, Tasman	A I I	Notolabrus	40/00/0000	Matus & Sebastian	NI-
MAP42	вау	Abei	cellaotus	16/02/2009	Hernandez	NO
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP43	Вау	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP44	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP45	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP46	Bay	Abel	celidotus	16/02/2009	Hernandez	No
	•				Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP47	Bay	Abel	celidotus	16/02/2009	Hernandez	No
	,				Aleiandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP48	Bay	Abel	celidotus	16/02/2009	Hernandez	Yes
	Duy	71001	oomaotao	10,02,2000	Aleiandro Perez-	100
	Manua Tasman		Notolabrus		Matus & Sebastian	
ΜΔΡ49	Bay	Abel	celidotus	16/02/2009	Hernandez	Ves
	Day	Abei	cenuolus	10/02/2003	Aleiandro Perez-	163
	Manua Taeman		Notolabrus		Matus & Sobastian	
	Napua, Tasman	Abol	nololabrus	16/02/2000	Hornondoz	Vaa
MAP 30	Day	Abei	cenuolus	10/02/2009	Aleiandre Derez	res
	Manua Taaman		Matalahuun		Alejandro Perez-	
	Mapua, Tasman		Notolabrus	40/00/0000	Matus & Sebastian	
MAP51	вау	Abei	cellaotus	16/02/2009	Hernandez	Yes
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP52	Вау	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP53	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP54	Bay	Abel	celidotus	16/02/2009	Hernandez	No
					Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP55	Bay	Abel	celidotus	16/02/2009	Hernandez	Yes
	-				Alejandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP56	Bav	Abel	celidotus	16/02/2009	Hernandez	Yes
	,				Aleiandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP57	Bav	Abel	celidotus	16/02/2009	Hernandez	Yes
					Aleiandro Perez-	
	Mapua, Tasman		Notolabrus		Matus & Sebastian	
MAP58	Bay	Abel	celidotus	16/02/2009	Hernandez	Yes
1111 11 000	Duy	71001	oonaotao	10,02,2000	Aleiandro Perez-	100
	Manua Tasman		Notolabrus		Matus & Sebastian	
	Bay	Abel	celidotus	16/02/2009	Hernandez	Ves
MAI 33	Day	Abei	cenuolus	10/02/2003	Aleiandro Perez-	163
	Monuo Toomon		Notolohrun		Matua & Sabastian	
	Rayua, Tasman	Abol	celidatus	16/02/2000	Hornandoz	Voc
MAFOU	Бау	Abei	Centolius	10/02/2009	Aleiandre Derez	165
			Matalahuun		Alejandro Perez-	
00004		A I I	NOLOIADIUS	7/00/0000		NI-
GOB01	Golden Bay	ADEI	ceildotus	7/03/2009	Hernandez	NO
					Alejandro Perez-	
00	<u> </u>		Notolabrus		Matus & Sebastian	
GOB02	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB03	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
	-				Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB04	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No

Sample ID Location Population Species Sampler In this study? GOB06 Golden Bay Abel Notolabrus 703/2008 Heurandez Alejandro Prez- Matus & Sebastian No GOB06 Golden Bay Abel Notolabrus 703/2008 Matus & Sebastian No GOB07 Golden Bay Abel celidotus 7/03/2008 Matus & Sebastian No GOB07 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB08 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB09 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB10 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB11 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB13 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB13 Golden Bay <th></th> <th></th> <th></th> <th></th> <th></th> <th></th> <th>Used</th>							Used
Sample ID Location Population Species sample Samplers study? GOB05 Golden Bay Abel Notlabrus Trolszob Matus & Sebastian GOB06 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB07 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB06 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB07 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB08 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB10 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB11 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB12 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB13 Golden Bay Abel celidotus Trolszob Matus & Sebastian GOB14 G					Date		in this
GOB05 Golden Bay Abel Notolabrus celidotus 7/03/2008 Hernandez Hernandez No GOB06 Golden Bay Abel Notolabrus celidotus 7/03/2008 Hernandez Hernandez No GOB07 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB07 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB08 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB09 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB10 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB11 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB13 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB14 Golden Bay Abel celidotus 7/03/2008 Hernandez No GOB15 Golden Bay	Sample ID	Location	Population	Species	sampled	Samplers	study?
COBBDS Colden Bay Abel Notifiabrus Matus & Sebestian No GOB06 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB06 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB07 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB08 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB09 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB10 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB11 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB12 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB13 Golden Bay Abel celidotus 7/03/2009 Hemandez No GOB14 Golden Bay Abel celidotus 7/03/2009						Alejandro Perez-	
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GOB26 Golden Bay Abel Notolabrus celidotus Matus & Sebastian GOB26 Golden Bay Abel celidotus 7/03/2009 Hernandez No GOB27 Golden Bay Abel celidotus 7/03/2009 Hernandez Yes Alejandro Perez- Notolabrus 7/03/2009 Hernandez Yes Alejandro Perez- Notolabrus 7/03/2009 Hernandez Yes GOB28 Golden Bay Abel celidotus 7/03/2009 Hernandez No		,				Alejandro Perez-	
GOB26 Golden Bay Abel celidotus 7/03/2009 Hernandez No Alejandro Perez- Notolabrus Matus & Sebastian Matus & Sebastian GOB27 Golden Bay Abel celidotus 7/03/2009 Hernandez Yes Alejandro Perez- Notolabrus 7/03/2009 Hernandez Yes Alejandro Perez- Notolabrus Matus & Sebastian Matus & Sebastian GOB28 Golden Bay Abel celidotus 7/03/2009 Hernandez No				Notolabrus		Matus & Sebastian	
GOB27 Golden Bay Abel Celidotus 7/03/2009 Hernandez Yes Alejandro Perez- Notolabrus 7/03/2009 Hernandez Yes Alejandro Perez- Notolabrus Matus & Sebastian Yes GOB28 Golden Bay Abel celidotus 7/03/2009 Hernandez Notolabrus	GOB26	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
Notolabrus Matus & Sebastian GOB27 Golden Bay Abel celidotus 7/03/2009 Hernandez Yes Alejandro Perez- Notolabrus Matus & Sebastian GOB28 Golden Bay Abel celidotus 7/03/2009 Hernandez Yes						Alejandro Perez-	
GOB27 Golden Bay Abel <i>celidotus</i> 7/03/2009 Hernandez Yes Alejandro Perez- <i>Notolabrus</i> Matus & Sebastian GOB28 Golden Bay Abel <i>celidotus</i> 7/03/2009 Hernandez No	0000-		A I	Notolabrus	7/00/0000	Matus & Sebastian	N -
Alejandro Perez- Notolabrus Matus & Sebastian GOB28 Golden Bay Abel celidotus 7/03/2009 Hernandez No	GOB27	Golden Bay	Abel	cellaotus	7/03/2009	Hernandez	Yes
GOB28 Golden Bay Abel celidatus 7/03/2009 Hernandez No				Notolohrun		Alejanuro Perez-	
	GOB28	Golden Rav	Abel	celidotus	7/03/2009	Hernandez	No

						Used
				Date		in this
Sample ID	Location	Population	Species	sampled	Samplers	study?
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB29	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
			Notolohruo		Alejandro Perez-	
COB30	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Ves
00000	Colden Day	Abei	cenaolas	1100/2000	Aleiandro Perez-	103
			Notolabrus		Matus & Sebastian	
GOB31	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Yes
	-				Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB32	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Yes
					Alejandro Perez-	
00000	O aldara Dava	A I I	Notolabrus	7/00/0000	Matus & Sebastian	N
GOB33	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Yes
			Natalahrua		Alejandro Perez-	
COB34	Coldon Bay	Abol	noloiabrus	7/03/2000	Hornondoz	Voc
60834	Golden bay	Abei	cenuolus	1103/2009	Aleiandro Perez-	165
			Notolabrus		Matus & Sebastian	
GOB35	Golden Bav	Abel	celidotus	7/03/2009	Hernandez	Yes
					Aleiandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB36	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Yes
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB37	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
					Alejandro Perez-	
00000	O aldara Dava	A I I	Notolabrus	7/00/0000	Matus & Sebastian	NI-
GOB38	Golden Bay	Abei	cellaotus	7/03/2009	Hernandez	NO
			Notolohrus		Alejandro Perez-	
COB30	Golden Bay	Abol	celidatus	7/03/2000	Hernandez	No
00003	Colden Day	Abei	Cenuolus	1103/2009	Aleiandro Perez-	NO
			Notolabrus		Matus & Sebastian	
GOB40	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
	,				Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB41	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
					Alejandro Perez-	
000.0			Notolabrus		Matus & Sebastian	
GOB42	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	NO
			Notolohrun		Alejanuro Perez-	
GOB43	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Ves
00040	Colden Day	Abei	cenaolas	1100/2000	Aleiandro Perez-	103
			Notolabrus		Matus & Sebastian	
GOB44	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Yes
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB45	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Yes
					Alejandro Perez-	
00040	O aldara Dava	A I I	Notolabrus	7/00/0000	Matus & Sebastian	N
GOB46	Golden Bay	Abei	cellaotus	7/03/2009	Hernandez	Yes
			Notolohrun		Alejanuro Perez-	
COB47	Golden Bay	Abol	celidatus	7/03/2000	Hernandez	Vec
00047	Colden Day	Abei	cenuolus	1103/2003	Aleiandro Perez-	163
			Notolabrus		Matus & Sebastian	
GOB48	Golden Bav	Abel	celidotus	7/03/2009	Hernandez	Yes
	,				Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB49	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
					Alejandro Perez-	
			Notolabrus		Matus & Sebastian	
GOB50	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	No
			NI-4-1-1-		Alejandro Perez-	
CODE4	Coldon Davi	Abal	NOTOIADrus	7/02/2000	Matus & Sebastian	Vaa
GOR21	Golden Bay	ADEI	Cellaotus	1/03/2009	Aleiandre Berez	res
			Notolehrus		Matus & Sebestian	
GOB52	Golden Bav	Abel	celidotus	7/03/2009	Hernandez	Yes

0 1 10				Date		Used in this
Sample ID	Location	Population	Species	sampled	Sampiers	study?
					Alejandro Perez-	
00050	0.11 B		Notolabrus		Matus & Sebastian	
GOB53	Golden Bay	Abel	celidotus	7/03/2009	Hernandez	Yes
			Matalahuus		Alejandro Perez-	
00054	Calden Dav	Ahal	Notolabrus	7/02/2000	Matus & Sebastian	Vaa
GOB54	Golden Bay	Abei	cellaotus	7/03/2009	Hemandez	res
			Notolohrua		Alejanuro Perez-	
CORSE	Coldon Ray	Abol	celidatus	7/03/2000	Hornandoz	Voc
GOB55	Golden Day	ADEI	cendolus	1103/2009	Aleiandro Doroz	res
			Notolahrus		Matus & Sobastian	
CORFE	Coldon Pov	Abol	nolidatus	7/02/2000	Walus & Sebasilan	Voo
00000	Golden bay	ADEI	Centolius	1103/2009	Alejandro Perez-	165
			Notolabrus		Matus & Sebastian	
GOB57	Golden Bay	Ahel	celidatus	7/03/2009	Hernandez	Ves
00007	Colden Bay	Abei	centottas	1/03/2003	Alejandro Perez-	103
			Notolabrus		Matus & Sebastian	
COB58	Golden Bay	Abol	celidatus	7/03/2000	Hernandez	Vec
00000	Obluen Day	Abei	Centolius	1103/2009	Alejandro Perez-	163
			Notolabrus		Matus & Sebastian	
GOB59	Golden Bay	Ahel	celidatus	7/03/2009	Hernandez	Ves
CODOU	Colden Buy	71001	001100100	1100/2000	Alejandro Perez-	100
			Notolabrus		Matus & Sebastian	
GOB60	Golden Bay	Ahel	celidatus	7/03/2009	Hernandez	No
CODOO	Obluen Day	Abei	Centolus	1103/2009	TICHIAIIUCZ	NO
	Darling Harbour		Notolabrus			
DHA01	Lyttelton	Banks	celidotus	11/04/2009	Surrey Scott	No
DINIOT	Lyttenton	Danko	001100100	11/04/2000	Carley Coold	
	Darling Harbour		Notolabrus			
DHA02	l vttelton	Banks	celidotus	11/04/2009	Surrey Scott	No
210.02		Danno				
	Darling Harbour		Notolabrus			
DHA03	l vttelton	Banks	celidotus	11/04/2009	Surrey Scott	No
211/100	Lyttonon	Danko	oonaotao	1 1/0 1/2000		110
	Port William		Notolabrus			
PWI01	Stewart Island	Stewart Is	celidotus	14/12/2009	Catherine Jones	Yes
		eterra tie				
	Port William.		Notolabrus			
PWI02	Stewart Island	Stewart Is	celidotus	14/12/2009	Catherine Jones	Yes
	Port William,		Notolabrus			
PWI03	Stewart Island	Stewart Is	celidotus	14/12/2009	Catherine Jones	Yes
	Port William,		Notolabrus			
PWI04	Stewart Island	Stewart Is	celidotus	14/12/2009	Catherine Jones	Yes
	Port William,		Notolabrus			
PWI05	Stewart Island	Stewart Is	celidotus	14/12/2009	Catherine Jones	Yes
	Port William,		Notolabrus			
PWI06	Stewart Island	Stewart Is	celidotus	14/12/2009	Catherine Jones	Yes
	Port William,		Notolabrus			
HSB01	Stewart Island	Stewart Is	celidotus		Catherine Jones	No
	Horseshoe Bay,		Notolabrus			
HSB03	Stewart Island	Stewart Is	celidotus		Catherine Jones	Yes
	Horseshoe Bay,		Notolabrus			
HSB04	Stewart Island	Stewart Is	celidotus		Catherine Jones	Yes
	Horseshoe Bay,	o	Notolabrus			
HSB05	Stewart Island	Stewart Is	ceiidotus		Catherine Jones	Yes
	Hamash D		NI-4-1-1			
	Horseshoe Bay,	0.	Notolabrus			N
HSB06	Stewart Island	Stewart Is	cellaotus		Catherine Jones	NO
	Llorosches D		Matclah			
	Horseshoe Bay,	Stowart la	INDIOIADIUS		Cathoring Janas	Vac
N360/	Stewart Island	Slewart IS	Cendolus		Callenne Jones	res
	Horeeshoo Pou		Notolahrua			
HSB08	Stewart Island	Stewart le	celidatus		Catherine Jones	Yes
	Stowart Island	Stomart 13	301140143			100

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
HSB09	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB10	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB11	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB12	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB13	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB14	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB15	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB16	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB17	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	Yes
HSB18	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	No
HSB19	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus		Catherine Jones	No
HMB01	Horseshoe Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB02	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB03	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB04	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB05	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB06	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB07	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB08	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB09	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB10	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB11	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB12	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB13	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
HMB14	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB15	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB16	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB17	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB18	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB19	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB20	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB21	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB22	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB23	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB24	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB25	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB26	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB27	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB28	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB29	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB30	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB31	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB32	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB33	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	No
HMB34	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus	7/12/2009	Catherine Jones	Yes
HMB35	Halfmoon Bay, Stewart Island	Stewart Is	Notolabrus celidotus Notolabrus	7/12/2009	Catherine Jones	Yes
NAP03	Napier		fucicola Notolabrus	23/03/2009	Surrey Scott	No
NAP05	Napier		fucicola Notolabrus	23/03/2009	Surrey Scott Alejandro Perez-	Yes
KAP01	Kapiti Island		fucicola	21/01/2009	Matus	No

				Date		Used in this
Sample ID	Location	Population	Species	sampled	Samplers	study?
KAP02	Kapiti Island		Notolabrus fucicola	21/01/2009	Alejandro Perez- Matus	Yes
KAP03	Kapiti Island		Notolabrus fucicola	21/01/2009	Alejandro Perez- Matus	No
KAP04	Kapiti Island		fucicola Notolabrus	21/01/2009	Alejandro Perez- Matus	No
KAP05	Kapiti Island		fucicola Notolabrus	21/01/2009	Alejandro Perez- Matus	Yes
KAP06	Kapiti Island		fucicola Notolabrus	21/01/2009	Alejandro Perez- Matus	No
KAP07	Kapiti Island		fucicola	21/01/2009	Alejandro Perez- Matus	No
KAP08	Kapiti Island		fucicola	21/01/2009	Matus	No
KAP09	Kapiti Island		fucicola Notolabrus	21/01/2009	Matus	No
KAP10	Kapiti Island		fucicola Notolabrus	21/01/2009	Matus	No
KAP11	Kapiti Island		fucicola	21/01/2009	Matus	No
KAP12	Kapiti Island		fucicola Notolabrus	21/01/2009	Matus	No
KAP13	Kapiti Island		fucicola	21/01/2009	Matus	No
KAP14	Kapiti Island		fucicola	21/01/2009	Matus	No
KAP15	Kapiti Island		fucicola Notolabrus	21/01/2009	Alejandro Perez- Matus	No
KAP16	Kapiti Island		fucicola Notolabrus	21/01/2009	Matus	No
KAP17	Kapiti Island		fucicola Notolabrus	21/01/2009	Matus	No
KAP18	Kapiti Island		fucicola Notolabrus	21/01/2009	Matus	No
KAP19	Kapiti Island		fucicola Notolabrus	21/01/2009	Matus	No
KAP20	Kapiti Island		fucicola	21/01/2009	Matus	No
WLG14	Wellington Harbour		Notolabrus fucicola	2008-9	Alejandro Perez- Matus	Yes
	Wellington		Notolabrus		Alejandro Perez-	
WLG17	Harbour		fucicola	2008-9	Matus	Yes
WLG39	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
	Wellington		Notolabrus		Alejandro Perez-	
WLG46	Harbour		fucicola	20/01/2009	Matus	No
WLG47	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG48	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG49	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
	Wellington		Notolabrus		Alejandro Perez-	
WLG50	Harbour		fucicola	20/01/2009	Matus	No
WLG51	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG53	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG55	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
WLG57	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG58	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG62	Wellington Harbour Wellington		Notolabrus fucicola Notolabrus	20/01/2009	Alejandro Perez- Matus	No
WLG63	Harbour		fucicola	20/01/2009	Matus	No
WLG65	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG66	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG72	Wellington Harbour		Notolabrus fucicola	20/01/2009	Alejandro Perez- Matus	No
WLG74	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG96	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG97	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG98	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG99	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG100	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG101	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG102	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG103	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG104	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG105	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG106	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG107	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG108	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG109	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG110	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG111	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
WLG112	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG113	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG114	Wellington Harbour		Notolabrus fucicola	23/02/2009	Alejandro Perez- Matus	No
WLG115	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG116	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG117	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG118	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG119	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG120	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG121	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG122	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG123	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG124	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG143	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG144	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG145	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG146	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG147	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG148	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG149	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG150	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG151	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG152	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
WLG153	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
WLG154	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	Yes
WLG155	Wellington Harbour		Notolabrus fucicola	2/06/2009	Alejandro Perez- Matus	No
JKB01	Jackson Bay		Notolabrus fucicola	13/04/2009	Surrey Scott	Yes
JKB02	Jackson Bay		Notolabrus fucicola Notolobruo	13/04/2009	Surrey Scott	Yes
JKB03	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB04	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB05	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB06	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB07	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	Yes
JKB08	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB09	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB10	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB11	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB12	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB13	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB14	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB15	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB16	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB18	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB19	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB20	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB21	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB22	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB23	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB24	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB25	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	NO
JKB26	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	NO
	Jackson Bay		tucicola Notolabrus fuoioolo	13/04/2009	Surrey Scott	
	Jackson Bay		Notolabrus	13/04/2009	Surrey Scott	t es
JKB29	Jackson Bay		tucicola Notolabrus fueicola	13/04/2009	Surrey Scott	INO
JKB30	Jackson Bay		iucicoia Notolabrus fueicela	13/04/2009	Surrey Scott	NO
JKB33	Jackson Bay		Notolabrus fucicola	13/04/2009	Surrey Scott	
011002	Juonoon Day		10010010	10,07,2000	Sundy Oboli	110

Sample ID	Location	Population	Species	Date sampled	Samplers	Used in this study?
JKB33	Jackson Bay		Notolabrus fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB34	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB35	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB36	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB37	Jackson Bay		fucicola Notolabrus	13/04/2009	Surrey Scott	No
JKB38	Jackson Bay		fucicola	13/04/2009	Surrey Scott	No
HSB02	Horseshoe Bay, Stewart Island		Notolabrus fucicola	1/12/2009	Catherine Jones	Yes
NINS01	Kermadec Islands		Notolabrus inscriptus		Te Papa collection	No
NINS02	Kermadec Islands		Notolabrus inscriptus		Te Papa collection	No
NINS03	Kermadec Islands		Notolabrus inscriptus Pseudolabrus		Te Papa collection	Yes
JKB17	Jackson Bay		miles	13/04/2009	Surrey Scott	Yes