An Experimental Approach to the Translocation of the North Island Saddleback (*Philesturnus carunculatus rufusater*) to Bushy Park Reserve, Wanganui

North Island Saddleback. Photo: Joanne Thorne

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ABSTRACT

Translocation, the intentional release of a species into a new location, is a key technique used in the conservation of New Zealand's threatened species. Despite the frequency with which translocations are carried out, factors affecting their outcome are not fully understood and greater emphasis on research based approaches is required for improvement. The translocation of North Island saddlebacks (*Philesturnus carunculatus rufusater)*, an endangered forest passerine, from Mokoia Island, Lake Rotorua, to predator fenced reserve Bushy Park, Wanganui provided the opportunity to investigate some key aspects that were identified *a priori* as factors that may affect its outcome. A greater understanding of these factors may increase the success of future saddleback translocations to the mainland.

The enforcement of complex disease screening programmes during translocation is a routine part of New Zealand translocations, yet the impacts these procedures have on post release survival is unknown. The saddleback translocation was designed to experimentally test these impacts by comparing the post release survival of four treatment groups that underwent different regimes of quarantine and prophylactic disease treatment (used to prevent stress induced disease) as part of a standard disease screening programme. However the detection of a *Plasmodium* in four of the translocated saddlebacks required a change in the original experimental design and subsequent comparison of post release survival between groups was difficult due to confounding factors. Despite this, the disease screening process resulted in difficulties in identifying which diseases were of concern, inaccurate diagnostic tests, increased cost, mortality during captivity and poor post release survival. These factors served to highlight some serious downfalls in the current 'guess work' approach applied to regulating disease risk during translocations and alternative approaches are discussed.

Population Viability Analysis (PVA) indicated that the population had 0% probability of extinction within the next five years. The model was based on data collected during the first year after release and therefore had a high degree of uncertainty. However, it provides a framework for adaptive management of the population in the future. As new data are collected under various management strategies the model can be updated to determine the most effective strategy. Breeding biology of the saddlebacks was

generally similar to island saddleback populations but fecundity rates were lower than that seen in other low density populations of North Island saddlebacks. This may have been due to the effect of the translocation which can lower reproduction and survival in the first year after release.

The saddleback's colonisation of Bushy Park was used as a natural experiment to investigate habitat selection. Eight out of nine saddleback pairs established home ranges around the periphery of the reserve in primarily dense secondary vegetation. The relationship between ten habitat variables and site occupancy was analysed in programme MARK. The best variable for predicting occupancy of a site was the complexity of the shrub tier (30 cm – 6 m). A complex habitat may represent a superior habitat by providing greater food availability and high quality nest sites. Caution is required when selecting release sites on the mainland as they tend towards mature forest which may not be high quality habitat for saddlebacks. Habitat quality at a release site is a vital consideration for ensuring a successful translocation outcome.

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CONTENTS

LIST OF TABLES

TABLE

LIST OF FIGURES

FIGURE

LIST OF PLATES

1

Introduction

With species extinction rates at an all time high, the world is currently facing a massive biodiversity crisis. When comparing past extinction rates to present, there is no doubt that humans are the cause of much of this loss. The current rate of extinction is estimated to be in the region of 100 times what it was before *Homo sapiens* spread from Africa (Tennyson & Martinson 2006). Separated from Gondwanaland for some 80 million years, New Zealand's original array of distinctive and important island biota makes our extinctions some of the most tragic of all. Described by Wilson (2004) as our 'once distinctive, now-tattered biota', it is estimated that around 41% of our endemic birds are now extinct and many more are currently threatened or endangered (Wilson 2004). The threat to New Zealand's biota is ever present as habitats continue to be degraded, the human population continues to grow and the risk of spreading introduced species intensifies as people and freight move freely among countries. Soule (1985) has referred to the field of conservation biology as a 'crisis discipline' within which ecologists and conservation managers require effective techniques and knowledge to conserve endangered species. New Zealand's isolation has posed some unusual challenges and encouraged the development of pioneering approaches to conservation management (Wilson 2004). The potential of our offshore islands for species recovery has long been recognized and has led to the evolution of conservation strategies such as island pest eradication and translocation. In fact, these strategies have played a central role in the recovery of some of our most threatened species (Saunders & Norton 2001).

One endemic bird that has benefited from these pioneering approaches to conservation is the saddleback (*Philesturnus carunculatus*). Disappearing from the mainland in the 1890s, the North Island saddleback (*Philesturnus carunculatus rufusater*) was restricted to a single island before it was translocated to numerous offshore islands whose predators had been eradicated (Lovegrove 1996a). Recently, efforts to conserve the North Island saddleback have been directed towards establishment at selected mainland sites.

This thesis investigates aspects of the translocation and establishment of 40 North Island saddlebacks from Mokoia Island, in Lake Rotorua, to the fenced reserve Bushy Park near Wanganui, in an attempt to increase the current body of information related to the recovery of the North Island saddleback, particularly on the mainland

1.1. TRANSLOCATIONS

Translocation is defined as the intentional release of animals to the wild in an attempt to establish, re-establish or augment a population (IUCN 1987). It is a conservation technique that was pioneered in New Zealand by Richard Henry in the 1890s (Atkinson 1990) and has saved several species, such as the black robin (*Petroica traversi*) and South Island saddleback (*Philesturnus carunculatus carunculatus*) from extinction (Atkinson & Bell 1973, Butler & Merton 1992). Today, translocation continues to be an important and commonly used tool in the conservation of New Zealand's threatened species.

1.1.2. An Experimental Approach

Historically, translocations have been carried out as management exercises with little emphasis on research based approaches, post release monitoring or even clear objectives (Armstrong & McLean 1995, Seddon *et al.* 2007). Consequently, there have been few detailed records of procedures followed and the factors influencing outcomes of translocations are often poorly understood (Seddon *et al.* 2007).

The impending reduction in worldwide biodiversity demands closer scrutiny of translocation methodology and results, and a clearer understanding of which factors are

associated with success (Griffith *et al.* 1989). Repeated calls have therefore been made in the literature for translocations to be designed as experiments and to involve careful post release monitoring and information exchange (Armstrong *et al.* 1994, Seddon *et al.* 2007). Although there is a growing interest in approaching translocations in this way, Seddon *et al.* (2007) classified 454 peer-reviewed papers on wildlife translocations according to their primary approach and found only a small percentage had been designed to test hypotheses or scientifically evaluate translocation techniques. Sixty four percent of these papers included some research, while the remaining 36% of papers related to general planning, progress reports or the development of guidelines. The majority of papers that took a research based approach (65%) were descriptive and made opportunistic evaluations of specific parameters rather than adopting a rigorous experimental or adaptive management approach. Twelve percent were classified as primarily experimental and were designed to test hypothesis about translocation strategies. The remaining 23% used population viability analysis (PVA) models to project population growth and viability under particular circumstances. A further application of PVA modelling is adaptive management where population models are used to test alternative management strategies in a 'learning while doing' manner. Reasons for an overwhelming majority of descriptive studies over experimental or modelling studies include poor planning, inadequate financial resources, small sample sizes and lack of statistical controls (Seddon *et al.* 2007).

Despite the growing number of research papers addressing translocations, greater emphasis must be placed on developing specific goals and identifying the biological and technical limitations of a given translocation (Armstrong *et al.* 1994, Seddon *et al.* 2007). Evaluation of the translocation outcome should include both experimental and modelling approaches. This approach will increase our understanding of threatened species and the processes which will help to save them rather than using translocations primarily as a management tool to prevent the extinction of small populations.

My thesis takes a research based approach to the translocation of North Island saddlebacks to Bushy Park. I investigated aspects of the translocation that were identified *a priori* as factors that may potentially affect its outcome, yet have received little attention to date. A greater understanding of these factors may improve translocation success:

1. *Disease screening*. Despite scant evidence of disease being implicated in the failure of a translocation, disease screening animals during a translocation is now routinely enforced in New Zealand. A typical disease programme involves screening for disease and a quarantine period of around two weeks. Because captivity is probably stressful for wild animals (Reed & Stockdale 1994), prophylactic treatment is often given for stress induced diseases. The effect these procedures have on translocated individuals is rarely considered. I designed the saddleback translocation as an experiment to test the effects of different regimes of quarantine and prophylactic treatment on the post release survival of the birds.
2. *Population modelling*. The translocation of saddlebacks to the mainland raises some specific issues that may affect the viability of these populations. For example, suitability of the habitat (see below) and dispersal out of a reserve are two factors that may affect the long term viability of mainland populations. Modelling a founder population is important for two main reasons: 1) it is a key component of post release evaluation by assessing the viability of a founder population and identifying factors affecting its viability; 2) basic models can be used for adaptive management of the population. Management strategies can be evaluated by updating models with population parameters collected under particular strategies. I developed a PVA model based on data collected during the first year after translocation. This model provides the framework for future management of the population in relation to factors that may affect its persistence such as habitat suitability and dispersal out of the reserve.
3. *Habitat quality of release sites*. A vital component of a translocation is selecting a release site that meets the habitat requirements of the species involved (Armstrong & McLean 1995). Documenting the habitat selection of a newly released species offers a unique opportunity to identify their niche requirements as they are likely to colonise preferred habitats first which are also likely to be higher quality habitats (Fretwell & Lucas (1970). Saddleback habitat selection has been studied on islands where a preference for dense, secondary vegetation has been recorded (Hooson & Jamieson 2004, Armstrong *et al.* 2005, Steffans *et al.* 2005). This raises uncertainty about the suitability of mainland release sites which may tend towards mature forest. I investigated the habitat selection of the newly released saddlebacks and discuss implications for the selection of future mainland release sites.

1.2. THE SADDLEBACK

1.2.1. Family Callaeidae

The Callaeidae family comprises three endemic New Zealand wattlebirds, the Huia (*Heteralocha acutirostris*), thought to have become extinct around the mid 1920s (Tennyson and Martinson 2006), the Kokako (*Callaeas cinerea)* and the Saddleback. It is thought that the New Zealand wattlebirds had an ancient origin, probably arising in the early Tertiary period some 65 million years ago (Fleming 1962).

1.2.2. North Island Saddleback

The North Island saddleback is a medium sized (length 25 cm) endemic forest passerine (Plate 1.1). The North Island saddleback and South Island saddleback have traditionally been considered to be suspecies, but Holdaway *et al.* (2001) recently re-classified them as separate species. I follow the older classification here because it continues to be used by the New Zealand Department of Conservation (e.g. Hitchmough *et al.* 2007). The North and South Island saddleback differ in plumage characteristics, especially in juveniles, and in size, the South Island subspecies being somewhat larger. Adult birds are glossy black with a chestnut colored 'saddle' across the back and similar colorings around the base of the tale. The North Island species has a strip of gold across the mantle. Bright orange-red wattles hang from the gape, and the beak is slender and sharply pointed. The juvenile North Island saddleback is primarily brownish black with a dull chestnut saddle, lacks the gold strip across the mantle, and has small pale-orange wattles.

Although primarily insectivorous, the saddleback also feeds on nectar and fruits of a variety of plant species (Atkinson and Campbell 1966, Merton 1966, Blackburn 1967, Jenkins 1976, Pierre 2000, 2001) and uses a range of techniques while foraging for food on the ground, foliage and live and dead wood (Atkinson 1966, Atkinson and Campbell 1966, Blackburn 1967, Pierre 2000, Pierre 2003).

Saddlebacks have a recorded longevity of up to 17 years and form monogamous pairs that are usually permanent once a pair has bred (Jenkins 1976, Lovegrove 1980),

although translocation typically results in the break up of established pairs (Lovegrove 1992, Armstrong & Craig 1995). Pairs hold territories throughout the year, and territory boundaries may vary in relation to time (O'Callaghan 1980), habitat quality (Blackburn 1964) and population density (Pierre 2003). Breeding season varies annually and with location, with clutches consisting of one to four eggs and up to four clutches being laid each season (Craig 1994, Hooson & Jamieson 2003). Reproduction rates are density dependant (Hoyle 1993, Armstrong *et al.* 2005). In low-density populations up to four clutches of four eggs per pair have been recorded (Craig 1994), but fecundity declines in established high-density populations (Hoyle 1993, Armstrong *et al.* 2005). Nests (Plate 1.2) are built in natural cavities and other secluded areas (Jenkins 1976, Lovegrove 1980, Hooson & Jamieson 2003), although artificial nest boxes are readily used (Lovegrove 1992). The female alone incubates eggs for 18-20 days and broods young nestlings (Blackburn 1966, Lovegrove 1980, Hooson & Jamieson 2003). Both males and females feed late-stage nestlings and fledglings, which leave the nest at about 27 days of age (Blackburn 1966, Lovegrove 1980, Hooson & Jamieson 2003).

Plate 1.1 Adult North Island saddleback. Photo: Joanne Thorne

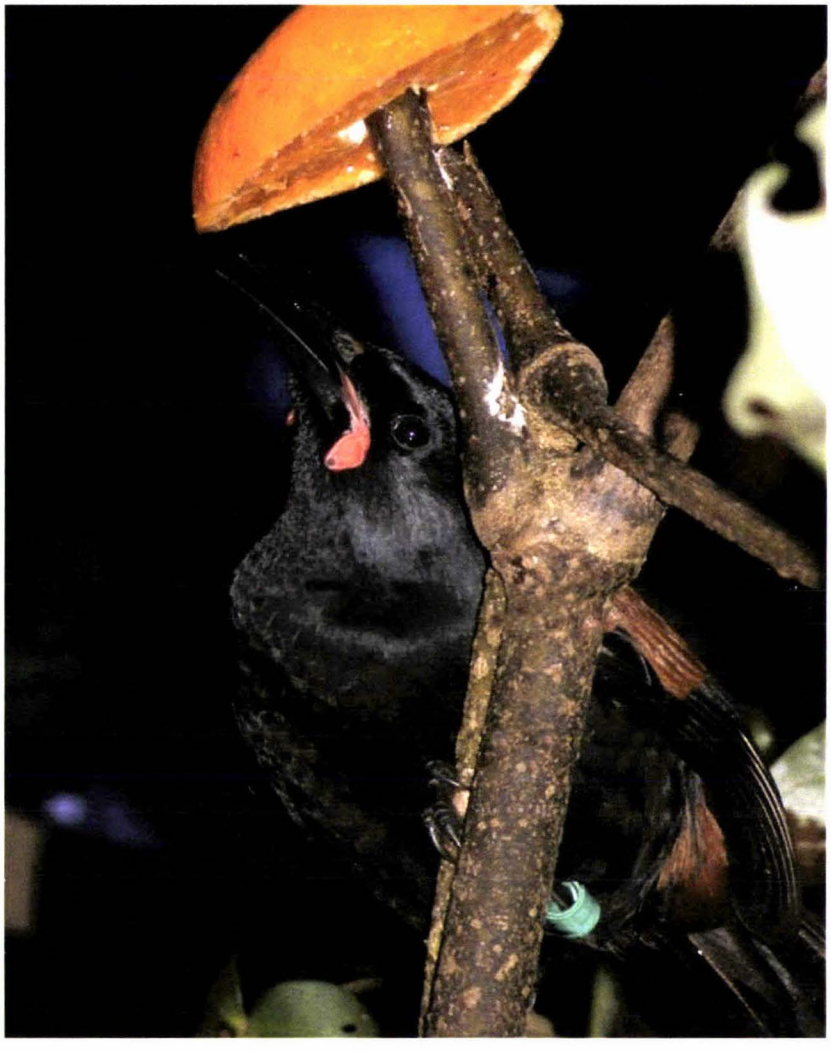


Plate 1.2 North Island saddleback nest. Photo: Kelly Brider

Status and distribution

Once common throughout the North Island and its offshore islands, the North Island saddleback was thought to have virtually disappeared from the mainland by the 1890s (Williams 1976), existing only on Hen Island off the east coast of Northland (Merton 1965, Hooson & Jamieson 2003). There were thought be about 400 saddlebacks on Hen Island in 1939 (Blackburn 1968). The reason for their decline was predation by introduced mammals, particularly the ship rat (*Rattus rattus*) (Atkinson & Campbell 1966, Atkinson 1973, Lovegrove 1992, Lovegrove 1996), which became widespread throughout the North Island by about 1860 (Atkinson 1973). Several aspects of saddleback behavior, such as an inquisitive and fearless nature, frequent foraging on the ground, selection of nest and roost sites low to the ground and poor flying ability may have heightened their susceptibility to predation (Merton 1965, Lovegrove 1996b, Hooson & Jamieson 2003).

Efforts towards their recovery began with translocation attempts in the 1920s (Lovegrove 1996a), and a review of the distribution and status of saddleback populations by Hooson and Jamieson (2003) suggested that the North Island saddleback population had grown to approximately 6630 by 2002. Today, the North Island Saddleback is listed as 'range restricted' (Hitchmough *et al.* 2007) by the New Zealand Department of Conservation under the New Zealand Threat Classification System and is present on 13 offshore islands and two fenced mainland reserves, the Karori Wildlife Sanctuary in Wellington (Hooson & Jamieson 2003) and the Bushy Park Reserve near Wanganui

Translocations of the North Island Saddleback

After two failed attempts to establish North Island saddlebacks on Little Barrier and Kapiti islands in 1925 and one attempt to Lady Alice island in 1950 (Lovegrove 1996a), the successful establishment of birds on Middle Chicken Island in 1964 (Merton 1965) was the beginning of a largely successful translocation history for the North Island saddleback. Several aspects of saddleback behaviour, such as limited dispersal, small territories, adaptability to a broad range of habitats and high reproductive rate at low densities make them especially suitable for translocation (Lovegrove 1996a).

A few saddleback translocations have taken an experimental approach to answer underlying factors affecting the outcome of a translocation. For example, the release of saddlebacks to Kapiti Island in 1988 provided Lovegrove (1992) with an opportunity to test the benefits of a delayed release versus an immediate release. Results showed no significant difference in survival between the birds that were held in captivity prior to release (delayed group) and birds that were released immediately after translocation to the island (immediate group). Armstrong and Craig (1995) tested whether familiarity among translocated groups of saddlebacks affected the outcome of a transfer to Mokoia Island. They found no evidence to suggest that using familiar birds would increase the success of a translocation; an important finding given that the composition of the founder group is an essential part of planning for a translocation. Experiments such as these provide valuable data for future translocations and for the conservation of saddlebacks.

The North Island saddleback was successfully transferred to fenced mainland site Karori Wildlife Sanctuary in 2002 however an attempt to establish them at unfenced Boundary Stream Mainland Island (BSMI) in 2004 failed. Primary reason for failure to establish was attributed to predation by mammalian predators (Sullivan 2006). The outcome of this translocation suggests that North Island saddlebacks are not suitable for reintroduction to mainland sites with important predators present. Supporting this is the results of a review of 45 saddleback translocations carried out between 1925 and 1994 by Lovegrove (1996a). The primary reasons for failure to establish were attributed as too few birds being released and predators present at the release site. Taylor *et al.* (2005) modelled translocation success in saddlebacks in relation to numbers released and introduced mammalian predators and cited predators as the primary cause for extinction. Considering these findings it seems prudent that sites considered for transfer to the mainland should be, for the near future, confined to fenced reserves.

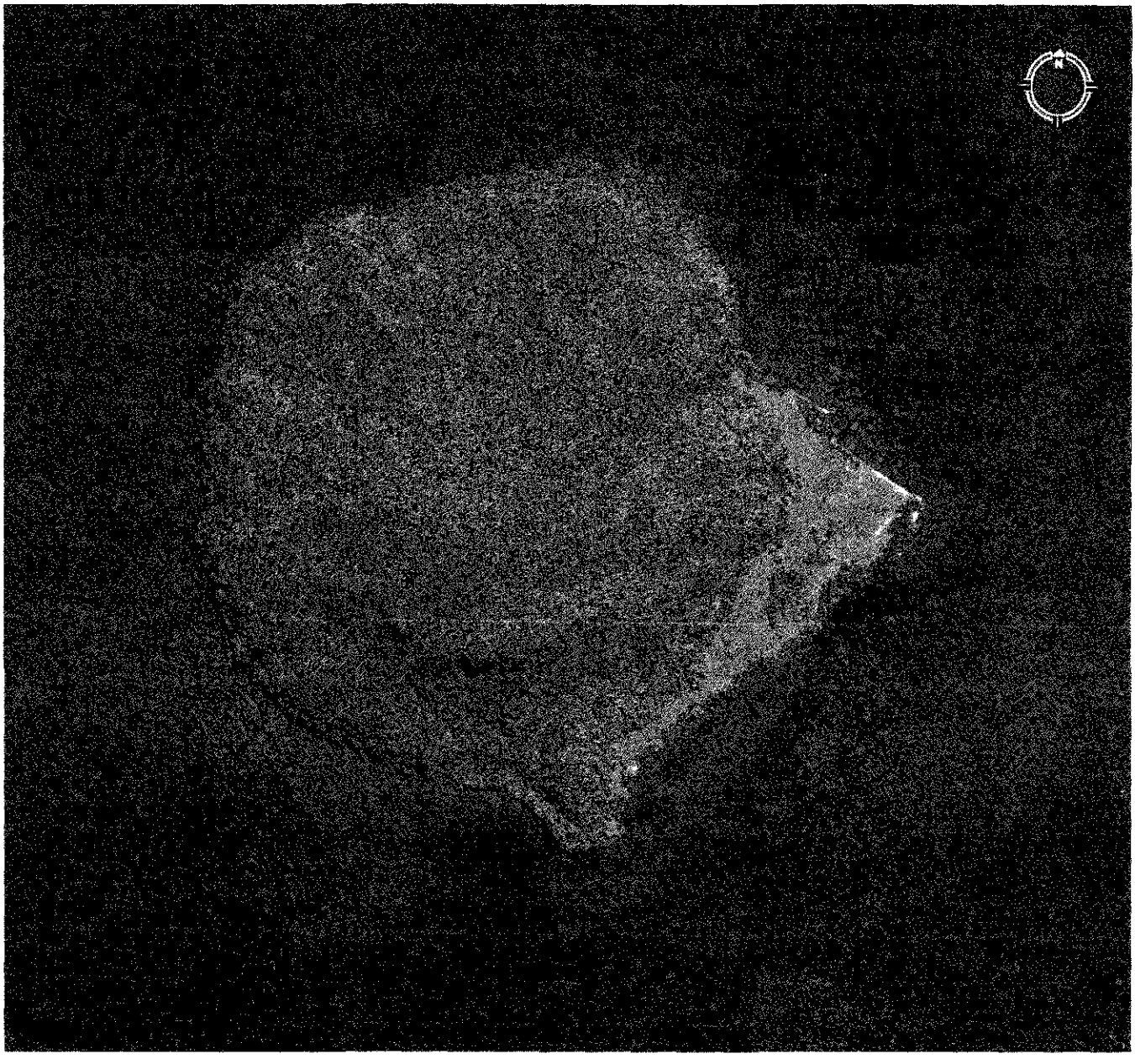
1.3. SOURCE SITE, MOKOIA ISLAND

Mokoia Island is a 135 ha island that lies at 38°06'S latitude and 175°55'E longitude in Lake Rotorua in the North Island (Plate 1.3). Mokoia is the largest inland island in New Zealand and at its shortest distance is about 2.1 km from the mainland.

The island has a long history of human habitation and is highly modified. Maori occupied the island for hundreds of years, during which time much of the island was burnt and cleared to grow crops in the fertile soil (Andrews 1992). The island was made a Wildlife Refuge in the 1950s by which time cultivation had ceased. The first restoration attempts began in the 1960s and natural regeneration of the forest has been occurring for about 55 years (Perrott & Armstrong 2000). Mokoia island now has good secondary growth that is dominated by mahoe (*Melicytus ramiflorus*), kohuhu (*Pittosporum tenufolium*), five-finger (*Pseudopanax arboreus*) and mamaku tree ferns (*Cyathea medullaris*) (Beadel 1990). Vegetation is scrubby on the ridges and summit but there is a closed canopy forest in the gullies and near the lake side.

Goats, sheep and rats were eradicated from the island by the Department of Conservation during 1989-1990 and mice were eradicated in 2001. Since the eradication of these mammalian pests several native bird species have been translocated to the island: the New Zealand robin (*Petroica australis*) in 1991 (Jansen 1993), the North Island saddleback in 1992 (Armstrong and Craig 1995), the hihi (*Notiomystis cincta*) in 1994 (Armstrong *et al.* 1999), a small group of male kokako in 2007 and North Island brown kiwi (*Apteryx australis mantelli*) (B. Evans pers comm.). The hihi population was removed from the island in 2002 after failing to grow despite intensive management (Armstrong *et al.* 2007).

Plate 1.3 Aerial photograph of Mokoia Island, Lake Rotorua (sourced from Google™ earth images).



1.4. RELEASE SITE, BUSHY PARK RESERVE

Bushy Park is a 97 ha reserve that lies at 39°47'S latitude, 174°55'E longitude situated 24 km northwest of Wanganui (Plate 1.4), and is one of 85 protected natural areas in the Manawatu Plains Ecological District. The reserve is surrounded by an Xcluder™ pest proof fence (Plate 1.5), and is actively managed to be free of mammalian predators. The majority of Bushy Park consists of a forest remnant of 87 ha with an additional 10 ha consisting of grazing land and a 100-year-old homestead with its adjoining out

buildings and gardens. Once privately owned, the reserve is now overseen by the Bushy Park Trust, formed in 1994.

The 87 ha forest remnant consists of lowland coastal pukatea-tawa-podocarp-mixed broadleaf with emergent rimu (*Dacrydium cupressinum*) and northern rata (*Metrosideros robusta*). Tawa (*Beilschmiedia tawa*) and pukatea (*Laurelia novae-zelandiae*) are the dominant canopy trees and northern rata, rimu, hinau (*Elaeocarpus dentatus*) and miro (*Prumnopitys ferruginea*) are found throughout on ridges and hillslopes. One indigenous tree of note is 'Ratanui', a northern rata some 43 m high that is thought to be the largest such specimen in New Zealand.

Bird species that inhabit the reserve include the New Zealand robin reintroduced in 2001 and 2004, North Island saddleback reintroduced in 2006, kereru (*Hemiphaga novaeseelandiae*), tui (*Prosthemadera novaeseelandiae*), tomtit (*Petrocia macrocephala*), bellbird (*Anthornis melanura*), morepork (*Ninox novaeseelandiae*), waxeye (*Zosterops lateralis*), New Zealand falcon (*Falco novaeseelandiae*), fantail (*Rhipidura fuliginosa*), paradise shelduck (*Tadorna variegata*), harrier hawk (*Circus approximans*), grey warbler (*Gerygone igata*) and shining cuckoo (*Chrysococcyx lucidus*). The reserve is also used to raise juvenile North Island brown kiwi in a free range environment until they reach a predator proof weight, at which time they are released back into the wild.

Bushy Park is an isolated forest remnant surrounded by sheep and cattle farming country with occasional grain growing. Such forest remnants are termed 'habitat islands' (Saunders & Norton 2001). Within the surrounding farms there are some small residual areas of degraded forest, the nearest of which is a 13 ha patch of mixed exotic/native vegetation located 98 m to the South-West of the reserve. This patch is in turn isolated from other bush patches by a minimum of 374 m. A corridor of mixed native scrub and exotic trees down either side of the Bushy Park driveway connects to a narrow strip of primarily exotic roadside vegetation along Rangitatau East Road. A 24 ha block of regenerating native bush is situated to the South of the main entrance gate and immediately adjacent to the main bush reserve. This block has no predator control, and is separated from the reserve by the Xlcuder™ pest proof fence and a cleared strip of grass approximately 15 m wide.

Xcluder™ Fence

In May 2005 a 4.2 km pest proof Xcluder™ fence was erected around the perimeter of the reserve (Plate 1.5). A pest eradication programme followed in late August and early September 2005 in an effort to create a habitat free of exotic mammalian predators. This consisted of two aerial applications of brodifacoum (Talon T20 pellets) carried out 5 weeks apart, making a total application of 600 kg of brodifacoum. The reserve has 13 trap lines running parallel in a North-South direction, and these lines are used in the ongoing monitoring of the reserve. Tracking tunnels, traps, poison and predator dogs are used to detect any pests that were not eradicated during the poison drop or that breach the fence. Outside the fence, DoC 200 traps, fenn traps and Talon blocks are placed around gateways and areas of the fence known to be 'mustelid highways'. Mice (*Mus musculus*) were detected in the reserve in November 2006 (T. O'Connor, pers. comm.) and attempts are being made to reduce numbers and eventually eradicate them through trapping and use of Talon poison blocks. With the exception of mice and low numbers of hedgehogs (*Erinaceus europaeus*) the reserve is thought to be free of exotic mammals (T. O 'Connor, pers. comm.).

Plate 1.4 Aerial photograph of Bushy Park Reserve and surrounding farmland.

Digital map data supplied by Critchlow Associates Ltd. Sourced from Land Information New Zealand.
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NORTH
Scale 1:11,380
Printed 20/11/2007

Plate 1.5. Xcluder™ Pest Proof fence, Bushy Park reserve, Northern aspect. Photo: Joanne Thorne

1.5. THESIS AIMS

While numerous saddleback translocations to offshore islands have occurred since the mid 1920s, translocation to the mainland is a relatively new component in the conservation of the North Island saddleback. Our efforts to establish a viable population at Bushy Park was only the third attempt to do so on the mainland and provided the opportunity to investigate aspects of the translocation and subsequent establishment of the population that were identified as factors that may affects its outcome. Three data chapters are presented in this thesis.

Chapter 2: The Effects of Disease Screening during Translocation

I explain how the saddleback translocation was designed as an experiment to test the effects of a typical disease screening programme on the post release survival of the birds.

Objectives

i. Determine whether a quarantine period affects the post-release survival of saddlebacks.
ii. Determine whether prophylactic treatment for stress induced diseases affects the post-release survival of saddlebacks.
iii. Determine whether a combined regime of quarantine and prophylactic treatment affects the post release-survival of saddlebacks.

Chapter 3: Population Viability Analysis and Breeding Biology

I investigate the short term viability of the saddleback population using PVA and describe the breeding biology during the first breeding season after release.

Objectives

i. Assess the viability of the saddleback population at Bushy Park over a period of five years.
ii. Identify which demographic parameter estimates have the greatest impact on the population and make recommendations for future management of the population.
iii. Compare the breeding biology of the Bushy Park population to that of saddleback populations on islands, given the contrasting habitats between island and mainland sites.

Chapter 4: Habitat Selection

I use the colonization of Bushy Park as a natural experiment to investigate the habitat selection of the newly released saddlebacks.

Objectives

i. Identify environmental cues that may predict habitat occupancy using generalized linear models.
ii. Identify specific habitat types that represent high quality saddleback habitat and relate this to the selection of suitable release sites on the mainland.

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2

Disease Screening

2.1. INTRODUCTION

Since the 1880s, the translocation of endangered species has played a crucial role in New Zealand's conservation history. Translocations have saved several species from the threat of extinction (e.g. Merton 1975 for saddleback; Butler & Merton 1992 for black robin) and techniques used have been refined through the years. As the use of translocations in New Zealand gains popularity (Saunders 1995, Armstrong & McLean 1995), there has been an increased focus on developing guidelines to aid managers in executing successful translocations rather than using the *ad hoc* approach that has sometimes been employed in the past (Saunders 1995).

To improve the success of translocations, the New Zealand Department of Conservation produced the 'New Zealand transfer guidelines for indigenous terrestrial fauna and flora' in 1990; then replaced this document with the 'Standard Operating Procedure for the Translocation of New Zealand's indigenous flora and fauna' in 2001. These guidelines cover a broad range of topics from objectives and justifications for a translocation, founder group details, release site suitability, monitoring requirements and public perception of the proposed translocation. A significant development in the Standard Operating Procedure was greater emphasis on management of pathogenic disease during a translocation, with reference to an accompanying workbook,

'Developing quarantine and health protocols for native animal movements within New Zealand' (Jakob-Hoff 2000a).

Disease can potentially have major impacts on the conservation of endangered species (Alley 2002, Tompkins & Gleeson 2006), and its effects may be magnified by low genetic diversity often associated with small populations (Hale & Briskie 2007). Although there are few documented cases of disease endangering species in comparison to other factors such as habitat loss and over hunting (Smith *et al.* 2006), there are some notable cases. Avian malaria (*Plasmodium relictum*) is believed to have caused the extinction of many endemic Hawaiian birds since the 1920s and continues to influence their distribution, abundance and behaviour (Woodworth *et al.* 2004). The presence of canine distemper in the last known colony of the black-footed ferret (*Mustela nigripes*) in 1985 led to the extinction of the species in the wild, and ecologists were left with just 18 individuals of poor sex ratio and high relatedness with which to start a captive breeding programme (Thorne & Williams 1988). Despite its isolation, New Zealand's indigenous fauna are also affected by pathogens, sometimes with serious outcomes (Alley 2002). In particular, exotic pathogens pose a risk to endemic fauna that have not had an opportunity to evolve strong immune responses to such pathogens (Tompkins & Gleeson 2006). Examples include the highly endangered black robin (*Petroica traversi*) suffering mortalities due to avian pox (Tisdall & Merton 1988), captive New Zealand dotterel (*Charadrius obscurus*) found to be infected with avian pox and malaria (Jakob-Hoff 2000b), and a recent Salmonella outbreak on Tiritiri Matangi Island that resulted in an estimated 26% mortality rate in the resident population of hihi (*Notiomystis cincta*) (Ewen *et al.* 2007).

Historically, disease management has been overlooked during the translocation of animals, both worldwide (Viggers *et al.* 1993) and in New Zealand (Griffith *et al.* 1993), yet there is growing concern that disease may endanger the outcome of the translocation (Viggers *et al.* 1993, Reed & Stockdale 1994, Cunningham 1996). This perceived risk can be divided into two general scenarios that may occur during translocation:

1. An infected animal is transferred into a site where the pathogen has not occurred before, potentially transmitting the pathogen to animals with no previous exposure to it.
2. An animal with no previous exposure to a pathogen is transferred into a site that contains infected populations of the same species or different species.

Recently, however, a growing awareness of disease issues has led to a greater emphasis being placed on the threat of disease during the translocation of animals (Mathews *et al.* 2006). As a result, disease screening and quarantine programmes are frequently included in translocations in New Zealand. However, this process is not always straightforward and can pose a range of challenges during a translocation, including the practical aspects of quarantining a large number of birds and the associated costs and expertise required. Additionally, gaps in our knowledge of wildlife diseases make it difficult to identify diseases of concern during a translocation (Jakob-Hoff 2000a), and so creating an appropriate disease-screening programme often involves a lot of 'guess work'.

A quarantine period involves the physical isolation of the animals for a period of time that is dependent on the maximum incubation period of diseases of concern (Viggers *et al.* 1993). Because little is known about wildlife disease in New Zealand fauna, an effective length of quarantine is often hard to establish. The confinement of wild animals during a quarantine period may cause stress that arises from poor nutrition, an unnatural social environment, inadequate hygiene standards and overcrowding (Reed & Stockdale 1994). Elevated stress levels can pre-dispose birds to diseases such as aspergillosis (Alley *et al.* 1999, Jakob-Hoff 2001) and coccidiosis (Jakob-Hoff 2001), hence a procedure intended to prevent disease spread can potentially facilitate it. Consequently, quarantined birds are routinely treated with preventative drugs to lower the disease risk while in captivity.

The translocation of 40 North Island saddlebacks from Mokoia Island, Lake Rotorua, to Bushy Park, Wanganui, provided the opportunity to experimentally test the effects of a 'typical' disease-screening programme on the survival of the founder group. The aim of my experiment was to compare the survival of translocated saddleback that underwent

four different regimes of quarantine and prophylactic disease treatments. Specifically, I aimed to address the following questions:

1. Does quarantine affect the post-release survival of translocated saddlebacks?
2. Does prophylactic treatment for stress-induced diseases affect the post-release survival of translocated saddlebacks?
3. Does a combined regime of prophylactic treatment and quarantine have an effect on the post release survival of translocated saddlebacks?

Unfortunately circumstances arose during the translocation that caused confounding factors and subsequently limited the conclusions that could be drawn from the experimental design. However some valuable lessons were learnt and recommendations for future translocations are discussed.

2.2. METHODS

2.2.1. Experimental Design

The capture and translocation of 40 saddlebacks was undertaken during two trips to Mokoia Island two weeks apart. Twenty birds were translocated to Bushy Park on 17 May 2006 and a further 20 birds on 1 June 2006. Staggering the transfers in this way meant all birds could be released simultaneously at the end of the proposed experimental treatments. This ensured that the immediate release birds did not have the advantage of being released before the quarantined birds.

To tease out the effects of quarantine and preventative treatment on birds I divided the 40 birds into four groups of 10, with each group receiving a different treatment as follows:

Group 1: Quarantine + prophylactic disease treatment. These birds were to be quarantined for two weeks in holding aviaries at Bushy Park and treated for coccidiosis with one oral dose of Baycox (also used for piglets and containing Toltrazuril 50g/L) at capture. The dosage was calculated to be 0.03 mL for 60-70 g birds and 0.04 mL for 70-100 g birds. These birds were also to be treated for aspergillosis with Sporonox Oral

Solution (Itraconazole 10 mg/L) throughout the quarantine period. The Sporonox dosage was calculated to be 0.04 mL for 60-80 g birds and 0.05 mL for 80-90 g birds. Rather than giving Sporonox to individual birds, the combined dosage for all birds was added daily to water and jam water dishes that were spread around the aviary to allow access to all individuals.

Group 2: Quarantine, no prophylactic disease treatment. These birds were to be quarantined for two weeks at Bushy Park but receive no preventative disease treatment

Group 3: No quarantine, prophylactic disease treatment. These birds were to be treated for coccidia at capture and for aspergillosis during transfer but released immediately upon arrival at Bushy Park.

Group 4: No quarantine, no prophylactic disease treatment – These birds were to undergo no quarantine or disease treatment and be released immediately upon arrival at Bushy Park

Approval of this experimental design was conditional on the first 20 birds being free of any harmful pathogens (Table 2.1) so that the second 20 birds could be released immediately. If one of the nominated pathogens were present, the translocation could only proceed following advice from the Department of Conservation and Massey University wildlife veterinarians as to how to proceed.

2.2.2. Ethics

Massey University Animal Ethics Committee approved all methods involving the capture, translocation and disease screening of the saddlebacks.

2.2.3. Translocation proposal and Tangata Whenua endorsement

A translocation proposal detailing all aspects of the translocation, disease screening and experimental treatments was submitted to the Department of Conservation at the Wanganui and Bay of Plenty Conservencies for approval. A permit to capture, handle and transfer the saddlebacks was issued by the Bay of Plenty conservator. Tangata Whenua consultation was carried out at the source site with the Mokoia Island Trust and the release site with Te Kaahui o Rauru and Nga Rauru Iwi Authority Society.

2.2.4. Transfer Techniques

Mistnetting teams of two or three people set up 9 m and 12 m mistnets (38 mm mesh) in several different locations around Mokoia Island. Birds were lured into mistnets by playing taped saddleback calls and using soft toy decoys (obtained from Nativez®). If no birds were caught at a site within 15-20 minutes, the nets were moved to a different location. Once removed from mistnets, birds were placed into bird bags and taken to holding aviaries for processing. In order to keep birds in Groups 1 and 2 separate, two aviaries were set up inside a small hut on Mokoia Island (Plate 2.1). The aviaries were constructed of windbreak mesh, each approximately 1.5 x 3 m wide and 1.8 m high. A captive diet was supplied at two feeding stations within each aviary so that each type of food was available at both stations. The aviary floors were covered in newspaper, and fresh leaf litter and rotten logs were spread out on the floor. Birdbaths were supplied and clusters of kawakawa (*Macropiper excelsum*) branches were added for perching and roosting areas.

Plate 2.1. Saddleback holding aviaries set up on Mokoia Island.

After capture each bird was processed in the following way:

1. The bird's weight and relative age (adult or juvenile) was assessed from plumage characteristics (Jenkins and Veitch 1991) and wattle size.
2. The bird was banded with a metal band and three colour bands, size D, forming a unique combination.
3. Measurements of tarsus length, head to bill, wattle (length and width) and cloaca (length, width and angle) were recorded.
4. One or two feathers were taken to provide DNA for sexing.
5. A 0.1-0.2 ml blood sample was taken from the brachial vein directly into heparinised capillary tubes. One drop of blood was fixed as a thin blood smear by immersing in 99% methanol for approximately 30 s. The remainder of the blood was added to vials containing a lysis buffer for molecular diagnosis of blood parasites using the polymerase chain reaction (PCR).
6. A cloacal swab was taken to test for bacterial infection.

The first 10 birds caught were assigned to Group 1 and held in the first aviary. The next 10 birds caught were assigned to Group 2 and held in the second aviary. All 20 birds were caught by the end of the second day. Faecal samples were collected from the holding aviary of each group 3 days after the first birds were captured. Samples from each aviary were pooled and analysed for coccidia. Further pooled faecal samples were taken from each aviary at Bushy Park at the conclusion of the quarantine period to assess the long-term effectiveness of Baycox treatment on coccidia levels.

The next morning, between 09:30-11:30, all birds were caught with a hand net, offered a drink of jam water, and placed into cardboard transfer boxes (Plate 2.2, 2.3). Each transfer box contained invertebrates, sultana cake and fruit and held two birds. Each bird in Group 1 was dosed with Sporanox before being placed in a transfer box to ensure it received its dose for that day. Birds were then transferred from Mokoia Island to Rotorua by a short boat ride. Upon reaching the mainland at approximately 12:30, the birds were loaded into cars and driven to Wanganui. This trip took 4-5 h and we stopped after 2 h travel for a 20 minute rest period during which water and jam-water were placed inside each box to prevent dehydration of the birds. On arrival at Wanganui (18:30 h) the birds were placed in a dark room for the night. Fresh food, jam-water and

water were added to each box. The following morning, the birds were driven to Bushy Park, and walked for 10 minutes into the reserve to the holding aviaries. The birds were released into two separate aviaries (3.5 x 9m x 5m) (Groups 1 and 2 kept separate). All birds appeared to have travelled well and no injuries were sustained.

Catching and transfer methods on the second trip were the same as for the first trip. Once again, the 20 birds were divided into two groups (3 and 4) where Group 3 was treated with Baycox and Sporonox solution and kept separate from Group 4. All birds were caught by the end of the second day and sustained no injuries on transfer to Bushy Park. Pooled faecal samples were taken from each aviary 3 days after the first birds were captured and analysed for coccidia.

While in the Bushy Park aviaries, the birds were fed a captive diet supplemented with fresh vegetation, rotting logs, leaf litter, and fruiting branches of *Coprosma* spp. and five-finger (*Pseudopanax arboreus*) added every other day.

2.2.5. Disease screening

All 40 birds were screened for a set of pathogens (Table 2.1) that were thought to pose the highest disease risk during the translocation. The pathogens tested for were representative of a typical disease-screening regime during a bird translocation in New Zealand. Samples were tested at Massey University, Palmerston North (Endoparasites and enteric bacteria), and Landcare Research, Dunedin (Haemoparasites).

Plate 2.2. Outside of Saddleback transfer box showing large ventilation windows covered with windbreak.

Plate 2.3 Inside of Saddleback transfer box showing perch, three food dishes and rubber grip mat on floor.

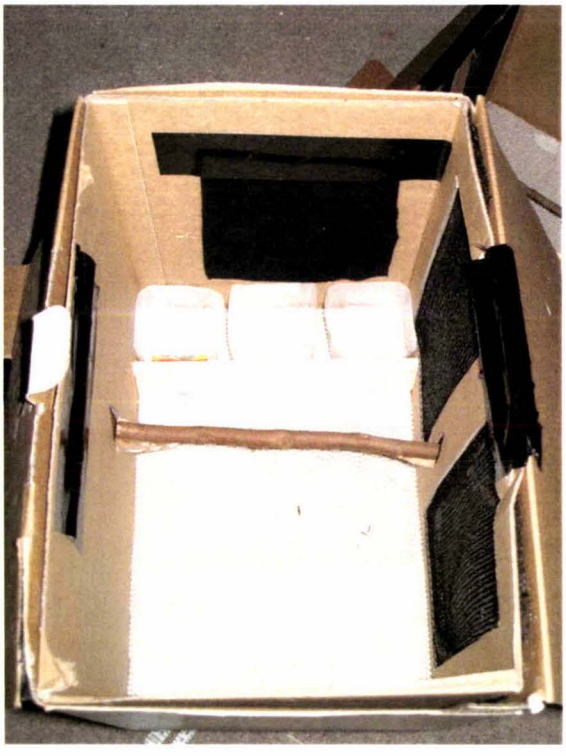

Table 2.1. List of pathogens screened for in saddlebacks transferred to Bushy Park. CBC = Complete Blood Count, WBC = White Blood Count, PCR = Polymerase Chain Reaction. * indicates pathogens nominated as requiring a change in the experimental treatments and release protocol.

Disease	Screening Method	Action if positive
Haemoparasites*	Blood smear, CBC, PCR	Reject as source depending on organisms (e.g. avian malaria – reject).
Endoparasites	Faecal sample, pool together	None
Salmonella spp.*	Faecal culture	Reject as source or treat depending on species.
Yersinia spp.*	Faecal culture	Reject as source or treat depending on species.
Aspergillosis	Physical exam, WBC	Reject individual if overt clinical signs
Avian pox	Physical exam, WBC	Reject individual if overt clinical signs

2.2.6. Saddleback surveys

I collected survival data for the released birds by conducting searches of the park, fortnightly for the first four months, then monthly for the next seven months. The park was searched fairly evenly by walking 13 North to South rat trap lines through the reserve (Fig 2.1). Saddlebacks respond to loud noises and usually approach any noise or disturbance produced near them. I stopped at intervals of about 100 m and played recordings of North Island saddleback song or made loud noises such as breaking a rotten log to attract any saddlebacks that were close. If no saddlebacks were seen or heard within 4-5 minutes I continued walking. I attempted to locate and identify any bird that was seen or heard during these searches. I identified birds by their unique combinations of coloured leg bands and recorded their location, activities and any interactions with conspecifics. Each search took two days to complete.

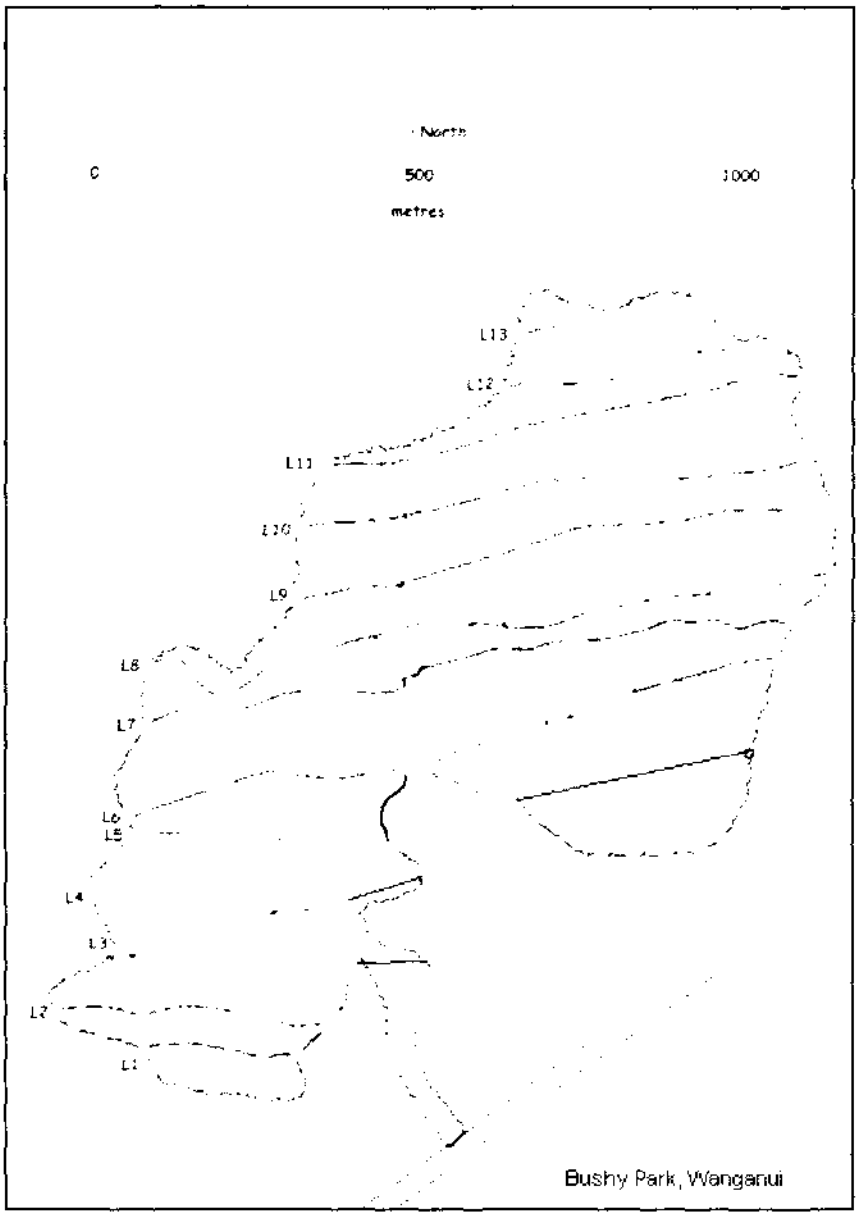

Figure 2.1. Map of Bushy Park showing the 13 tracking tunnel lines used when searching for saddlebacks.

2.2.7. Survival Analysis

I analysed saddleback survival in MARK (White & Burnham 1999; http://www.cnr.colostate.edu/~gwhite/mark/mark.htm). MARK is a comprehensive software application for the analysis of data from marked individuals. The data were analysed using the Cormack-Jolly-Seber (CJS) model for live recaptures (Lebreton *et al.* 1992, White & Burnham 1999).

The CJS model has several underlying assumptions: 1) every marked animal present in the population at time i has the same probability of recapture, p_i; 2) every marked animal in the population immediately after time i has the same probability of surviving to time i + 1; 3) marks are not lost or missed; 4) all samples are instantaneous, relative to the interval between occasions i and i+1; 5) each release is made immediately after the sample (White & Burnham 1999). MARK allows the time intervals between captures to be unequal and also allows assumptions (1) and (2) to be relaxed by creating groups of animals with various survival (Φ) and resighting (P) probabilities. The CJS model calculates separate survival and resighting rates for each interval, however MARK allows the model to be simplified by constraining parameters.

Encounter histories of a population of marked individuals are used by MARK to estimate survival and resighting rates. Animals are marked and released at time t_1 and are encountered when they are seen alive again (or captured) at times t_2, t_3, t_4....t_n. Encounter histories are coded as 1s if the animal is seen (captured) alive or 0s if the animal is not seen at each encounter occasion.

The encounter histories file for this analysis included eight fortnightly surveys followed by seven monthly surveys from the time of release (19 June 2006) which gave a total of 16 encounter occasions. I set the fortnightly surveys at time intervals of 0.5 and the monthly surveys at time intervals of 1 to give monthly survival probabilities. Survival was modelled using the logit link. This is the standard link function used to model survival data because it constrains probability to be between 0 and 1 (Armstrong & Cassey 2007). I initially coded the re-sighting data as two groups, male and female, without distinguishing between treatment groups. This allowed me to explore the data with a set of basic models that reflected hypotheses formed regarding factors affecting saddleback survival and resighting. I formulated a set of candidate models based on factors such as before and after breeding season (*b*), first month after release (*m*) and sex (*s*). MARK can fit models with interactions between particular effects e.g. (*m***s*) or without interaction e.g. (*s*+*m*).

I used $\{\Phi_{s+m} P_{s*b}\}$ (d.f. = 20) as the global, or starting, model for this set of data. This model assessed the separate effects of sex (*s*), and first month after release (*m*), on survival probability, and assessed the effect of an interaction between sex (*s*), and

before and after breeding season (*b*), on resighting probability. The global model (most parameterised model) must be tested to see if it fits the data adequately before attempting to produce simpler (reduced parameters) models. This is done by a Goodness of Fit (GOF) test which is an important consideration to ensure that the arrangement of the data meet the underlying CJS assumptions (see above) of the global model (Cooch & White 2006). When attempting to quantify the fit of the global model we measure the variance inflation factor, or c-hat. When c-hat = 1 the model fits the data but if c-hat $\neq$ 1 some degree of lack of fit is indicated. A new approach to GOF testing is the 'median c-hat goodness of fit' procedure. MARK performs a logistic regression analysis on a series of simulated c-hat values to estimate the c-hat value where the proportions of the deviance c-hats are equal (i.e. where the number above the observed value is equal to the number below the observed value). I performed a median c-hat test on the global model to test whether it adequately fit the data.

I then altered the design matrix of the global model to code survival and/or resighting parameters according to effects (*b*), (*m*) and (*s*) to create more parsimonious models. The design matrix is used to constrain parameter estimates in order to progressively simplify the model that is fitted to the data.

I assessed the information value of the models by comparing Akaike's Information Criterion (AICc) which is given by

$$-2\text{Log}(L) + 2K + 2K(K + 1)/(M - K - 1)$$

where L is the likelihood, K is the number of parameters estimated and M is the effective sample size. AICc model selection allows for the selection of the model with the least discrepancy between the unknown 'true model' and the approximated data-based model (Burnham *et al.* 1995). The most parsimonious model is that with the lowest AICc value. Likelihood Ratio Tests (LRT's) can also be used to test for statistically significant differences between models. However, this approach has several limitations and the general use of AICc for model selection is becoming increasingly popular (White & Burnham 1999). Models that have similar AICc values (ΔAICc<1-2) cannot be distinguished on statistical grounds (Burnham *et al.* 1995), and each should

be given consideration according to their Akaike weight (w_i), or relative support for the model. Akaike weights are calculated as

$$w_i = \exp(-\Delta AICc/2)/\sum\{\exp(-\Delta AICc/2)\}$$

I then adjusted the encounter histories file to recognize each treatment group and modelled the re-sighting data again. Because of the changes in experimental treatments, I was unable to compare survival between all four treatment groups. Instead, I combined treatment groups 3 and 4 into one group (referred to as Group 3) and coded the resighting data to recognize three treatment groups. I did not code the encounter histories to distinguish between sexes for this analysis because this would have reduced the sample size of each group even further. I began with the global model $\{\Phi_{g*m}\ P_b\}$ (d.f. = 20). This model assessed the effect of an interaction between treatment group and first month after release ($g*m$), on survival probability, and assessed the effect of before and after the breeding season (b), on resighting probability. I performed a median c-hat test and then progressively simplified the model, once again comparing AICc values to select the most parsimonious model. I created models testing the effects of group (g), before and after breeding season (b), first month after release (m) and a group effect for the first month after release only (gm), as well as interactions between effects e.g. ($g*m$).

2.3. RESULTS

2.3.1. Disease screening

Cultures from cloacal swabs showed no isolates of Yersinia, Salmonella or Campylobacter. One bird had a positive result for Citrobacter bacteria, a normal soil organism.

The only pooled faecal sample that showed no coccidia from capture to release was from Group 1 (Table 2.2). Group 2 had low levels of coccidia on Mokoia Island, but none was detected in the pooled faecal samples collected from their aviary at the end of the quarantine period. Although all birds in Group 3 were treated for coccidia on capture, there was still a low amount of coccidial oocysts found in their pooled sample

A (Table 2.2). Group 4 had the highest level of coccidiosis (91,500 coccidial oocysts/gm) on capture. Due to a *Plasmodium* spp being detected during the translocation we were unable to immediately release birds from groups 3 and 4 as originally planned. Instead, birds from these groups were housed together in one aviary for a quarantine period. Combined faecal samples from Groups 3 and 4 at the end of the quarantine period showed 4,350 coccidial oocysts/gm. This was an increase in levels for Groups 3 but a decrease of original levels for Group 4. Tapeworm and mite eggs were present in all pooled faecal samples (Table 2.2).

Table 2.2. Presence of parasite eggs and coccidial oocysts in transferred saddleback. Groups 1 and 3 were orally treated with Baycox on capture. Groups 2 and 4 had no treatment. Pooled faecal samples were collected from holding aviaries on Mokoia Island 1-3 days after capture (Sample A) and from quarantine aviaries at Bushy Park on the day of release (Sample B). Faecal sample B from groups 3 and 4 were combined because birds from these groups were housed together in one aviary for a quarantine period rather than being immediately released due to *Plasmodium* spp being detected during the translocation.

Group	Coccidial oocysts/gm		Tapeworm and Mite eggs	
	Sample A	Sample B	Sample A	Sample B
1	0	0	Yes	Yes
2	675	0	Yes	Yes
3	861	4,350	Yes	Yes
4	91500		Yes	

No haemoparasites were detected in any of the blood films, however, one bird returned a positive PCR result for a *Plasmodium* spp and three birds returned a 'weak positive' PCR result for the same parasite. The Plasmodium was of unknown strain, although it was not *Plasmodium relictum*. All four birds were transferred to Auckland Zoo quarantine facilities by airfreight in late June 2006 for more extensive sampling and monitoring. Three repeat PCR tests were performed on the three 'weak-positive' birds during the following four months and all results were negative for the *Plasmodium* spp. The fourth bird, an adult female, returned two more positive PCR results during July and August. At this time she also developed a swollen digit that did not respond to anti-inflammatory or antibiotic treatment. The digit was eventually amputated, after which the bird recovered quickly. Two more PCR tests in September and October returned negative results for this bird. None of the four birds displayed any clinical signs of the

Plasmodium spp. during quarantine at Auckland Zoo. They were air freighted back to Bushy Park in early December 2006 and released into the reserve. All four birds were known to be alive one year after release and the adult female who returned three positive PCR tests went on to successfully fledge two chicks during the first breeding season. The four birds initially sent to Auckland zoo were not included in the survival analysis.

2.3.2. Changes to experimental treatments

Because a *Plasmodium* spp was detected in four birds from the first transfer of saddlebacks we were unable to release Groups 3 and 4 immediately as originally planned in the experimental design (Table 2.3). Instead, we held all 20 birds from these groups in one aviary (7 m x 3 m x 2 m) adjacent to the aviaries containing Groups 1 and 2 and all 40 birds were held in captivity at Bushy Park for longer than originally intended. As the birds in groups 3 and 4 were held together in one smaller aviary, we treated all 20 birds for aspergillosis as a precaution against stress caused by possible overcrowding. Hence treatment with Sporonox was given to birds in Group 1, 3 and 4 (Table 2.3). The change in the experimental treatments resulted in confounding factors arising from different sized aviaries used to house birds, different quarantine lengths between groups and the housing of treated birds with non-treated birds (Group 3 treated with Baycox held with Group 4, no treatment) and hence comparison of survival between treatment groups must be treated with caution.

2.3.3. Survival from capture to release

Forty saddlebacks were caught during two catching trips to Mokoia Island. Of these, two adult males died in the Bushy Park aviaries due to hypothermia, and four birds, (2 adult males, 1 adult female and 1 juvenile female) were positive for a *Plasmodium* spp and therefore unable to be immediately released. This reduced the numbers in experimental treatment Groups 1, 2 and 3 to eight rather than the originally planned ten (Table 2.3).

Table 2.3. Original experimental design compared with actual experimental design as a result of a *Plasmodium* spp being detected during the translocation. * indicates the two groups of birds that were held together in one aviary.

Group 1		**Group 2**	
Original	*Actual*	*Original*	*Actual*
N = 10	N = 8	N = 10	N = 8
Sporonox & Baycox treatments	Sporonox & Baycox treatments	No treatment	No treatment
Quarantine 14 days	Quarantine 33 days	Quarantine 14 days	Quarantine 33 days
Group 3		**Group 4**	
Original	*Actual**	*Original*	*Actual**
N = 10	N = 8	N = 10	N = 10
Sporonox & Baycox treatments	Sporonox & Baycox treatments	No treatment	Sporonox treatment
Immediate release	Quarantine 18 days	Immediate release	Quarantine 18 days

2.3.4. Quarantine periods

Groups 1 and 2 spent a total of 33 days in quarantine at Bushy Park, while Groups 3 and 4 spent a total of 18 days in quarantine at Bushy Park (Table 2.3). This length of time was due to a combination of waiting for permission to release the birds after the detection of a *Plasmodium* spp, and then waiting for a window of fine weather during which to release the birds. This was thought important, as the weather at the time was generally heavy rain and extremely cold temperatures, and conditions were not ideal for a release. Thirty-four saddlebacks (12 females and 22 males) were released at Bushy Park on 19 June 2006 between 08:00 and 13:00 at a central site within the reserve. The remaining four birds were released on 7 December 2006.

2.3.5. Recovery of dead birds

Only one body was recovered after release, a sub adult male found on 3 August 2006. A post-mortem examination diagnosed a trauma to the head but the body was too decomposed to determine if predation had occurred. This bird was not seen alive

between the time of release and recovery of its body so I treated this individual as alive on release and undetected or dead on subsequent surveys.

2.3.6. Post release survival

The first set of models initially produced in MARK distinguished between sexes but not treatment groups. The global model for this set of data, $\{\Phi_{s+m}\ P_{s*b}\}$ (d.f. = 20), had a median c-hat = 1.06 (SE = 0.01) indicating that it had a good overall fit to the data. Comparison of the models using AICc values identified $\{\Phi_{s*m}\ P_b\}$ as the best model in the set, although the model $\{\Phi_{s*m}\ P_{s+b}\}$ also had support (ΔAICc = 0.12). $\{\Phi_{s*m}\}$ estimated lower survival rates for females (0.69) than males (0.91), during the first month after release. Subsequent monthly survival was higher for both males (0.96) and females (0.99). The resighting model $\{P_b\}$ revealed differences between resighting probabilities before and after the breeding season. In this model resighting probability was constrained for both sexes and was estimated at 0.41 in the period before the breeding season and increased to 0.86 during the breeding season. The resighting model $\{P_{s+b}\}$ estimated resighting probability to be lower during the period before the breeding season (0.35 and 0.44 for females and males respectively) than during the breeding season (0.84 and 0.88 for females and males respectively).

The global model for treatment group survival, $\{\Phi_{g*m}\ P_b\}$ (d.f. = 20), had a good fit to the data (median c-hat = 1.04, SE = 0.01). The resighting model remained as $\{P_b\}$ in all additional models. Comparison of group models (Table 2.4) showed that $\{\Phi_m P_b\}$ best explained the data as it had the lowest AICc value and approximately twice the support of the next best model. This model estimated survival probability for all groups to be 0.79 during the first month after release and 0.94 during subsequent months. However, the model $\{\Phi_{g+m}\ P_b\}$ also had some support (ΔAICc<2), indicating that it is unclear whether there was a group effect on survival in addition to an effect of first month after release. The remaining models had less support with ΔAICc>2 although they should still be given consideration based on their Akaike weights (w_i).

Table 2.4. A series of models for factors affecting saddleback survival. Factors considered were treatment group (*g*), first month after release (*m*), group effect for the first month after release only (*gm*), with interaction (*) or without (+). The re-sighting model was $\{P_{b}\}$ in all cases, reflecting a difference in re-sighting probability before and after the breeding season. AICc is the criterion on which models were selected, the lowest value indicating the most parsimonious model. ΔAICc is the difference in AICc between the best model and the current model. w_i is the AIC weight, indicating the relative support for the model. *K* is the number of parameters in the model.

Model	AICc	ΔAICc	w_i	*K*
Φ_{m}	499.89	0.00	0.47	4
Φ_{g+m}	501.32	1.44	0.23	6
Φ_{gm+m}	502.60	2.72	0.12	6
Φ_{g}	502.94	3.05	0.10	5

Under the global model $\{\Phi_{g*m}\ P_{b}\}$, estimated survival during the first month after release was similar for Group 1 (0.88) and Group 3 (0.86), while Group 2 had a lower survival (0.65) (Table 2.5). Estimated survival for subsequent months was similar between all groups.

Table 2.5. Estimated monthly survival probabilities with 95% confidence intervals for each treatment group under the global model $\{\Phi_{g*m}P_{b}\}$.

	Survival probability during 1st month after release	Subsequent monthly survival probability
Group 1	0.88 (0.44, 0.98)	0.98 (0.89, 1.00)
Group 2	0.65 (0.29, 0.89)	0.97 (0.82, 0.99)
Group 3	0.86 (0.57, 0.97)	0.92 (0.86, 0.96)

2.4. DISCUSSION

The translocation of the North Island saddleback from Mokoia Island to Bushy Park presented an opportunity to experimentally test the effects of quarantine and prophylactic disease treatment on the outcome of a translocation. The motivation for this experiment arose due to the growing trend of costly and complicated disease screening procedures routinely being enforced during translocations. The detection of a

Plasmodium in four captured saddlebacks caused confounding factors in my experimental design and subsequently only limited conclusions about the effect of disease screening could be drawn. Interestingly, while being unable to complete my experiment as originally planned, the resulting situation served to highlight some of the precise concerns about today's disease-screening process that led the experiment to be devised in the first place. Difficulties in identifying which diseases were of concern, inaccurate diagnostic tests, increased cost and labour, mortality during captivity and poor post release survival were just some of the obstacles that arose following the required disease screening of the saddlebacks translocated to Bushy Park.

2.4.1. Survival from capture to release

All saddlebacks survived the capture on Mokoia Island and translocation to Bushy Park. The boxes used in transfer (Plate 2.2 and 2.3) were our own design with features drawn from several types of transfer boxes. They worked well, and no injuries were sustained in transit. A previous translocation of saddlebacks from Cuvier Island to Boundary Stream Mainland Island (BSMI) resulted in the deaths of three birds in transit (Sullivan 2004). One bird injured its beak on the wire mesh of a wooden transfer box and subsequently died and an additional two birds died from suspected heat stress due to lack of ventilation while being transferred in modified cardboard cat travel boxes. We were able to prevent mortalities by putting only two birds in each box, having adequate ventilation to prevent heat stress and having the boxes composed entirely of cardboard and windbreak to eliminate wire injuries. The cardboard construction also made them light and one person easily carried two boxes, but they may not have been sturdy enough had we used air travel.

Two birds died during the long quarantine period at Bushy Park. This can almost certainly be attributed to poor aviary design, in particular the lack of adequate shelter for all 20 birds during extremely wet and cold weather conditions. Both birds were from Groups 3 and 4 that were held together in a small aviary that was erected at short notice. This unanticipated situation arose from the detection of the *Plasmodium* in four birds. All birds in Groups 1 and 2 survived these harsh weather conditions as they were housed in large aviaries prepared well ahead of the transfer with roost boxes and extra vegetation for shelter. The death of these two saddlebacks highlights the need for all

translocations that undergo a disease screening programme to have a contingency plan in place that can supply extra funding and captive management expertise for situations where quarantine periods need to be extended, additional birds need to be quarantined or where the translocation needs to be postponed.

Although the quarantining of birds during a translocation is now routinely enforced, past research has shown that 'immediate release' birds may have better survival after release than 'delayed release' birds. During a translocation of hihi to Kapiti Island, Castro *et al.* (1994) found that birds released immediately had a higher survival rate than delayed release birds. However, in this study the delayed release birds were released after the immediate release birds, making it difficult to separate the effects of captivity from the advantages of being released first and becoming established in preferred habitat. Nevertheless, Lovegrove and Veitch (1994) recommend that wild caught birds should be released immediately, and argue that a 'delayed release' is not only costly, but probably stressful on birds and increases the risk of injury or disease. Reed and Stockdale (1994) note that factors encouraging avian disease are most applicable to captive birds through overcrowding, poor nutrition and inappropriate social conditions, all of which cause stress and aid the transmission of pathogens. For instance, injured or sick African penguins (*Spheniscus demersus*) brought into rehabilitation centers in South Africa are prone to acquiring diseases in captivity. These diseases may then be transferred back into the wild once the penguins are released, and can have considerable effects on wild populations (Brossy *et al.* 1999). A captive population of New Zealand dotterels destined for release underwent pre-release disease screening that revealed infections of both avian pox and a *Plasmodium*. Investigation into the health of wild dotterels revealed that neither of these diseases were present in wild populations and it was thought too risky to release the infected captive birds. It was noted that the concentration of birds in the aviaries may have made them more susceptible to disease (Jakob-Hoff 2000b), highlighting the potential risks of captivity.

Further investigation into the risks associated with a quarantine period is essential now that disease management is a compulsory part of translocations in New Zealand. It may be that a process intended to minimise disease risk is inadvertently increasing it instead.

2.4.2. Saddlebacks infected with a *Plasmodium*

As a result of the disease-screening programme undertaken during the translocation, a *Plasmodium* was detected in four saddlebacks. The *Plasmodium* was found through molecular diagnosis by PCR, which magnifies DNA from the parasite. This test has a high sensitivity for *Plasmodium* blood parasites (Fallon *et al.* 2003) and is a far more reliable method than traditional microscopy (Richard *et al.* 2002). No blood parasites were detected in the individual blood smears taken during the translocation, indicating that the level of infection was probably low (Richard *et al.* 2002, Castro & Howe 2007). This demonstrates the importance of using appropriate diagnostic tests for a disease-screening programme to be effective; had the PCR test not been included in the disease screening, the *Plasmodium* would not have been detected.

Further investigation into the *Plasmodium* on Mokoia Island suggests that the strain is native, and if so, may have a history of co-evolution with saddlebacks (Castro & Howe 2007), a theory that is supported by the low level of infection shown in the infected birds and the presence of native mosquito species which are known to feed on birds' blood. In fact, none of the affected birds showed any clinical signs of the disease and one female went on to fledge two chicks during the first breeding season despite being released late in the season, indicating that the *Plasmodium* infection was chronic rather than acute. This raises the question of whether the parasite should be actively transferred with the birds. Windsor (1995) advocates 'equal rights for parasites' and argues that conservation of parasite species should be equally important if our aim is to preserve biological diversity. At the very least, having a better understanding of this parasite may enable future translocations of saddlebacks from Mokoia Island to proceed in the knowledge that this specific strain of *Plasmodium* does not pose a high threat to the founder population or release site and further, that this particular host-parasite bond will be preserved!

The fact that this particular strain of *Plasmodium* does not cause high mortalities does not mean, however, that saddlebacks will be resistant to other species of *Plasmodium* (Castro & Howe 2007), of which there are many (Bensch *et al.* 2004). For instance, a *Plasmodium* infection in South Island saddlebacks on Long Island caused high mortalities (M.R. Alley pers comm.), indicating that the birds had low immunity to that

particular strain of *Plasmodium*. The effects of the outbreak may have been further magnified by the reduced genetic diversity within the saddleback population. A recent study by Hale & Briskie (2007) suggests that species that have undergone severe bottlenecks, such as the South Island saddleback have reduced immune function and may therefore be more susceptible to disease outbreaks.

Discovery of the *Plasmodium* highlighted our lack of knowledge on the presence of disease in saddlebacks and some important information was gained. However, it threatened the success of the translocation by increasing costs and compromising the birds' welfare with unnecessarily long quarantine periods because no plan was in place for how, or if, the translocation should proceed. If complex disease screening programmes are enforced during translocations then it is crucial that clear guidelines exist for how to continue should a new or unexpected disease be detected. In cases where known virulent organisms, such as virulent strains of *Salmonella* or *Plasmodium relictum* are detected, the appropriate steps are clear and postponement of the translocation would be justified. However, where a previously un-encountered organism is detected, the threat will be unknown and the plan of action less obvious. These are the situations that have the potential to jeopardise the outcome of a translocation because current guidelines are at best vague, resulting in extended quarantine periods while a solution is found.

2.4.3. Survival between treatment groups and the effect of prophylactic disease treatment

Initial pooled faecal samples of Groups 1 and 3 (treated with Baycox) showed little or no coccidial oocysts/gm, suggesting that treatment for coccidiosis is effective at immediately reducing coccidial oocysts (Table 2.2). However, it is difficult to say whether a one off Baycox treatment is effective or even necessary over a longer time frame such as a quarantine period, because both treated and untreated samples indicated a decrease in coccidiosis over time (Table 2.2). These results suggest that coccidiosis was not an infection of concern during the quarantine period and there was no real advantage in giving birds a one off dose of Baycox. It is possible though that the pooled faecal samples were not indicative of true levels of coccidial oocysts present in each aviary, as oocysts are not shed continuously. Pooling multiple faecal samples is more

practical than taking individual samples from each bird but may not give an accurate indication of an individual bird's parasite load (Matthews *et al.* 2006). Rather than treating each bird for coccidiosis on capture, a better strategy may be to monitor levels of coccidial oocysts throughout the quarantine period with numerous and repeated faecal samples and only treat with Baycox if levels become unacceptably high. Due to the contagious nature of coccidiosis, all birds in an aviary need to be dosed for the treatment to be effective. The age composition of the quarantined birds should also be considered when deciding whether to treat for coccidiosis, as high levels are generally associated with juvenile birds in captive situations (Jakob-Hoff 2001). This has caused mortalities in some endemic bird species including juvenile kiwi (Clemance 1995) and juvenile hihi (Cork *et al.* 1999). However, low levels of coccidiosis are common and harmless in most bird species (Jakob-Hoff 2001).

Sporonox oral solution was administered by calculating the dose for the whole group of birds and then adding it to several dishes of jam water throughout the aviaries. Some birds drank noticeably more treated jam water than others and the jam water was never finished completely, making it unlikely that each bird was getting the correct dose of Sporonox. Although this method of treatment was inaccurate, the option of catching each bird daily to dose with Sporonox would have been unacceptably stressful on the birds.

Because recovery of dead birds was low, the separate effects of treating for coccidiosis and aspergillosis could not be isolated. However survival probability under the global model $\{\Phi_{g*m} P_b\}$, was lowest for Group 2 (no prophylactic treatment) during the first month after release (Table 2.5). This suggests that treating birds with Baycox and/or Sporonox may result in higher survival during the period immediately after release. However it is difficult to be certain due to the confounding factors that arose between treatment groups.

Previous studies have shown that post translocation survival is often lower than long term survival rates (Slough 1989, Raeburn 2001) and although the factors influencing translocation success are not well understood, the stress of a translocation is thought to be an important contributing factor to the observed higher individual mortality immediately after release (Letty *et al.* 2000). Saddleback survival at Bushy Park was

lowest during the first month after release for all treatment groups under the global model $\{\Phi_{g*m} P_b\}$ (Table 2.5), however there were no 'immediate release' birds so it is uncertain to what extent the experimental treatments contributed to the low survival compared to other factors such as the general stress of the translocation during the first month. The best survival model, $\{\Phi_m\}$, estimated a survival probability for all groups of 0.79 during the first month. The survival of 40 North Island saddlebacks translocated from Cuvier Island to BSMI in 2004 that also underwent a complex disease screening and quarantine process was just 57% six weeks after release (Sullivan 2006). However, this particularly low survival rate may also have been due to predation from mammalian predators (Sullivan 2006) so the extent to which the disease screening programme affected survival is once again difficult to estimate.

Given the apparent decrease in coccidiosis levels in all groups over time, aspergillosis may have had the greater effect on survival. Aspergillosis is considered to be an opportunistic pathogen (Cork *et al.* 1999) that has caused mortalities in many New Zealand birds (Alley 2002), including the North Island saddleback (Sullivan 2004). The saddleback translocation to BSMI resulted in the deaths of at least two birds from aspergillosis following release after a nine day quarantine period (Sullivan 2004). The prognosis for infected birds is poor and prevention is the best way to control the disease (Joseph 2000). Minimisation of predisposing immunosuppressive factors, such as stress, is essential during translocations, and Sporonox treatment should be given during any captive period as a precaution to reduce the risk of unnecessary mortalities.

Longer term monitoring of the saddlebacks at Bushy Park showed that of the 38 birds released (including the four malaria birds) only nine females and twelve males survived for the first year (refer to Chapter 3), giving a survival rate of 55%. In previous translocations of North Island saddlebacks to sites with no mammalian predators and a very short holding period (2 - 4 days), the percentage of birds surviving the first year after release is often much higher than this. For example, translocation to Tiritiri Matangi Island resulted in 79% survival, translocation to Mokoia Island had 81% survival and translocation to Motuihe Island had 70% survival (Armstrong 1999). It is possible that the extended quarantine period that the Bushy Park saddlebacks endured contributed to this particularly low post release survival, however the above survival rates for other populations do not distinguish between the mortality immediately after

release versus longer term mortality when factors other than those associated with a translocation are likely to affect individual survival, so it is impossible to know how much mortality is attributable to the translocation process. Monitoring the pattern of post-release survival of individual birds is essential for gaining specific information on mortality associated with translocation. Translocation methods can then be refined in order to reduce their effects on post-release survival.

2.4.4. Avian disease in New Zealand

Although the extent to which disease contributes to the extinction of species is largely unknown, there is little conclusive evidence to implicate disease as the single causal factor of the extinction of a species (Smith *et al.* 2006). Of the 833 recorded species extinctions in the past 500 years worldwide, disease has been implicated in just 3.7% of cases (Smith *et al.* 2006). Similarly in New Zealand, while disease has been linked to the decline of some species (Falla *et al.* 1979 for weka; Craig & Douglas 1984 for bellbirds) there is little direct evidence in most cases. A study of 456 autopsies in both captive and wild New Zealand birds concluded that infectious disease outbreaks are uncommon (Johnstone & Cork 1993) and most outbreaks of disease are the result of poor captive management, which supports the expression of opportunistic pathogens (Johnstone & Cork 1993, Reed & Stockdale 1994). Despite this lack of evidence for disease driven extinctions, there is growing international concern that rates of disease emergence in wildlife populations are increasing (Lounibos 2002), and that failure to address disease issues is hindering our ability to secure the distribution and abundance of threatened species (Friend *et al.* 2001). Supporters of this view argue that little evidence for disease driven extinctions exists because of our limited knowledge on wildlife diseases, and failure in the past to investigate reasons for the decline of wildlife populations, particularly translocated ones (Griffith *et al.* 1993).

Diseases of concern in wild populations of New Zealand birds include aspergillosis, avian malaria, avian pox, coccidiosis and *Salmonella* (Alley 2002, Tompkins & Gleeson 2006), and while outbreaks are rare there are some noteworthy examples. In 2006 a *Salmonella* outbreak in hihi was documented on Tiri Tiri Matangi Island. This outbreak was thought to have occurred from human contamination and resulted in a planned translocation of the birds being postponed (Ewen *et al.* 2007).

Although disease screening is now a compulsory part of most New Zealand translocations there are no published reports of disease threatening a population as a result of a 'wild to wild' translocation. In a review of translocations in Australia, Canada, New Zealand and the USA between 1973-1986, Griffith *et al.* (1993) noted their surprise that 'disease-caused translocation failure' was not more common. They do point out, however, that many of these cases may go undetected due to a lack of detailed post-release monitoring. Despite very little disease screening occurring during saddleback translocations in the past, a literature search on North and South Island saddleback translocations found no documented cases of disease threatening the success of a translocation. Primary reasons for failure have been attributed to too few birds being released (Lovegrove 1996) and introduced mammalian predators present at the release site (Lovegrove 1996, Taylor *et al.* 2005)

2.4.5. Challenges of effectively disease screening animals during translocation

Including an effective disease screening programme in a translocation can minimize the potential impacts of disease on wild populations at a release site (Griffith *et al.* 1993, Viggers *et al.* 1993, Reed & Stockdale 1994, Jakob-Hoff 2000b). However, it is a complex process and its effectiveness is limited by the current gaps in our knowledge of wildlife diseases. The value of screening for, and eliminating specific disease, is dependent on the prevalence and importance of the disease at both the source and release sites (Viggers *et al.* 1993). Both world wide and in New Zealand, we know little about diseases of native fauna or their current and historical incidence in wild populations (Jakob-Hoff 2000a, Matthews *et al.* 2006). This lack of knowledge makes it difficult to identify which diseases are of concern during a translocation, which in turn makes it hard to devise an effective disease screening programme (Matthews *et al.* 2006). The fact that there is little agreement on the protocols that disease screening should follow (Matthews *et al.* 2006) reflects the challenges that disease screening pose.

A further limitation to an effective disease-screening programme is the lack of sufficiently sensitive tests. The lack of such tests can result in a disease being incorrectly diagnosed (Reed & Stockdale 1994) or sub-clinical levels of disease being missed altogether (Viggers *et al.* 1993, Richard *et al.* 2002). Reed and Stockdale (1994) cite an example where *Chlamydia* testing of faecal samples from 121 native New

Zealand birds resulted in up to 75% false positives. This was due to the lack of specificity in the test used.

Lack of knowledge about wildlife diseases also makes establishing an effective length of quarantine difficult. In New Zealand, a preferred length is 30 days but for logistics and considerations of animal welfare while in captivity, a common length for birds to be quarantined prior to release is two weeks (K. McInnes pers. com). During the quarantine period observations are made for the development of symptoms of disease and then treated where necessary (Viggers *et al.* 1993). Consequently, any disease with an incubation period longer than the commonly used two week period may not be detected, making the process of quarantine less effective.

Finally, the logistics, cost and expertise required to carry out a successful disease screening programme are considerable and often beyond the means of many of the increasing number of community groups who are involved in translocations of threatened species to mainland sanctuaries.

Given these obstacles and the lack of direct evidence of disease caused translocation failure, the potential benefits of disease screening and quarantining animals during translocation must be weighed against the cost it may have on the outcome of a translocation. The translocation of 40 North Island saddlebacks from Cuvier Island to BSMI in 1994 illustrates some of the complications that may arise during a typical disease screening programme. *Salmonella* was falsely diagnosed in eight saddlebacks, leading to all 40 birds being transferred from Cuvier Island to Auckland Zoo for an additional nine days in quarantine, before being transferred and released at BSMI. This added a cost of approximately $9000 to the translocation budget due to additional disease screening, food, transport and labour costs (Sullivan 2004). At least five birds died from injury or stress related disease during transfer and immediately after release, and most birds disappeared soon after release (Sullivan 2004) indicating that the low post release survival could be attributed to effects of the translocation.

The translocation of 40 saddlebacks to Bushy Park, Wanganui, resulted in a quarantine period of 33 days for half the birds and 18 days for the remaining birds, additional aviaries to be built and four birds to be transported from Wanganui to Auckland return.

The associated cost for the extra building materials, saddleback food and transport is estimated at around $3000 and two birds died during quarantine. Furthermore, the four birds that initially tested positive for the *Plasmodium* spp. were eventually released into the park anyway, and three out of four went on to successfully breed during the second breeding season (K. Brider pers. comm.), indicating that the birds were in good health over the longer term.

2.4.6. Alternative methods for regulating disease risk

The difficulties associated with effectively disease screening wild animals during a translocation warrant the investigation of alternative methods to regulate disease risk. Regular and long-term health screening of source populations that are targeted for translocations would produce valuable baseline data on the normal health parameters of the population, helping to identify diseases of concern. Our current lack of knowledge on wildlife health is widely acknowledged amongst conservation biologists and veterinarians (e.g. May 1988, Deem *et al.* 2001, Jakob-Hoff 2000a, Alley 2002) and the idea of collecting baseline health data for threatened species has been put forward numerous times (e.g. Reed & Stockdale 1994, Boardman 1998, Deem *et al.* 2001, Matthews *et al.* 2006). The Department of Conservation has produced a document to complement the workbook 'Developing Quarantine and Health Protocols for Animal Movements' titled 'Guidelines for the Collection of Baseline Health Data in Wild Populations of Native Fauna'. This document provides conservation workers with guidelines on the planning and collection of baseline information for threatened species, and data for some species including kiwi, kakapo and takahe are now actively being collected by the Department of Conservation (Jakob-Hoff 2000a). If a population was regularly monitored, translocations could then take place without requiring extensive disease screening and quarantine periods, provided the population was deemed 'healthy' at that time. Besides contributing much needed information on the normal health parameters of species, this would decrease the cost and logistical complications of translocations and lower the incidence of stress related diseases and injury by allowing the immediate release of translocated individuals.

Little attention is given to the risk that diseases at a release site may pose to a translocated population, although its effects may be just as great if an animal with no

previous exposure to a pathogen is transferred into a site that contains infected individuals (Reed & Stockdale 1994). Given that most translocations in New Zealand involve threatened species (Saunders 1995), and that translocations are generally carried out in an effort to increase the abundance and distribution of that species (Griffith *et al.* 1989), perhaps the emphasis should be placed on investigating the disease risk at release sites rather than source populations. One case where disease at a release site was implicated in the failure of a translocation in New Zealand was the high incidence of aspergillosis in a translocated population of hihi on Mokoia Island. The birds suffered high mortality rates and the population was eventually removed from the island in 2002 (Armstrong e*t al.* 2007). Hihi appear to be particularly susceptible to infection from aspergillosis, possibly due to a stressful mating system that involves frequent forced copulation attempts (Alley *et al.* 1999) and the sequestration of carotenoids for the bright colours in the plumage of this sexually selected species (Ewen *et al.* 2006). However, comparison of Aspergillus fumigatus spore densities among sites suggests that the low survival on Mokoia could be associated with a particularly high prevalence of aspergillosis on the island. Several large predator-free sanctuaries now exist on New Zealand's mainland, including Karori Sanctuary, Maungatautari, Tawharanui Regional Park and Bushy Park. Many of these sanctuaries have long term objectives to translocate numerous threatened bird species. It may be valuable to carry out health monitoring of existing populations at these sites to gain insight into the occurrence of diseases at the release site and to aid decisions on which future species may be at risk from these diseases.

This approach of monitoring key source and release site populations to gain baseline health data may be limited by cost, time and expertise required to carry out the necessary research. However, it would allow us to gain a clearer picture of diseases of New Zealand wildlife at a time when the movement of threatened species is increasing (Reed & Stockdale 1994, Seddon *et al.* 2007) and the need for a clearer understanding of disease issues is more important than ever.

If the current disease screening requirements remain as they are, situations such as that experienced during the saddleback translocation to Bushy Park will continue to occur. It is therefore essential that we increase our knowledge of disease risk during translocations and the effects of a disease screening programme on the survival of

founder individuals. Applying an experimental approach to translocations to test these effects means we can then refine our approach to managing disease risks rather than use the 'guess- work' approach currently applied during translocations today. This will be important for the future if translocations are to remain a key tool in the conservation of our threatened species.

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3

Population Viability Analysis

3.1. INTRODUCTION

The primary aim of a translocation is to establish, re-establish or supplement a population of animals in the wild (Griffith *et al.* 1989) and the measure of a translocation's success is whether or not it results in a self-sustaining population. However, by nature, the outcome of a translocation is often uncertain and, despite their widespread use, reasons influencing their success or failure are not fully understood (Griffith *et al.* 1989, Armstrong & Mclean 1995). Careful post-release evaluation is an essential component of a translocation programme to gain the knowledge needed to improve translocation success (Seddon *et al.* 2007).

Population Viability Analysis (PVA) is a process that uses computer modelling to predict the likelihood that a population will become extinct within a specified time frame (Boyce 1992), and provides a framework for assessing the long-term outcome of a translocation. The use of PVA requires estimates of demographic and life history parameters for a species and can also incorporate the impact and frequency of catastrophes, and various environmental and genetic factors that may significantly affect the viability of a population (Possingham *et al.* 1993).

Translocations are often associated with small founder populations, particularly if there is a phase of high post-release mortality, leading to additional threats to population

persistence. Threats to small populations are often random or stochastic events and can be categorised into demographic, environmental and genetic stochasticity (Shaffer 1981). PVA can represent the dynamics of small populations by incorporating this risk of stochastic decline into the population model (Lacy 2000). Because random events can have a significant effect on the extinction probabilities of small populations, they are often the focus of PVA's (Boyce 1992) and it is now generally accepted that stochastic models are required to simulate the dynamics of natural populations (Burgman *et al.* 1993). PVA facilitates the development of management strategies and recovery plans, and guides research programs for threatened species (Lindenmayer *et al.* 1993) by highlighting parameters that have the most significant effect on population viability (Possingham *et al.* 1993). For these reasons, Seddon *et al.* (2007) recommend that some form of population modelling should be included in every translocation.

Perhaps the most important use of PVA is to assess the effect of alternative management options on a population's viability (Possingham *et al.* 1993, Seddon *et al.* 2007), allowing threatened species management to concentrate on the most effective options. This particular use of PVA is an adaptive management approach to species recovery (Boyce 1992, Possingham *et al.* 1993, Seddon *et al.* 2007) where systems are modelled and management policies are implemented as experiments in a 'learning while doing' manner (Walters 1997). The number of studies that use PVA as an adaptive management tool for re-introduced populations is increasing (Seddon *et al.* 2007), and several studies in New Zealand have applied this method to facilitate species recovery. Population modelling of a re-introduced North Island saddleback population was used to assess the long term effects of an aerial poison drop (Davidson & Armstrong 2002). It was shown that the population could not persist if subjected to repeated aerial poison drops. This information is highly applicable to the management of mainland saddleback populations because it highlights the need for consideration of alternative poison application techniques, such as permanent bait stations, where saddlebacks are present.

In this chapter I first discuss the breeding biology of the saddlebacks during the populations first breeding season at Bushy Park and compare it to the breeding biology of island populations, given the contrasting habitats between island and mainland sites. Recording accurate information on the breeding biology of threatened species is important for their conservation because fecundity has a large influence on recovery

(Hooson & Jamieson 2003). Additionally, reproductive data are a key requirement for PVA. I estimate survival and reproduction parameters using MARK and combine these into a stochastic PVA to model the saddleback population and explore its viability over the next five years. A number of factors specific to the Bushy Park translocation were identified as having the potential to affect the viability of the population. Firstly, the low post release survival of the saddlebacks after a prolonged quarantine period (refer to Chapter 2) may affect the longer term viability of the population by greatly reducing the size of the founder population. Secondly, differences between the habitat type at the release site (Bushy Park) and the source site (Mokoia Island) raised questions about the quality of the Bushy Park habitat for saddlebacks (refer to Chapter 4). It is possible that the mature forest habitat at Bushy Park may not be the most suitable for this species, which could lead to a lower density population than expected given population densities on islands of a similar size to Bushy Park. Thirdly, the degree to which the saddlebacks would disperse out of the park was unknown. If high rates of dispersal were experienced then the viability of the population may be compromised. The model developed in this chapter provides a framework for adaptive management of the population. The model can be updated based on new data collected under proscribed management strategies (related to the factors identified above), and population projections can then be used to evaluate alternative strategies.

3.2. METHODS

3.2.1. Saddleback monitoring

I surveyed the population from July 2006 to September 2007, approximately one year after their release (June 2006), to collect data on survival, reproduction and population size. I obtained adult survival and re-sighting data during 15 surveys from July 2006 to April 2006. Searches were initially carried out fortnightly for four months and then monthly for the remaining six months. I also conducted two additional surveys at the beginning of the second breeding season in September 2007 to estimate juvenile survival and re-sighting rates, and the total population size. Each survey took two days to complete, and birds were located by visiting known home ranges and by walking the network of tracks and tracking tunnel lines throughout the reserve (refer to Chapter 2 for a detailed description of survey techniques).

Reproduction data were collected during the first breeding season after release. Saddleback nests were located by checking nest boxes and other potential nest sites, by following the flight paths of parents transporting nest material or food back to nest sites, or by following the female back to the nest when she returned from feeding. If a female was observed continuously foraging for 30 minutes or more I concluded that the pair was not nesting. Once the nest was found, I recorded the contents of the nest, height of the nest rim from the ground, and a general description of the nest site including nest location (using a Garmin™ GPS 72). If the nest contained eggs I visited the site every 3-4 days to determine hatch date of nestlings. If the nest already contained nestlings I estimated age by size and plumage development. Once hatched, I did not visit the nest again until the chicks were ready to be banded between 12-20 days old. All chicks were weighed and banded with one metal and two color bands, size D, to form a unique combination. I defined 'number of fledglings' as the number that survived for a minimum of 10 days. This gave me a consistent measure for fledglings given that not all nests were found and it was difficult to detect fledglings until approximately 10 days of age. All chicks that survived for the first 10 days were easily detected, and none disappeared between 10 days and four weeks, at which time they were starting to become independent from their parents. A fledgling was deemed to be 10 days or older based on appearance such as plumage development and growth of tail. I visited each pair every 10 days and determined the number of fledglings by following parent saddlebacks for a maximum of 60 minutes. If no fledglings were detected after this time period I concluded that the pair had no dependent fledglings.

3.2.2. Survival analysis

Survival was analysed in MARK (White & Burnham 1999; http://www.cnr.colostate.edu/~gwhite/mark/mark.htm). Separate survival analyses were conducted for adults and juveniles, where a bird was considered a juvenile from the time of fledging to the start of its first breeding season (approximately 9 months). This age structure was added firstly because sexes of juveniles were not known and could not be included in the sex-specific adult survival models, and secondly because survival of juvenile saddlebacks may be lower than adult survival (Armstrong *et al.* 2005).

The encounter history file consisted of 16 encounter occasions beginning with the survey one month after release. Survival probability immediately after release may be lower due to the effects of the translocation (refer to Chapter 2), so the first two fortnightly surveys were not included in this analysis. Time intervals between surveys were entered as numbers of months, producing monthly survival probabilities. Survival data for the four saddleback positive for the *Plasmodium* were included in this analysis. I coded their encounter histories as '0' up until the point that they were released into the reserve in December 2006. The January 2007 survey was then coded as '1' for these birds to mark their entry into the population. The resighting data were treated as 'recaptures only' by MARK and was coded as two groups, male and female. I considered adult survival according to sex (s), time (t) and before and after breeding season (b). The global model $\{\Phi_s P_b\}$ (d.f. = 25) was tested for its fit to the data with a median c-hat test. This model assessed the effect of sex (s) on survival probability and the effect of before and after breeding season (b) on resighting probability and was based on information from the survival models developed in Chapter 2. I then altered the design matrix of the global model and sought more parsimonious models. The information value of these models was assessed by comparing Akaike's Information Criterion (AICc) and the best model was selected.

The encounter history file for juveniles consisted of three encounter occasions, the first occasion when they were detected as fledglings and the remaining two occasions representing the two September 2007 surveys. Rather than using separate fledgling dates for each juvenile I considered all detected juveniles to enter the population in January 2007, which was the average time of fledging. I set the first time interval at 1 to get the probability of a juvenile surviving to the breeding season. The second time interval was arbitrarily set at 0.5. The resighting data were treated as 'recaptures only' by MARK and modelled using the logit-link function. I began with the model $\{\Phi_t P_t\}$ (d.f. = 1) and tested its fit to the data with a median c-hat test. This model allowed both survival and resighting estimates to vary over time, denoted by (t). I then altered the design matrix to compare alternative models for describing juvenile survival. I only considered survival models that allowed survival to vary between time intervals, (Φ_t), as the relative lengths of the two time intervals were arbitrary due to the number of months varying for each juvenile. The best model was selected by comparing AICc values.

3.2.3. Population Model

An age structured population model with discrete time steps was constructed by D.P. Armstrong for the Bushy Park saddlebacks in a Microsoft Excel spreadsheet (White 2000), and was used to predict population growth for a time frame of five years. The model was a simplified version of that used by Armstrong & Davidson (2006). The model incorporated demographic stochasticity using Excel functions (see below) and combined estimates of population parameters derived from analyses of the survival and reproduction data for the first year with information from the saddleback reintroduction on Mokoia Island. Reproduction parameters were split into 'first-year female', defined as a female entering her first breeding season and 'older female', defined as a female who had undergone one or more breeding seasons. Reproduction was separated into two age-classes because previous research has shown that first-year females may have a lower reproduction rate than older females (Armstrong & Davidson 2006).

Starting Conditions at beginning of breeding season 2007

- *Number of first-year males and females*: Calculated by applying the resighting probability from the first time interval under the resighting model, $\{P_t\}$ (from juvenile survival analysis) to the number of juveniles found during the September 2007 surveys. Sexes of juveniles were not known so it was assumed that the sex ratio was even.
- *Total number of older males and females:* Results from the two September surveys were used to calculate the total number of older male and female saddlebacks present. During these two surveys I found only the adult birds that were known to be alive during the previous survey in April 2007, and I was confident that no birds had gone undetected during the September surveys as all adults in the park held stable territories and were easily detected. Resighting probability between the last April survey and the two September surveys was 100%, as was the resighting probability between the September surveys.

Parameter Estimates

To account for uncertainty in parameter estimates, vital rates were sampled randomly from a distribution defined by their estimates and standard errors. Reproductive rates were assumed to be log-normally distributed and survival rates were assumed to be

logit-normally distributed. Real parameter estimates and their standard errors were log transformed into Beta estimates (log of reproductive rate and logit of survival rate), and a random sample was generated from the log-normal or logit normal distribution. Random Beta estimates were then transformed back into real random values to be used in the model.

- *Fledglings per older female*: Estimated as the mean number of fledglings to survive for > 10 days per female, given that none of the females were probably first-year birds. Estimated from breeding season data.
- *Fledglings per first-year female*: No reproduction data were available for first-year females at Bushy Park. Therefore the proportional difference between reproduction rates of older females and first-year females was inferred from saddleback data collected on Mokoia Island by Armstrong *et al.* (2005). Using PROC GENMOD in SAS, the data were re-analysed by fitting them to the generalised linear model

$$\ln(f) = \alpha + \beta_a a + d$$

where f is the mean number of fledglings per female, a is the age of the female (0 for first-year birds, 1 for older), d is population density (females per ha), and α, β_a and β_d are the parameters of the model (D.P. Armstrong, unpub.). The parameter β_a represents the log of the proportional difference between the mean number of fledglings per older and first-year female, and was estimated to be 1.13, meaning older females were estimated to have 1.13 ($e^{1.13}$) times as many fledglings as first-year fledglings.

- *Probability a juvenile survives to breeding season*: Juvenile survival to breeding season was estimated using the survival probability of the first time interval under the survival model $\{\Phi_t\}$, in the juvenile survival analysis.
- *Probability an adult survives for 12 months*: Monthly adult survival was estimated in MARK and then raised to the power of 12 to obtain annual survival probabilities.
- *Probability of a recruit being a female*: The probability of a fledgling being either sex was assumed to 0.5.

Model flow

1. *Number fledged by first-year females*. Gets number of young from Poisson distribution, where mean is number of paired first-year females multiplied by the real random number of fledglings per first-year female.
2. *Number fledged by older females*. Gets number of young from Poisson distribution, where mean is number of paired older females multiplied by the real random number of fledglings per adult female.
3. *Number of total fledglings*. Adds values from steps 1 and 2 together.
4. *Number of recruits*. Gets number of recruits from Binomial distribution based on the total number of fledglings and the probability of their surviving to the breeding season.
5. *Number of female recruits*. Gets number of female recruits from Binomial distribution based on the total number of recruits and the probability of being female.
6. *Number of female recruits with mates*. Assumes that a female will only mate if she has a male and that older females will pair first with available males.
7. *Number of male recruits*. Difference between total recruits and female recruits.
8. *Number of adult females survivors*. Gets number of survivors from a Binomial distribution based on the number of females around last breeding season and their annual survival probability.
9. *Number of adult female survivors with mates*. Assumes that a female will only mate if she has a male and that older females will pair first.
10. *Number of adult male survivors*. Gets number of survivors from Binomial distribution based on the number of males around last breeding seasons and their annual survival probability.
11. *Total of number females at start of breeding*. Adds first-year and older females together.
12. *Total number of males at start of breeding*. Adds first-year and older males together.
13. *Total population number at start of breeding*. Adds total males and females together.
14. *Back to 1*. Time step = 1 year

Stochasticity

Demographic stochasticity was incorporated into the Bushy Park saddleback model in several places using Excel functions. The number of adult males and females surviving to the following year was obtained by using the Excel function CRITBINOM, which selected the number of survivors from a Binomial distribution based on the total number of individuals present in the last breeding season and their annual survival probability. The number of recruits was also obtained by using the function CRITBINOM, which selected the number of recruits from a Binomial distribution based on the total number of fledglings and the probability of them surviving to the breeding season. The number of female recruits was also obtained by using the function CRITBINOM, which estimated the number of female recruits from a Binomial distribution based on the total number of recruits and the probability of being a female. The number of male recruits was calculated as the difference between the total number of recruits and the number of female recruits. The number of young fledged was calculated using the PopTools function dPoissonDev(mean), which selected the number of young from a Poisson distribution based on the expected number produced (i.e. mean is the number of paired first-year or adult females multiplied by the reproduction rate for first-year or adult females). A stochastic model must be run many times to produce a frequency distribution of observed outcomes. Results presented in this chapter are based on 1000 runs of the model.

Parameter sensitivity analysis

A sensitivity analysis was performed on the population model. This is an important aspect of modelling that can highlight parameters that have the largest influence on the results of the model, and thus help establish effective management strategies and indicate which parameters ought to be most accurately measured (McCarthy *et al.* 1995). I varied the model's population parameters to investigate their effect on predictions of future population viability. When data are sparse, the behaviour of the population can be explored over a range of reasonable parameter values (Boyce 1992). Additionally, my parameter estimates may not accurately reflect the long term population dynamics of the Bushy Park saddlebacks because data was collected soon after their release when reproduction and survival rates may be lower (Armstrong & Ewen 2001). I varied adult and juvenile survival and reproductive rates independently over a range of realistic values (Table 3.1) to asses the influence these parameters had

on the results of the model. These values were based on data from other saddleback populations (e.g. Kapiti Island – Lovegrove 1991, Motuara Island – Pierre 1999, Mokoia Island - Davidson & Armstrong 2002, Ulva and Breaksea Island – Hooson & Jamieson 2004).

Table 3.1. Parameters that were varied during the sensitivity analysis. Values in bold indicate parameter values that were estimated from the one years data at Bushy Park. Remaining values for the three parameters were taken from estimates based on other saddleback populations. Parameter values were varied one at a time.

Parameter	Best	Estimated	Worst
Reproduction rate (fl/fem/yr)	3.7	**2.86**	0.90
Adult survival probability	0.95	**0.63**	0.20
Juvenile survival probability	0.85	**0.56**	0.15

3.3. RESULTS

3.3.1. Pair Formation

One week after release the saddlebacks had dispersed widely throughout the park. During this initial period after release, saddlebacks were often observed in groups of three or more, and several different male-female interactions were documented before stable pairs were formed (Table 3.2). However, some saddlebacks were paired up within three weeks of release and the seven surviving females were all paired by early October 2006. The number of pairs increased from seven to nine after the two females held at Auckland Zoo were released.

All pairs persisted over the course of the breeding season except for three cases where paired females lost their male partners (due to unknown reasons). Each female had paired up with a new male within a maximum of two weeks after the loss of her original mate, with one female newly paired within 2-3 days. In two of these cases the females had nestlings or fledged young, which the new male was observed to feed on repeated occasions. Males that paired up with newly single females were not necessarily from neighboring home ranges.

Table 3.2. Post release saddleback interactions observed at Bushy Park during fortnightly surveys. Saddlebacks were released on June 19 2007. M = Metal, B = Blue, R = Red, G = Green, Y = Yellow, W = White, Bk = Black. ♂ indicates Male. ♀ indicates Female. Pairs in bold indicate a pair that went on to breed.

Survey 1	Survey 2	Survey 3	Survey 4	Survey 5
♂GM-WB: ♂GM-RR	♂GM-BY: ♂GM-WW: ♀YY-RM : ♀GG-RM: ♂GM-WR	♂**RR-RM: ♀BkBk-RM**	♂**WG-RM: ♀YY-RM**	♂RG-RM: ♂GM-GW
♀GM-GG: ♂GM-BkW: ♂GM-BR		♂**GM-RY: ♀GM-BkY**		♂**GM-YY: ♀GG-RM**
	♀GM-BG: ♀RBk-RM			♂**GM-RY: ♀GM-BkY**
♀GM-BkY: ♀GM-BG				
	♂**RR-RM: ♀BkBk-RM**			♂GY-RM: ♀GM-BG

In addition to the nine adult pairs, one pair consisting of an adult male and a recently fledged female formed during the breeding season. This pair formed in early February 2007, a maximum of two months after the female fledged, and were observed on numerous occasions displaying the rituals that maintain a close pair bond, such as courtship feeding, 'bow-fan-warble' and quiet calls and pips. The pairing was permanent, as they were consistently observed together for a minimum of ten months and bred together at least once during the second breeding season in late 2007 (K. Brider, pers. comm.). Two further adult male/juvenile female pairs were observed towards the end of the 2006/07 breeding season and one of these appear to be permanent as the pair were consistently observed together during the second breeding season (K. Brider, pers. comm.).

3.3.2. Home ranges

Home ranges of pairs were spread throughout the park, but eight out of nine identified home ranges were situated around the perimeter of the reserve (refer to Chapter 4). I only witnessed one territorial display event between neighboring males during the study, indicating that such events were probably infrequent. The two males involved performed bow-fan-warble displays in close proximity to each other for approximately 20 minutes. The confrontation did not involve any physical contact between the males. All paired saddlebacks established permanent home ranges, although the size and shape

of most home ranges seemed to be flexible and frequently extended throughout the season, particularly when a pair had dependent fledglings. The remaining saddlebacks were all adult males, most of which moved continuously throughout the reserve rather than become established in one area.

3.3.3. Breeding season and nest sites

I located a total of 16 nests during the first saddleback breeding season, which lasted from early September 2006 to late April 2007, with the first clutch being laid on approximately 3 September and the last clutch on approximately 30 March.

Saddlebacks used a variety of sites to build nests, including nest boxes (Table 3.3). Most nests (13) were built within 10 m of the forest edge, and the majority were less than 2 m from the ground. The remaining three nests were built in Kahakaha epiphytes (*Collospermum hastatum*) between heights of 4 - 8 m. Nests sites were secluded and nest entrances were well hidden with surrounding dense vegetation (Plate 3.1, 3.2).

3.3.4. Clutch size, clutch number and number of fledglings

In total, eight saddleback females bred during the first breeding season (Table 3.3), including all seven of the original females that survived to September and one of the two females released in January. Eleven of the 13 clutches that I could access had two eggs, and the other two clutches had three eggs. Five of the females had at least three clutches, although two of these had at least one nest failure and one female deserted a nest with three eggs. The other two females present for the whole breeding season had at least two clutches. Some clutches may have gone undetected if they failed early. The seven females present throughout the breeding season had one to four fledglings, with an average of 2.9. A minimum of 22 chicks fledged and survived for at least 10 days.

On two occasions I noted a female saddleback incubating a new clutch while the male continued to feed dependent fledglings from the previous clutch. A further female was observed to be brooding two 4-5 day old nestlings while her male partner continued to feed a dependent fledgling from the previous clutch. One female was observed leaving her nest for approximately 17 minutes to chase away an unrelated juvenile saddleback that was foraging close to her nest site.

Plate 3.1. Secluded North Island saddleback nest entrance. Photo: Joanne Thorne

Plate 3.2. Closer view of the same nest site. Red arrow indicates tail of incubating female. Photo: Kelly Brider

Table 3.3. Summary of Bushy Park's saddlebacks first breeding season. Chicks were counted as fledged if they survived for a minimum of 10 days after fledging. * Indicates a new male that paired with female after her mate disappeared. ^ indicates birds that tested positive for avian malaria and were initially sent to Auckland Zoo.

Breeding pair		**No. of clutches detected**	**Clutch size**	**Nest location**	**Height from ground (m)**	**No. of fledged young detected**
Female	*Male*					
GM-BkY	GM-RY	3	2	Nest box	1.02	1
	GM-BR*		3	Nest box	1.05	2
			2	Nest box	0.70	1
RBk-RM	WW-RM	3	2	Fallen vegetation	1.20	2
			2	Fallen vegetation	0.55	0
			2	Fallen vegetation	0.68	1
WY-RM^	GM-WBk	1	Unknown	Epiphyte	8.00	2
	RG-RM*					
GM-GG	BkB-RM	2	Unknown	Unknown		1
			Unknown	Unknown		2
YY-RM	WG-RM	2	2	Ponga log	0.90	1
			Unknown	Epiphyte	4.00	0
GG-RM	GM-YY	3	2	Ponga log	0.68	2
			Unknown	Epiphyte	5.00	0
			2	Fallen vegetation	1.05	2
GM-BBk	GBk-RM	3	Unknown	Unknown		1
			Unknown	Unknown		1
			2	Fallen vegetation	1.46	1
BkBk-RM	RR-RM	3	2	Mahoe cavity	1.74	1
			3	Mahoe cavity	1.05	0
	GM-WW*		2	Nest box	0.71	1
RW-RM^	BW-RM^	0				0

3.3.5. Survival Analysis

I analysed adult survival in relation to sex (*s*), time (*t*) and before and after breeding season (*b*). The global model for this set of data, $\{\Phi_s\ P_b\}$ (d.f. = 25), had a median c-hat value of 1.01 (SE = 0.02) indicating that it fit the data well. Comparison of the resulting series of models (Table 3.4) indicated that $\{\Phi.\ P_b\}$ explained the data in the most parsimonious way as it had the lowest AICc value. The survival model $\{\Phi.\}$ constrained survival estimates to be constant between sexes and time intervals and gave a monthly adult survival probability of 0.96. The resighting model $\{P_b\}$ estimated resighting probability to be 0.39 before the breeding season and 0.87 during the breeding season. The model $\{\Phi_s\ P_b\}$ also had some support (ΔAICc <2), indicating that it is unclear whether there was a difference in survival probability between sexes. The remaining models had considerably less support for the data.

Table 3.4. A series of models for factors affecting adult saddleback survival and resighting probability. Factors considered were sex (s), before and after breeding (b), time (t) or constant (.) AICc is the criterion on which models were selected, the lowest value indicating the most parsimonious model. ΔAICc is the difference in AICc between the best model and the current model. w_i is the AIC weight, indicating the relative support for the model. *K* is the number of parameters in the model.

Model	AICc	ΔAICc	w_i	*K*
$\Phi.\ P_b$	472.51	0.00	0.59	3
$\Phi_s\ P_b$	473.53	1.02	0.35	4
$\Phi.\ P_t$	478.21	5.70	0.03	16
$\Phi_s\ P_t$	479.33	6.82	0.01	17
$\Phi_t\ P_t$	486.09	13.58	0.00	29
$\Phi.\ P.$	554.97	82.46	0.00	2

The global model used to analyze the juvenile resighting data, $\{\Phi_t\ P_t\}$ (d.f. = 1), allowed survival and resighting probabilities to vary for each time interval. This model fitted the data well, (median c-hat = 1.06, SE = 0.02), and comparison of the two models fitted to the data (Table 3.5) shows that it has the lowest AICc value and is therefore the best model. However the other model $\{\Phi_t\ P.\}$ also had some support (ΔAICc<2). The global model, $\{\Phi_t\ P_t\}$, estimated the probability of survival to the breeding season as

0.56, and probability of resighting between fledging and the start of the breeding season as 0.82.

Table 3.5. Two models for estimating juvenile saddleback survival and resighting probabilities. Models with (.) constrains estimates to be the same for each time interval, whereas models with (t) allows estimates to vary between time intervals. AICc is the criterion on which models were selected, the lowest value indicating the most parsimonious model. ΔAICc is the difference in AICc between the best model and the current model. w_i is the AIC weight, indicating the relative support for the model. K is the number of parameters in the model.

Model	AICc	ΔAICc	w_i	K
$\Phi_t P_t$	54.49	0.00	0.63	3
$\Phi_t P_.$	54.83	1.09	0.36	3

3.3.6. Population model

The population model started with 15 females and 18 males, of which six were first–year females, six were first–year males, nine were older females and twelve were older males. Mean fledglings per older female was 2.86 (SE = 0.5). Mean fledglings per first-year female was calculated by subtracting 1.13 (the log of the proportional difference between mean number of fledglings per older female and mean number of fledglings per first-year female) from a random sample based on the beta parameter of fledglings per older female. The beta value was then transformed into a real random value (Table 3.6).

Monthly adult survival was estimated as 0.96 under the survival model $\{\Phi. P_b\}$ (Table 3.4) which constrained survival probability to be the same for both males and females. This was then transformed to 12 monthly survival estimates to obtain the probability of an adult surviving for 12 months (Table 3.6).

$$\begin{aligned} \textit{probability (12 monthly survival)} &= \textit{probability (monthly survival)}^{12} \\ &= 0.96^{12} \\ &= 0.63 \end{aligned}$$

Standard error for adult monthly survival probability was converted to standard error for 12 month survival probability

$$SE(12\ month\ survival) = SE(1\ month\ survival) \times 12 \times p(monthly\ survival)^{12-1}$$
$$= 0.01 \times 12 \times 0.96^{11}$$
$$= 0.08$$

Juvenile survival to the start of the breeding season was estimated as 0.56 (SE = 0.1) under the survival model $\{\Phi_t P_t\}$ (Table 3.5).

Table 3.6. Estimates and standard errors for vital rates used in population model for Bushy Park saddlebacks, and procedure used to obtain random samples based on these rates. These values were used to calculate estimates and standard errors for beta parameters (log of reproduction rate, logit of survival probability), and random samples were drawn based on the beta parameters (assuming normal distributions) to incorporate uncertainty in parameter estimation into population projections. Fledglings per first-year female was calculated by subtracting 1.1.3 (the log of the proportional difference between mean number of fledglings per older female and mean number of fledglings per first-year female) from the beta parameter for fledglings per older female, and then transforming to a real random value. The random values shown are for 1 of 1000 runs of the model.

Parameter Estimates	REAL		BETA		RANDOM	
	Est	SE	Est	SE	Beta	Real
Fledglings per first-year female	Estimate inferred from Mokoia Island reproduction data				1.29335 – 1.13	1.1815
Fledglings per older female	2.86	0.5	1.0508	0.17483	1.29335	3.645
Prob. juvenile survives to breeding season	0.56	0.1	0.2412	0.40584	0.32408	0.5803
Prob. adult survives 12 months	0.63	0.1	0.5151	0.42712	0.55051	0.6343
Prob. of recruit being female	0.5					

Predictions for the viability of the Bushy Park saddleback population five years after translocation look promising. Over 1000 simulations the population never went extinct in five years, indicating a 0% probability of extinction over this time period. The population was projected to reach a mean population size of 95 individuals (95% CI = 10, 282) after five years (Figure 3.1).

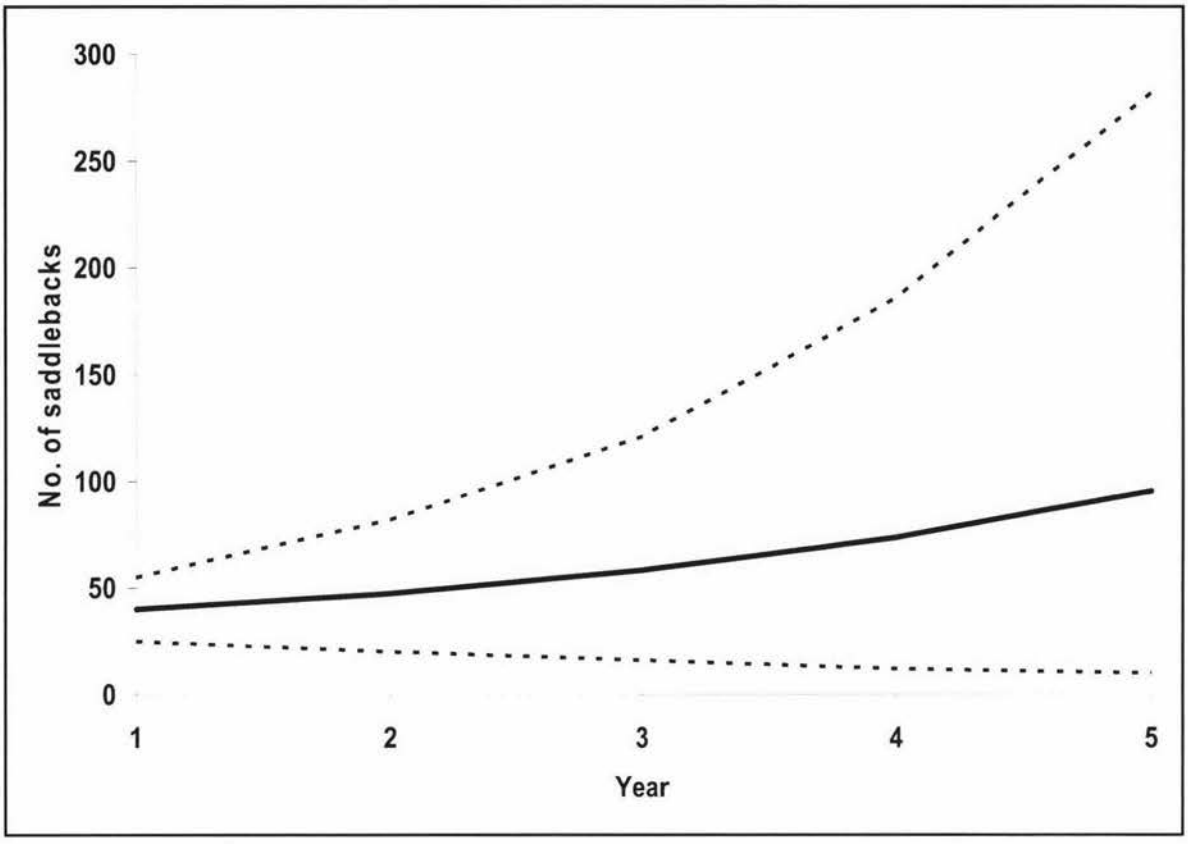

Figure 3.1. Projected growth in number of saddlebacks present in Bushy Park from September 2007 to September 2012 based on simulations incorporating demographic parameters collected during the first year after release. Trajectories show the mean population size (——) and 95% confidence interval (– – –).

Sensitivity analysis

Varying adult survival between 0.98 and 0.20 had the greatest effect on probability of the population going extinct within five years (Table 3.7), and produced the widest range of mean population sizes after 5 years under the varying scenarios. Varying fledglings/adult female rates produced the smallest range of mean population sizes over the three scenarios (Table 3.7) and had only a small probability of extinction (0.04) over five years under the worst scenario. Varying juvenile survival between 0.85 and 0.15 had the least effect on the probability of extinction (Table 3.7) but total population sizes ranged from 177 under the best survival rate to 16 under the worst survival rate.

Table 3.7. Expected mean population size with 95% confidence intervals for the Bushy Park saddleback population over a range of values for selected parameters. Results are based on 1000 runs and mean population number is measured at 5 years after the translocation. Parameters were varied one at a time.

Parameters	Total population number			Probability of extinction		
	Best	Predicted	Worst	Best	Predicted	Worst
Adult survival	187 (474, 34)	74 (221, 9)	5 (28, 0)	0	0	0.40
Fledglings/adult female/year	128 (373, 18)	74 (221, 9)	17 (72, 1)	0	0	0.04
Juvenile survival	177 (513, 77)	74 (221, 9)	16 (74, 1)	0	0	0.02

3.4. DISCUSSION

3.4.1. Post release behavior and breeding biology

The wide dispersal of the saddlebacks soon after release at Bushy Park is a common feature of both North Island and South Island saddleback transfers to islands (Armstrong & Craig 1995, Pierre 2003). The flocking behavior observed in the weeks following release is also commonly observed and may assist pair formation (Lovegrove 1996). The rapid pair formation at Bushy Park supports this idea as all available females were paired up by early September, less than three months after release.

All seven females that were present throughout the breeding season nested at least once and fledged between one and four fledglings. Island populations of newly released North and South Island saddlebacks have also been reported to breed successfully in the first breeding season after release (Armstrong & Craig 1995; Pierre 2003). Low-density saddleback populations, such as those after a translocation, typically have a longer breeding season, sometimes extending from August through to May (Craig 1994). The currently low density Bushy Park saddleback population mirrored this pattern as first clutches were laid in early September and pairs still had dependent fledglings in late April. Saddleback reproductive rates appear to be density dependant (Armstrong *et al.* 2002) and both the length of breeding season and reproduction rate may decline as density at Bushy Park increases.

Average number and size of clutches at Bushy Park were within the reproductive rates known for North and South Island saddleback island populations (e.g. Craig 1994,

Hooson & Jamieson 2003) and nest site characteristics were similar to those previously described for saddlebacks (e.g. Lovegrove 1980, Hooson & Jamieson 2003). However, considering the Bushy Park saddlebacks were at such low densities during their first breeding season, reproduction rates were slightly lower than expected, with an average of just 2.89 chicks fledged per pair for the entire season. In low density island populations North Island saddlebacks have been observed to successfully raise up to four clutches of four eggs during one season (Craig 1994). It should be noted however that reproductive rates may be lower immediately following a translocation (Armstrong & Ewen 2001), so fecundity of the saddlebacks at Bushy Park could be expected to increase before the effects of density dependence cause it to decline. Preliminary analysis of breeding data collected for the second breeding season at Bushy Park indicates that this may be the case (K. Brider, pers. comm.). Some nests were inaccessible and it was therefore difficult to determine due dates of fledging. Although I visited pairs at least every ten days, some chicks may have fledged but only survived for a few days and therefore gone undetected. Twenty-two fledglings were detected during the breeding season although this may be an underestimation of the number of chicks that actually fledged. Some of the reserves habitat type, such as the dense, secondary vegetation around the periphery, probably provides a large number of high quality nest sites (refer to Chapter 4) and the provision of extra nest boxes in these areas is probably unnecessary. However, the mature interior of the forest may contain lower quality sites and the provision of nest boxes in this area may facilitate breeding. Nest boxes can also be a useful tool for nest monitoring as nests built in artificial boxes are easily located.

The fact that territorial displays between neighboring pairs was rare is also likely to be a result of the low-density population (Armstrong & Craig 1995, Pierre 2003) and territorial displays would be expected to increase as the population grows (O'Callaghan 1980) and the gaps between neighboring territories are reduced.

Females that lost their male partners during the breeding season paired with free males in a short space of time; in one instance re-pairing took between just 2-3 days. Armstrong and Craig (1995) also observed a recently single female pair up with a new male after release on Mokoia Island although the time frame was within a month rather than days. Two of the new males at Bushy Park took up parental duties and fed nestlings and dependent fledglings that were not theirs. No published records of this

occurring previously in saddlebacks have been found, but it may be that the particularly low density of saddlebacks influenced this behavior in the same way that it can influence length of breeding season and reproduction rates. The formation of at least one pairing between an adult male and a recently fledged female was probably due to the lack of available adult females as Lovegrove (1992) suggests that juveniles may not be regarded as preferred mates. This is supported by Armstrong & Craig (1995), who observed that adults paired with each other rather than with juveniles during a translocation of North Island Saddleback to Mokoia Island. Saddlebacks will breed at one year of age, especially in low density populations (Craig 1994), and Lovegrove (1985) reported that some juveniles on Little Barrier Island formed pairs at six months old.

3.4.2. Population model

Population viability analysis is used to assess the future viability of a population of conservation concern and provides a framework for directing management strategies. It is an important component in the evaluation of a translocation and can provide information on viability, key vital rates and management strategies (Seddon *et al.* 2007). The Bushy Park model suggests that the Bushy Park saddleback population will be viable for at least the next five years. Because the population had only been present for a short time, my results were based on a single year's data, which is problematic. Armstrong & Ewen (2001) identify the three main problems; firstly, small sample sizes create uncertainty in the precision of parameters estimates; secondly, survival and fecundity rates can vary due to environmental changes and yearly estimates may be very different from long term mean values; thirdly, parameter estimates based on the first year after release may underestimate survival and fecundity rates due to the effects of the translocation. For example, reproduction rates of North Island robins translocated to Tiritiri Matangi Island were considerably lower in the first year than the long term mean, and a PVA based on the first years data substantially underestimated the probability of the populations' survival (Armstrong & Ewen 2001). This prediction led to an unnecessary follow up translocation being undertaken, consuming valuable resources that could have been allocated to research of the founder population. Therefore, it is important to monitor a newly translocated population for more than just the one year in order to get realistic estimates of survival and fecundity. Furthermore,

decisions about the management of the population, such as whether a follow up translocation is necessary, should not be made on the first year's data alone.

The application of a sensitivity analysis may improve the use of PVA's to the field of conservation biology by highlighting those parameters that have the largest influence on a population (McCarthy *et al.* 1995). A sensitivity analysis was performed on the Bushy Park model to rank population parameters that should be measured in the long term in order of precision required to build more accurate models in the future. For the Bushy Park population, survival of breeding birds had the greatest impact on the probability of extinction, indicating that future models for the population would be improved by careful monitoring of adult survival. Additionally, identifying and managing reasons for mortality in saddlebacks could increase the likelihood of population viability.

Although previous studies have shown that island saddleback populations undergo density dependant growth (e.g. Armstrong *et al.* 2005 for Mokoia Island saddlebacks; Armstrong *et al.* 2002 for Tiritiri Matangi Island saddlebacks) this was not incorporated into the Bushy Park model. Because the population was at low density during the study and the population projections were for five years only, we thought the effects of density dependence were unlikely to be significant.

While PVA is used extensively in conservation to predict the viability of threatened populations and steer management strategies, its predictions are often uncertain (Boyce 1992, McCarthy *et al.* 2003) and caution is needed when interpreting its results (Fieberg & Ellner 2000). PVA models are constrained by the amount of biological data available, and often this data is difficult to obtain from small populations that are threatened by extinction (Boyce 1992). Nevertheless, benefits of PVA far outweigh its limitations, and population modelling can be highly valuable when integrated with management strategies to improve the conservation status of threatened species within an adaptive management approach.

3.4.3. Adaptive management of the Bushy Park saddleback population

Attempts to re-establish the saddleback to parts of the mainland, even where exotic predators have been eradicated, is a relatively new approach to saddleback conservation

and may involve uncertainty about factors associated with success, such as habitat quality or dispersal out of the reserve. It is important to assess such factors and predict population viability in order to direct future management and aid decisions on future translocations (Armstrong & Ewen 2002). The model described in this chapter is a preliminary model based on just one year's data, but provides the framework for more reliable analysis in the future. The model predicts that under the current conditions, the Bushy Park population is viable for a minimum of five years. This result suggests that the low survival of birds during the first year after release did not affect the viability of the population. However, Taylor *et al.* (2005) note that translocation failures may occur within the first three years after release, suggesting that the population should be monitored for at least this long to detect a decline.

Long term monitoring of the population under various management strategies should be used to update this model to identify the most effective way to maintain a viable saddleback population. Current population projections may be too optimistic as the model did not take into account habitat quality or dispersal out of the reserve. Research into the habitat selection of the saddlebacks at Bushy Park has shown a preference for dense, secondary forest around the periphery of the reserve over the mature forest in the interior (refer to Chapter 4). It is possible that this will affect the future density, or even viability of the population, as poor habitat quality may be a limiting factor for a species. Management actions to improve the habitat quality at Bushy Park could involve large scale planting of more suitable plant species. The response of the population to these actions can then be monitored in terms of survival and reproduction parameters, and the population model updated to make more accurate population projections and to assess the effectiveness of management actions.

The extent to which dispersal out of the reserve will affect future population persistence is not known. Ongoing monitoring of individual birds, particularly juveniles who may be more likely to disperse in search of territories as opposed to adults holding established territories within the reserve, would allow the amount of dispersal to be measured. This information could be used to improve the PVA model and determine whether the population was likely to persist given the observed dispersal. This could in turn establish what, if any, management should be considered and whether translocations of saddlebacks to similar sites should proceed in the future.

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4

Habitat Selection

4.1. INTRODUCTION

The processes by which animals select one habitat over another are complex and have been the focus of much study. Definition of the key terms used in such studies is often inconsistent (Hall *et al.* 1997, Jones, 2001) and can result in inaccuracies and ambiguity. Therefore, this chapter shall begin with some clear definitions of the terminology used throughout. 'Habitat' is defined as the resources and conditions present in an area that produce occupancy by a given organism (Hall *et al.* 1997). 'Habitat selection' refers to a hierarchical process of behavioural responses that may result in the disproportionate use of habitats to influence survival and fitness of individuals (Jones 2001). Lastly, 'habitat quality' refers to the ability of an environment to provide the conditions that will support individual and population persistence (Hall *et al.* 1997).

When selecting a habitat, individuals respond to environmental cues that they can observe within a range of habitats (Kristan 2003) that relate to food availability, adequate nesting sites, competition and the presence of predators (Cody 1981). Habitat quality can vary greatly depending on the value and amount of resources it provides for survival, reproduction and population persistence, thereby producing a gradient in habitat quality (Smith & Shugart 1987). A number of studies have demonstrated that habitat structure is important to birds in terms of invertebrate prey abundance (Robinson & Holmes 1982, Smith & Shugart 1987, Huhta *et al.* 1998), the availability of nest sites

(Calder 1973, Makan 2006) and the provision of song perches (Smith & Shugart 1987). Birds may use a cue such as habitat structure to reliably determine the quality of a habitat in terms of food availability, cover from predators (Schlaepfer *et al.* 2002) or competition.

The optimal choice models of Fretwell and Lucas (1970) predict that habitats of higher quality are actively chosen over habitats of lesser quality (Fretwell and Lucas 1970, Ens *et al.* 1992, Muller *et al.* 1997). The characteristics of high quality habitats are associated with increased fitness, or an individual's contribution to future generations compared to other individuals in the population (Begon *et al.* 1986, Kristan 2003). Therefore, behaviors that allow animals to selection high-quality habitats should evolve through natural selection (Cody 1985). Luck (2002) demonstrated a positive association between habitat selection and certain measures of fitness in the rufous tree creeper (*Climacteris rufa*), an insectivorous passerine, supporting the theory that tree creepers were selecting sites to maximize their fitness.

When an environment is different from that which the species evolved in, and formerly reliable cues are no longer associated with habitat quality, animals may actively select poor quality habitats. Such maladaptive selection may cause animals to selectively move from 'source' habitats where natality exceeds mortality to 'sink' habitats where the reverse is true, hence the sink habitats may become 'ecological traps' that create problems for conservation of wildlife populations (Schlaepfer *et al.* 2002). Ecological traps are often associated with human modified habitats (Battin 2004). For example, native species in mainland New Zealand are not expected to be good habitat selectors as they did not evolve to select habitats with a low risk of mammalian predation.

Identifying and preserving high quality 'source habitats' is important for conservation (Dias 1996, Braden *et al.* 1997). Related to this, assessing the habitat quality of a release site is a vital consideration when planning a translocation (Armstrong and McLean 1995, Hooson & Jamieson 2004). A common method of choosing suitable release sites is to compare the habitat of existing populations to that of a potential release site (Armstrong & McLean 1995). However, if a species range has become reduced to a small proportion of its historical range, this method restricts the variety of habitats that would be considered for release (Armstrong & McLean 1995), and Gray and Craig

(1991) maintain that a species historical distribution should be given equal consideration when identifying release sites. An alternative, but less commonly applied method is to monitor the habitat selection of newly released individuals (Pierre 2003, Hirzel *et al.* 2004). This can be viewed as a natural experiment of colonization (Steffens *et al.* 2005) and can provide valuable information on the quality of the release site, and for the selection of future release sites (Pierre 2003, Hirzel *et al.* 2004). Identifying the environmental cues a species uses to chose one habitat type over another could assist in identifying the best release sites. However, because preferred habitat does not necessarily equal high quality habitat (Gray & Craig 1991), caution is required to ensure that specific environmental cues are associated with the best habitat.

Studying the habitat selection of newly released animals is especially relevant for many New Zealand translocations, where individuals are released at low density into sites that have no predators and few competitors (Steffens *et al.* 2005). Such situations give mobile individuals the opportunity to settle in preferred habitats, which, according to the optimal choice models of Fretwell and Lucas (1970), should also be the highest quality if the environmental cues used in the species' evolutionary history are still associated with high quality habitat. Several studies have attempted to quantify the preferred habitat requirements of a newly released species by studying the populations' pattern of colonization. For example, Hirzel *et al.* (2004) illustrate the value in monitoring the habitat selection of a newly released species through a study of a population of bearded vultures (*Gypaetus barbatus*) in the Alps. They modeled the ecological requirements of the bearded vulture by analyzing the relationship between the distribution of vulture sightings *post release* and a set of environmental descriptors. Results showed that vulture habitat selection is likely to be driven by food availability for immature birds and high quality nesting sites for mature birds. Steffens *et al.* (2005) investigated the spatial distribution of South Island saddleback breeding territories in relation to overall habitat availability one year after release onto Ulva Island. Results suggested that the saddlebacks preferred coastal forest fringe habitat rather than mature forest. The assumption that individuals will select high quality habitats in the absence of mammalian predators is supported by a study showing that the territory sites first selected by North Island saddlebacks reintroduced to Mokoia Island consistently had the highest reproduction success than those left unoccupied until later years (Armstrong *et al.* 2005). Findings from studies such as these may help guide future decisions on the

reintroduction and conservation of threatened species by providing specific information about their habitat requirements.

With a growing number of predator-free mainland sites becoming available, the translocation of saddlebacks to mainland habitats is sure to increase. Until recently, North Island saddleback translocations have been confined almost exclusively to predator-free offshore islands which tend towards a mosaic of habitats from mature forest to scrubby coastal vegetation. In contrast, mainland reserves are more likely to consist mainly of tall mature forest. Results from saddleback habitat selection studies on offshore islands (e.g. Steffens *et al.* 2005) suggest that saddlebacks tend to select scrubby, high diversity habitats, indicating that a typical mainland habitat may not be the best habitat for them.

In this chapter I used the saddleback's pattern of colonization of Bushy Park as a natural experiment to investigate habitat selection in terms of habitat structure. I employed a height frequency sampling method to measure habitat variables in the home ranges of nine saddleback pairs, and compared them to habitat variable measurements in nine randomly selected 'unoccupied' sites using a logistic regression analysis. I aimed to identify the environmental cues that saddlebacks use to select habitats in order to help define the characteristics of appropriate release sites for future mainland saddleback translocations.

4.2. METHODS

4.2.1. Identifying home ranges

I collected habitat data from the home ranges of all nine adult pairs of North Island saddlebacks during their first breeding season after release into Bushy Park. All birds were banded with a unique combination of three colour and one metal band for individual identification. Home ranges were estimated by first locating and then following either male or female birds of a known pair for periods of between 60-90 minutes, and recording their locations in relation to features of the park such as streams, fence lines and tracking tunnel lines. I did this repeatedly for each pair over a period of four months from December 2006 to March 2006, by which time I was able to map out

approximate home ranges. I did not sample home ranges of single birds, all of which were adult male, as they tended to move around the park rather than settle on a fixed home range.

4.2.2. Habitat Sampling

I used a variation of the Height Frequency Method (Scott 1965, Makan 2006) to sample habitat at Bushy Park. This method involves measuring the frequency at which each plant species appears in successive layers within the vegetation.

Three central sampling points were located in each of the nine saddleback home ranges by randomly selecting three compass coordinates from $0\text{-}360^0$ and three distances from 0-120 m from the centre of the home range, given that the mean radius of territories was about 120 m. Compass coordinates were selected from a list of random numbers between 0-360 and distance was selected from a list of random numbers between 0-120. If a selected distance fell outside the reserve or obvious home range boundaries I discarded this distance and selected another. Four 20 m long transects radiated from each central sampling point along each primary compass direction. At the central sampling point and four points along each transect (spaced 5 m apart), a 2 m sampling pole was held vertically from the ground and the frequency of all species was recorded by noting the presence of any foliage within a 10 cm radius of the sampling pole (Table 4.1). An additional tier of 0-30 cm was used to measure presence of foliage at ground level. The pole was then lifted vertically to a height of 2 m to sample all vegetation within the next 2 m tier (2-4 m). From 4 m and above the projection of the sampling pole was estimated by eye and the presence of foliage was noted in each 2 m tier up to the canopy. I also estimated the percentage of canopy and ground cover at each sampling point along each transect over an area of 1 m^2. I estimated the distance in metres between each central sampling point and the nearest forest edge to get a 'distance to edge' measurement

In addition to sampling the habitat within home ranges, I randomly chose nine sites in areas of the reserve unoccupied by saddlebacks. Random sites were chosen by dividing the unoccupied areas of the reserve into 120 m by 120 m squares and numbering them 1-55. Grid squares were chosen by randomly selecting a number from 1-55 and the

three central sampling points in each chosen grid were selected and sampled using the same techniques as described above for the occupied sites. If a chosen square overlapped an occupied home range this square was discarded and another was selected. Similarly, if a chosen square fell outside the reserve by more than 50% it was discarded. Distance to the nearest forest edge was also estimated for each central sampling point.

Table 4.1. Example of a raw data sheet for the collection of habitat data using the Height Frequency method. Four 20 m transects were sampled at each of three sites within nine occupied and nine unoccupied habitats. Points were sampled at 5 m intervals along each transect where the presence of foliage types were noted in successive vertical tiers of the forest. Data sheet below shows the habitat data collected for one 20 m transect.

Site	1a				
Distance from edge	45 m				
	Sampling points along transect				
Tier	*0 m*	*5 m*	*10 m*	*15 m*	*20 m*
0– 30 cm	Fern, Kawa Kawa, Pukatea	Fern, Supple Jack	Pigeon wood	Pigeon wood, Nikau	Fern, Kawa Kawa
30cm – 2 m	Pukatea, Kawa Kawa	Nikau, Rangiora	Pigeon wood, Mahoe	Nikau, Mahoe, Tawa	-
2 m – 4 m	Fern, Kawa Kawa, Pukatea	Supple Jack	Pigeon Wood	Pigeon Wood, Supple Jack	Kawa Kawa, Konano
4 m – 6 m	Pukatea	Nikau,	Pigeon wood, Tawa	Nikau	Titoki
6 m - 8 m	Pukatea, Supple Jack	Pigeon wood	Tawa	Pigeon wood, Mahoe	Titoki, Supple Jack
8 m – 10 m	Pukatea, Rata	Nikau, Mahoe, Tawa	Tawa	Mahoe, Tawa	Pukatea
10 m – 12m	Rata	Tawa	Tawa	Mahoe, Tawa	Pukatea
12 m – 14 m	Rata	Tawa	Tawa	Tawa	Pukatea
Ground Cover	60%	40%	40%	60%	80%
Canopy Cover	30%	60%	60%	40%	40%

4.2.3. Statistical analysis

I summarized the raw data (Table 4.1) to obtain measurements for ten habitat variables at each of the 18 sites (Table 4.2). I chose the habitat variables that were most likely to be important factors in predicting occupancy based on aspects of saddleback ecology such as nesting and foraging behavior, and the results of previous saddleback habitat selection studies. This prior information indicated that saddlebacks prefer a secondary growth habitat with high complexity and density. I attempted to measure habitat in terms of habitat structure as I believed this was a key environmental cue used by saddlebacks selecting habitat.

I used MARK to fit logistic regression models to the relationship between occupancy (the binary dependant variable) and ten habitat structure characteristics (explanatory variables). These models take the form

$$\ln(P/(1 - P)) = \alpha + \beta x$$

where P is the probability that a site is occupied, x is the explanatory variable and α and β are the parameters of the model. MARK uses iterative maximum likelihood estimation to obtain estimates for model parameters (White & Burnham 1999).

The summarized habitat data were formatted as an input file for MARK's 'known fate' model where the first column represents fate (10 = occupied site, 11 = unoccupied site), the second column shows the number of sites with that fate and set values for explanatory variables (a 1 in all cases in this analysis) and the remaining columns show the 10 habitat variables as individual covariates (Table 4.3). The number of encounter occasions and attribute groups was set as 1. I specified that individual covariates would be used, and set the number of individual covariates at 10, labeling them as: S-W index, ground cover, canopy cover, species richness, distance from edge, ground complexity, shrub complexity, sub canopy complexity, canopy complexity and total complexity. I modeled the data using the logit-link function. Due to the small dataset (n = 18 sites), I investigated single variable models only. This was done by modifying the design matrix of the 'constant' model (no habitat variables included) to include one habitat variable at a time and running each model separately. For a particular model the estimate of

survival is constrained to be a function of the selected habitat variable. There was one 'encounter occasion' where a site is occupied or unoccupied, and two parameters (the intercept term and one habitat variable).

The model that predicated site occupancy the best was chosen based on Akaike's Information Criterion (AICc) values, where the lower values indicate better models. I tested the significance of each single variable model in comparison to the constant model using the likelihood ratio test in MARK. The likelihood ratio statistic (-2Log(likelihood)) reflects the significance of the unexplained variance in the dependant variable. The likelihood ratio test is a test of the significance of the difference between the likelihood ratio for the selected model minus the likelihood ration for the constant model. Significance was set at 0.005 using the Bonferroni adjustment. This procedure is used when multiple comparisons of the same data set are made and ensures that the experimentwise error rate remains at 0.05 with 10 possible comparisons made.

Table 4.2. Description of explanatory variables used in the study and method of measurement.

Variables	**Measure**
S-W	A single Shannon-Weiner diversity index was calculated for the vegetation data from the summed values for all 12 transects at each site.
Ground cover	Mean ground cover at each site. This was derived by summing all ground cover values for a site and dividing by 51 (the number of ground cover values recorded for each site).
Canopy cover	Mean canopy cover at each site. This was derived by summing all canopy cover values for a site and dividing by 51 (the number of canopy cover values recorded for each site).
Species richness	Total number of plant species summed across all 12 transects at each site.
Distance to edge	Mean distance to edge of forest for the three central sampling points at each site.
Total complexity	Habitat complexity was calculated as a single summed height frequency value. This was calculated for each site by summing the occurrences of all species in all tiers across each transect. Total values for each transect at a site were combined.
Ground complexity	Ground tier was calculated as the complexity in the 0 – 30 cm tier.
Shrub complexity	Shrub tier was calculated as the complexity in the 30 cm – 6 m tier.
Sub-canopy complexity	Sub-canopy tier was calculated as the complexity in the 6 m – 12 m tier.
Canopy complexity	Canopy tier was calculated as the complexity in the 12 m and above tier.

Table 4.3. An example of the format for habitat data analysed by MARK using the 'known fate' model. 10 = occupied site, 11 = unoccupied site. **N** = the number of individuals with a specific set of covariate values. Individual covariates represent the values for each habitat variable collected at each site.

Fate	N	Individual covariates									
10	1	1.08	26	61	22	27	53	187	205	62	507;
11	1	1.02	17	80	14	420	65	76	87	166	394;

4.3. RESULTS

All paired saddlebacks had established permanent home ranges by the start of the first breeding season (early September 2006). The size and shape of most home ranges was flexible, and frequently extended throughout the season, particularly when a pair had dependant fledglings. Home ranges were spread throughout the park, but eight out of nine identified home ranges were situated around the periphery of the reserve (Figure 4.1), primarily in dense secondary forest tending towards tall mature forest near the inner boundaries. The only home range that was not placed on the periphery of the reserve was located approximately 75 m from the forest edge at its nearest point (Figure 4.1, solid black area numbered '2'). Notably however, this home range was in an area of extensive tree fall, with dense and scrubby undergrowth, similar to the edge habitat of the reserve.

Mean values of occupied and unoccupied sites for the ten habitat variables are shown in Table 4.4. The best single variable model for explaining occupancy of a site was the 'shrub complexity' model, which constrained occupancy to be a function of the complexity of vegetation in the shrub tier (30 cm – 6 m). This model had the lowest AICc score and a likelihood ratio test showed that it was highly significant ($\chi^2 = 20.37$, df = 1, $P < 0.0001$) (Table 4.5). A higher complexity in the shrub tier was associated with site occupancy (Table 4.4). Other single variable models that were useful predictors of occupancy were 'total complexity' ($\chi^2 = 14.50$, df = 1, P = 0.0001), 'S-W index' ($\chi^2 = 10.78$, df = 1, P = 0.001) and 'distance to edge' ($\chi^2 = 10.73$, df = 1, P = 0.001) (Table 4.6). A shorter distance (m) to the forest edge, a higher S-W index and a higher total complexity were associated with site occupancy (Table 4.4). However the ΔAICc between these models and the 'shrub complexity' model was large, with the

shrub complexity model having almost all of the relative support (Table 4.5), clearly indicating that this was the best model.

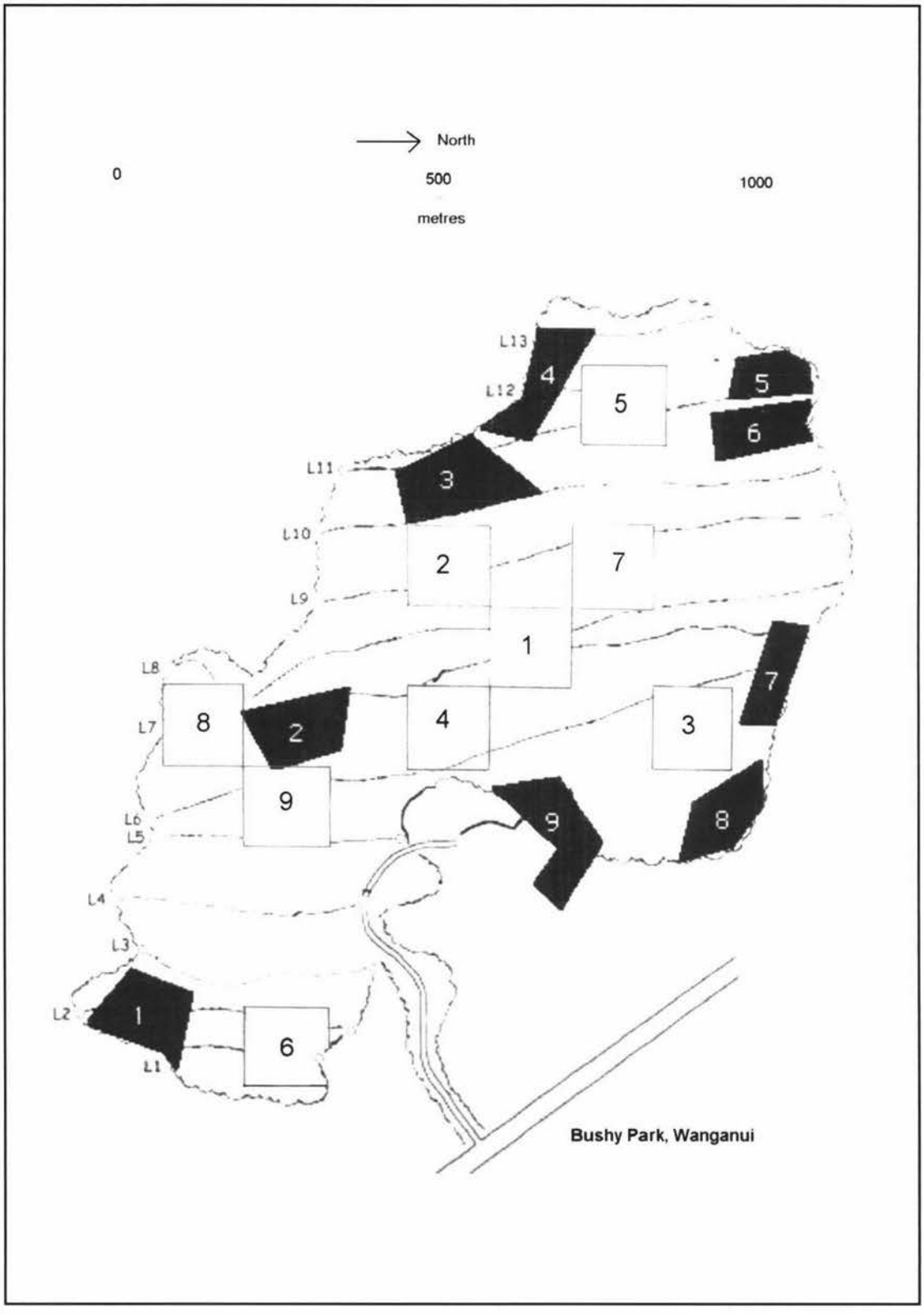

Figure 4.1. Map of Bushy Park showing the approximate boundaries of the nine saddleback home ranges that were sampled (solid black areas numbered 1-9) and the nine unoccupied sampling sites (open boxes numbered 1-9). Thirteen tracking tunnel lines running North-South also shown.

Table 4.4. Mean values for occupied and unoccupied sites for each habitat variable. Standard deviation shown in brackets

	Occupied Sites (n = 9)	**Unoccupied Sites (n = 9)**
S-W index	1.08 (0.06)	1.01 (0.04)
Ground cover	25.33 (5.00)	23.89 (11.67)
Canopy cover	49.67 (10.07)	64.44 (18.63)
Spp richness	18.89 (4.04)	14.56 (2.92)
Distance to edge (m)	39.33 (21.18)	177.78 (147.14)
Complexity		
Ground	64.67 (13.46)	43.33 (18.24)
Shrub	277.44 (43.33)	144.11 (43.99)
Sub Canopy	195.33 (32.56)	149.11 (39.79)
Canopy	117.22 (33.89)	132.00 (29.84)
Total	654.67 (81.09)	468.55 (84.69)

Table 4.5. Comparison of logistic regression models for the relationship between habitat variables and site occupancy by saddlebacks. AICc is the criterion on which models were selected, the lowest value indicating the most parsimonious model. w_i is the AIC weight, indicating the relative support for the model. Significant effects ($P < 0.005$ using Bonferroni adjustment) are in bold.

Model	χ^2	**P**	**-2Log (likelihood)**	**AICc**	w_i
Shrub	20.37	**<0.0001**	2.29	9.38	0.9315
Total complexity	14.50	**0.0001**	5.23	15.26	0.0493
S-W Index	10.78	**0.001**	7.10	18.98	0.0076
Distance to edge	10.73	**0.001**	7.11	19.02	0.0075
Ground	7.34	0.02	8.79	22.38	0.0014
Species richness	7.03	0.01	8.96	22.72	0.0011
Sub canopy	6.50	0.01	9.23	23.26	0.0009
Canopy cover	4.25	0.04	10.35	25.50	0.0002
Constant model	-	-	12.48	27.45	0.0001
Canopy	1.04	0.31	11.96	28.71	0.0000
Ground cover	0.13	0.7	12.41	29.62	0.0000

4.4. DISCUSSION

4.4.1. Basic pattern of colonization

Eight out of nine saddleback pairs established home ranges around the periphery of Bushy Park reserve (Figure 4.1) where the majority of habitat consisted of dense, secondary vegetation in contrast to the mature podocarp-broadleaf forest in the interior. These results are consistent with previous studies on saddleback habitat selection. North Island saddlebacks on Hen Island were observed to feed more in secondary and coastal forests rather than mature forest (Atkinson & Campbell 1966). Lovegrove (1980) noted that regenerating forest on Cuvier Island was ideal habitat for saddlebacks due to its rich source of berry producing plants and deep litter layer. Similarly, South Island saddlebacks on Ulva Island (Hooson & Jamieson 2004, Steffens *et al.* 2005) and Breaksea Island (Hooson & Jamieson 2004) established territories that were almost exclusively distributed in coastal fringe habitat around the periphery of the islands.

4.4.2. The process of habitat selection

Historical records show that the North Island saddleback was once widespread throughout the North Island (Williams 1976) and would have occupied mature forest prior to their extinction on the mainland (Lovegrove 1996a). It is interesting therefore that this habitat type was largely avoided by saddlebacks at Bushy Park. Conceivably, the observed preference for habitats with dense, secondary vegetation may be due to the familiarity of this habitat type for the translocated birds. Vegetation on Mokoia Island, the source site, has a similar scrubby, regenerating forest makeup (Perrott & Armstrong 2000) and the saddlebacks habitat preference may be related to factors such as familiarity and cultural transmission rather than habitat quality (Gray & Craig 1991).

However, it seems more likely that the edge habitat with higher shrub complexity was indeed the best habitat available, and in selecting this habitat saddlebacks were making an adaptive choice that has evolved over time, consistent with the optimal choice models of Fretwell and Lucas (1970). The importance of 'shrub complexity' and 'total complexity' in predicting habitat occupancy indicates that complexity may be one of the environmental cues that saddlebacks use to select habitat.

Previous habitat studies have given evidence to suggest that a complex habitat structure is positively correlated to high invertebrate abundance and diversity. Halaj *et al.* (2000) tested the effect of habitat structural diversity on patterns of arthropod abundance and diversity by manipulating needle density and branching complexity of Douglas-fir branches. Results showed that arthropod diversity increased with habitat complexity, implying that levels of habitat complexity can be used as a meaningful measure of habitat quality (Huhta *et al.* 1998, Halaj *et al.* 2000) because a more complex habitat may provide greater food availability. Further evidence supporting this idea was shown in a study on the hihi and its habitat requirements. Hihi breeding success was shown to be positively associated with increasing complexity of the sub-canopy tier (6 m – 12 m) on Kapiti and Little Barrier Islands (Makan 2006). This tier of the forest is thought to be important for the hihi in terms of foraging and nesting behaviours. For saddlebacks, the shrub tier has been shown to be a preferred and important foraging location. Lovegrove (1980) studied foraging heights of North Island saddlebacks on Cuvier Island. Although the height at which birds foraged showed seasonal variation, the majority of foraging observations were between ground level up to six metres. This pattern in foraging behaviour could explain why 'shrub complexity' was the most important predictor of site occupancy. Because saddlebacks show a preference for foraging in the ground and shrub tiers, a higher complexity at this level may provide greater food availability.

The relationship between habitat structure and relative prey abundance seems to be relatively constant (Smith & Shugart 1987), further suggesting that the evolution of habitat selection based on structural cues is plausible. Habitats selected to provide adequate resources on arrival would therefore continue to provide adequate resources in the future rather than vary in quality in an unpredictable pattern.

Pairs may be selecting a more complex habitat for reasons other than increased food supply. Although Bushy Park has many potential nest sites, the fact that breeding pairs selected home ranges that were close to the forest edge and consisting of dense vegetation suggests that saddlebacks probably prefer sunny, well hidden nest sites. If so, this habitat would provide many good quality nest sites in contrast to the more damp, dark and comparatively open interior of the forest. During the first breeding season after release at Karori Wildlife Sanctuary, Wellington, saddleback chicks from nests in damp or cold sites appeared vulnerable when females started to leave the nest for longer

periods of time (Empson 2003). Numerous studies on saddleback breeding biology suggest a preference for secluded nest sites located in the shrub tier. North Island saddlebacks on Cuvier Island nested at a mean height of 3.4 m (Lovegrove 1980) and a study of the breeding biology of South Island saddlebacks on three offshore islands noted a mean nest height of 1.50 m (Hooson & Jamieson 2003). Similarly, 13 out of 16 saddleback nests at Bushy Park were situated within 2 m of the ground, although four of these were built in artificial nest boxes (refer to Chapter 3). Additionally, a more complex habitat may afford greater protection from predators. Recently fledged saddlebacks can be cryptic and display anti-predator strategies such as quietly hiding in dense, leafy vegetation (Lovegrove 1996b). It is possible that a greater complexity in the shrub tier represents a superior habitat to breeding saddlebacks by providing a greater number of high quality nest sites and fledgling protection in terms of dense vegetation cover.

It is likely that the significance of the 'distance to edge' variable reflects the saddlebacks evolved preferences for complex vegetation. This preference may have led the birds to seek out the diverse habitat found primarily on the periphery of Bushy Park reserve. The creation of an edge can affect forest structure by increasing the incident light, which in turn promotes plant growth (Chen *et al.* 1992). Stronger winds and greater variation in temperature also occur near forest edges (Ranney 1977) leading to higher tree mortality and an increase in the number of fallen trees (Chen *et al.* 1992). The resulting high density of the shrub tier and fallen trees at the edge may result in increased availability of food (Murcia 1995) and high quality nesting sites.

4.4.3. Implications for translocation to mainland sites

Although saddlebacks are thought to be flexible in their habitat requirements (Lovegrove 1996a), results from this, and previous studies, indicate that careful consideration is required when selecting release sites. In the past, where saddleback translocations to islands have been the norm, the determining factors for selecting release sites have been the presence or absence of important predators, size of the island and distance to the mainland. While these factors, particularly those relating to predation risk, remain important in the selection of high quality release sites, due consideration should be given to the habitat type of a release site.

Griffith *et al.* (1989) noted that species released into the centre of their historical range had a greater success rate than those released on the periphery of, or outside their historical range, however this may not be the case when a species historical distribution contains a large variety of habitat types, and the current distribution is restricted to just a few refuge habitats at the edge of its historical distribution (Hooson & Jamieson 2004). Until recently, North Island saddlebacks were absent from the mainland for over 100 years, existing only on offshore islands, most of which contain a mosaic of habitat types. Their long absence from the mainland should perhaps elicit caution when attempting to re-establish them within their historical range. I believe that saddlebacks are making an adaptive choice to settle in high quality habitats consisting of dense secondary vegetation, and translocation to poor quality habitats may result in lower density populations compared to island populations or even failure to establish.

The pattern of habitat selection at Bushy Park suggests that a 'source-sink' system could develop over time. As the perceived high quality habitat becomes full, birds will be forced to establish themselves in the previously avoided mature forest. Comparison of fecundity rates between pairs in edge and interior habitat in the future could therefore confirm whether the initially selected habitat has the highest quality, as suggested by the reproduction data on Mokoia. Considering the uncertainty of the suitability of habitat at Bushy Park, the future viability of the population could be improved by an adaptive management approach. For example, using the PVA model developed in Chapter 3, the effectiveness of management strategies such as the planting of more suitable plant species or the provision of nest boxes in less complex habitat, could be evaluated by monitoring the population under such strategies and then updating the population model. Additionally, the results from this study imply that the original population projections made in Chapter 3 may be too optimistic as the current habitat quality of Bushy Park may limit the growth of the population. If the interior habitat does represent a 'sink', then future release sites on the mainland will need to contain some minimum amount of dense, secondary forest rather than consisting of exclusively tall, mature forest. This raises some interesting issues about how big a mainland release site must be to support a viable saddleback population. For instance, although Bushy Park reserve has 87 ha of forest, it potentially has a much smaller area of suitable habitat for saddlebacks and, without careful management it may never support a high density population. Using the size of islands that currently support saddleback populations as a

guide to how large a mainland site should be is not advisable unless careful thought has gone into whether the habitat type at the mainland site is of a high quality for saddlebacks. For saddlebacks, habitat complexity may be used as a proximate measure of habitat quality.

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Synthesis

Translocation is one of New Zealand's most powerful tools for the conservation of its endangered species. But, whilst the number of translocations is increasing (Seddon *et al.* 2007), there is still a greater need for the application of research based approaches and post release evaluation techniques in order to gain knowledge to improve their success. This thesis investigated aspects of a North Island saddleback translocation in an attempt to add to the body of information relating to saddleback conservation, particularly on the mainland. It is hoped that a greater understanding of the processes affecting the outcome of this translocation may contribute towards the successful establishment of saddlebacks to mainland sites in the future.

Although I was unable to conclusively say what effect a typical disease screening process has on the outcome of a translocation, the saddlebacks at Bushy Park did experience a low survival rate during the first year after release compared to other populations that did not undergo a long quarantine period and were released into predator free sites. Additionally, the situation arising from the detection of the *Plasmodium* served to emphasize some major downfalls in the current management of disease risk that must be addressed. Situations such as these will continue to occur while such complex disease screening procedures are in place and could jeopardise translocation outcomes. Long quarantine periods, inaccurate diagnostic tests, and increased costs are just some of the obstacles that may arise. Given that little evidence

exists for disease related failure of a translocation, I recommend that further research into the effects of routine disease screening programmes is required to asses the costs and benefits to the outcome of a translocation. Furthermore, emphasis on the collection of baseline health data at both source and release populations may increase our knowledge on wildlife diseases in New Zealand and thus reduce the need for extensive disease screening during translocation.

The post release behaviour and breeding biology of the saddlebacks was similar to that seen in newly released island populations. However, reproduction rates were somewhat lower than would be expected for such a low density population. This may be due to the effects of the translocation process as previous research has shown that both survival and reproduction rates may be lower during the first year after release (Raeburn 2001). Preliminary analysis of data collected during the second breeding season indicates that reproduction rates are increasing (K. Brider pers. comm.), supporting the assumption that the effects of the translocation decreased fecundity.

Population modelling indicated that the population had a 0% probability of going extinct within the next five years. Because the model was based on survival and reproduction data collected in the first year after release it had a high degree of uncertainty, and management decisions should not be made on these initial projections (Armstrong & Ewen 2001). However, I propose that the model be used as the basis for future models using an adaptive management approach. Factors that are likely to affect long term population persistence are dispersal out of the reserve and habitat suitability. The original population projections may be overly optimistic as the model did not take these factors into account. Therefore, the extent to which they will affect viability should be explored by continuing to monitor the population and then predicting persistence with an updated model that includes the new data collected. Alternative management strategies should be evaluated in the same manner.

Saddlebacks showed a preference for the dense, secondary habitat around the periphery of the reserve over the primarily mature forest in the interior. My results suggested that habitat complexity, particularly in the shrub tier (30 cm – 6 m) is one of the environmental cues that saddlebacks use to assess the resources that a habitat may provide. A more complex habitat, such as that found around the edge of the reserve,

may represent a higher quality habitat by supplying greater prey abundance and diversity (Halaj *et al.* 2000), and high quality nest sites. The preference for this particular habitat type may therefore represent an adaptive choice that has evolved through natural selection. Ongoing monitoring would indicate whether the mature interior of Bushy Park will be a limiting factor for population growth and if this is the case, strategies to improve the habitat quality of the reserve may be valuable. For example, the provision of nest boxes in the mature interior of the forest and the creation of more dense, scrubby habitat may increase the habitat quality of Bushy Park. The effectiveness of these strategies could then be evaluated with updated population models as part of an adaptive management approach. My findings illustrate the need for careful selection of future mainland release sites which may tend toward mature forest. I recommend that release sites should be selected based on the amount of high quality habitat they contain specific to the species in question, rather than the total size of the site. In the case of saddlebacks, the habitat complexity of a site may provide a proximate assessment of habitat quality.

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