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**The Impact of Paradise Shelducks (*Tadorna variegata*)
on Pastoral Communities and their Role as Reservoirs
of Agricultural Diseases**

A thesis submitted in partial fulfilment of the requirements for the degree of
Masters of Science in Conservation Ecology,
Massey University, Auckland.

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2007

Abstract

Since its habitat expansion, due to human land clearance for farmland, paradise shelducks (*Tadorna variegata*) have established a firm foothold in the New Zealand agricultural environment. Paradise shelducks feed primarily on agricultural pasture and consequently compete directly with livestock for resources. As a result many farmers consider paradise shelducks to be a pest. In addition, it is a common perception that paradise shelducks contaminate agricultural land with their faeces. Although there is a wealth of information on the impacts of waterfowl on agricultural industries and diseases associated with waterfowl, no studies have specifically looked at the potential impact paradise shelducks pose on New Zealand's agricultural practices. The aims of this study were to 1) determine the presence and prevalence of pathogenic micro-organisms in paradise shelduck faeces and their associated environment, 2) evaluate the findings in terms of transmission routes and the relative risk to livestock and humans, 3) determine whether paradise shelducks have an affect on primary pasture production and composition, and 4) estimate the daily food intake rates of paradise shelducks.

This study was based on a population of paradise shelducks in Tawharanui Regional Park over each of four seasons from 2006-2007. The prevalence of pathogenic micro-organisms was determined by paradise shelduck faecal surveys for selected bacteria and parasites. Surveys were conducted for flock birds and breeding pairs. Additionally, faecal samples of sympatric species and water troughs were analysed. The impacts of paradise shelducks on pastoral communities was assessed by means of an exclusion experiment, consisting of two types of enclosure; a 'closed' enclosure to exclude all animals including paradise shelducks, and an 'open' enclosure to exclude livestock, but to allow access for paradise shelducks. Daily food intake rates for paradise shelducks were estimated from observational foraging data and necropsies of paradise shelducks.

Results show that no isolates of *Salmonella*, *Campylobacter*, *Yersinia*, *Cyrtosporidium* or *Giardia* were found. Relatively low prevalences of non haemolytic and alpha haemolytic *Streptococci*, *Enterococcus*, *Bacillus*, *Clostridium perfringens*, *Proteus mirabilis*, strongyle eggs and *Coccidia* eggs were found. Additionally, *E. coli* was consistently isolated from the faecal samples throughout the sampling period. However, the serotypes of the micro-organisms isolated were not determined, so no conclusions could be drawn in relation to their pathogenicity. Furthermore, no significant

correlations were found between the number of accumulated faeces sampled and the presence or prevalences of the micro-organisms isolated. It also appears that sampling during the driest times of the year will yield the highest presence of micro-organisms in paradise shelduck faeces. An array of micro-organisms, similar to those found in paradise shelduck faeces, were found in pukekos and house sparrow faeces as well as high contamination levels of faecal indicators in troughs. No conclusive transmission routes for the micro-organisms were found. Paradise shelducks were found to have a significant impact on pasture production and to selectively graze white clover (*Trifolium repens*). Furthermore, it was estimated that the paradise shelducks had a foraging intake rate of 104 ± 15 g/day of pasture dry matter. The results confirmed that paradise shelducks can have an affect on agricultural land. A more long term study in different regions is required to evaluate the full extent to which paradise shelducks affect agricultural production in New Zealand.

Acknowledgements

The first person I would like to thank is my supervisor, Associate Professor Dianne Brunton, for her advice, support and enthusiasm. I wish to also acknowledge Dr. Weihong Ji, Dr. Rosemary Barraclough, Dr. Nathalie Patenaude for their guidance.

I would also like to give a special thanks to Nicole Taylor and my parents, Terence and Delize Delaney for their support and patience.

Thanks to Fish & Game New Zealand and the Auckland Regional council who supported this project with funds. A special thanks to John Dyer and Tim Lovegrove for their help and advice. Additionally, I would like to thank Maurice Pucket, Colin Ward and TOSSI for their work at Tawharanui Regional Park.

Many thanks to everyone who helped me in the field and in catching those pesky ducks; Mark Casey, Nicholas East, Haden Henderson, Luis Otriz Catedral, Taneal Cope, Birgit Ziesemann, Mark Lowe, Mark Seabrook-Davison, Kevin Parker, Michael Anderson and Marleen Baling. Additional thanks goes to Ian and Tamsin Delaney, Brett 'Party-House' Hammond, Luke Meurant, Matt Payne and Sam Cox for his enthusiasm. A special thanks to Chris Wedding for all his help in the field and for the company up at Tawharanui.

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CHAPTER 1: General Introduction



Plate 1.1. Photo by M. Delaney 2006.

1.1 Diversity of Waterfowl in New Zealand

Because of their historical importance for hunting, domestication and aviculture, the family Anatidae (ducks, geese and swans) are the most well understood of all wild birds (Livezey 1986, Batt 1992). Anatidae or waterfowl have a dorso-ventrally flattened bill with a distinct hook nail at the tip. This characteristic bill is what differentiates this group from other birds. Although within the group bill characteristics are highly variable (Batt 1992). Waterfowl have a nearly cosmopolitan distribution, with Antarctica being the only continent without a waterfowl species (Batt 1992). The group are diverse in their anatomy, physiology, and behaviour and as a result, the estimated 150 species extant, inhabit practically every environment associated with water (Batt 1992). While most waterfowl are specifically adapted for aquatic habitats, there are some species which are nearly entirely terrestrial, such as shelducks and some geese (Batt 1992).

Like most other countries, New Zealand has its share of both native and introduced waterfowl species. Currently, New Zealand hosts 20 known species from the Anatidae family (Table 1.1). Of these, 12 are introduced, four are native and an additional four are endemic. Moreover, New Zealand is home to two species from the genus *Tadorna* (shelducks); the chestnut-breasted shelduck (*T. tadornoides*) and the more abundant paradise shelduck (*T. variegata*).

1.2 The Shelduck

Shelducks belong to the subfamily Anatinae and are one of 15 species in the tribe Tadornini (sheldgeese and shelducks) (Batt 1992). They are a group of mid-sized and often semi-terrestrial Old World waterfowl, and are present on every continent except North America and Antarctica. The shelduck is unusual and can be seen as an intermediate between geese and ducks. The sexes are dimorphic in most species, and all have a characteristic upper-wing colouration when in flight. They lack an eclipse plumage, and nest extensively in ground burrows (Patterson 1982). Shelducks combine grazing and dabbling feeding methods, and their diet usually consists mainly of plants, such as grasses, as well as small shore invertebrates, like crustaceans and insects (McKinney 1992). They have a long term pair bond but a relatively short period of parental care.

Table 1.1. Anatidae species found in New Zealand. E=Endemic, N=Native, V=Vagrant, I=Introduced. Data from (Robertson & Heather 1999, Heather & Robertson 2000, Kelly 2005).

Genus	Species	Common name	E	N	V	I	New Zealand Distribution
<i>Cygnus</i>	<i>atratus</i>	Black swan				*	North, South and Stewart Island
	<i>olor</i>	Mute swan				*	East Coast of North and South Island
<i>Branta</i>	<i>canadensis</i>	Canada goose				*	North, South and Stewart Island
<i>Cereopsis</i>	<i>novaehollandiae</i>	Cape Barren goose				*	Uncommon/Sporadic
<i>Anser</i>	<i>anser</i>	Feral goose				*	North, South and Stewart Island
<i>Tadorna</i>	<i>variegata</i>	Paradise shelduck	*				North, South and Stewart Island
<i>Tadorna</i>	<i>tadornoides</i>	Chestnut-breasted shelduck		*			Northern South Island
<i>Hymenolaimus</i>	<i>malacorhynchos</i>	Blue duck	*				Central North Island and West Coast of South Island
<i>Chenonetta</i>	<i>jubata</i>	Australian wood duck				*	Uncommon/Sporadic
<i>Dendrocygana</i>	<i>eytoni</i>	Grass whistling duck				*	Uncommon/Sporadic
<i>Anas</i>	<i>platyrhynchos</i>	Mallard				*	North, South and Stewart Island; offshore island groups
	<i>superciliosa</i>	Grey duck		*			North, South and Stewart Island; offshore island groups
	<i>rhynchotis</i>	Australian shoveler		*			North, South and Stewart Island
	<i>clypeata</i>	Northern shoveler				*	Uncommon/Sporadic
	<i>gracilis</i>	Grey teal		*			North Island and East Coast of South Island
	<i>castanea</i>	Chestnut teal				*	Uncommon/Sporadic
	<i>aucklandica</i>	Brown teal	*				East Coast of Northern North Island and West Coast of Southern North and South Island
<i>Malacorhynchus</i>	<i>membranaceus</i>	Pink-eared duck				*	Uncommon/Sporadic
<i>Aythya</i>	<i>australis</i>	White-eyed duck				*	Uncommon/Sporadic
	<i>novaeseelandiae</i>	New Zealand scaup	*				Northern and Central North Island and Northern and West Coast of South Island

Families break up when the parental pairs leave their breeding territory to migrate to a safer location for the annual wing moult (Williams 1979b, McKinney 1992). The same pairs will often reform in successive years, after the wing moult but mate switches do occur occasionally and rivalries over mates and territories are intense (Williams 1979b, Patterson 1982, Batt 1992, McKinney 1992).

Territoriality seems to be an especially significant component of the shelduck social behaviour. Breeding pairs are loud and conspicuous with persistent calling coupled with movements of the head and neck. These signals appear to be intended principally to act as a deterrent to territorial intruders and sexual rivals. This type of display signal is appropriate for long-distance communication in the open habitats shelducks occupy (Williams 1979b, McKinney 1992) and these behaviours are characteristic of the paradise shelduck in New Zealand.

1.3 The Paradise Shelduck

Like most other shelducks, paradise shelducks are sexually dimorphic, monogamous and goose-like in their feeding behaviour (Williams & Imber 1970, Williams 1971). The drake has a black head with a greenish gloss, the body being dark grey and barred with black, while the under-tail and tertials are orange chestnut. In contrast, the duck has a white head and the body is a bright orange chestnut. The paradise shelduck is a grazing species, mainly feeding on agricultural pasture (McAllum 1965, Williams & Imber 1970, Williams 1971, Bisset 1976). Paradise shelducks are generally found in two different habitats: (i) hill-country farmland, which is typical of the North Island and (ii) the tussock grasslands of the South Island (Williams 1979b, 1981). The ecology of the paradise shelducks described in the present study refers to hill-country farmland populations, unless otherwise stated.

1.3.1 Annual Cycle

In December, paradise shelducks start to gather in large flocks for their annual wing-moult. The flocks normally form concentrations of between 50 – 1500 birds (Williams 1979a) but moulting flocks have known to get as large as 4000-5000 birds. Initially, only non-breeding juveniles arrive at the moult sites. These young birds are followed later by the failed breeders and finally the successful breeding pairs, who are often

accompanied by their fledglings (Fitzgerald 1966, Williams 1979b). For the majority of paradise shelducks, moult migration does not exceed 35 km and generally the same moulting sites are used each year (Fitzgerald 1966, Williams 1979a, Barker 1990, Barker *et al.* 2005). Although, Barker *et al.* (2005) found that an estimated 30% of paradise shelducks in the Wanganui District permanently emigrated from their moulting sites. Moulting sites characteristically have a large open area of pasture accompanied by a large body of water close to allow for a safe retreat when threatened. During the moult, each bird is flightless for 3-4 weeks but will often remain much longer with the moulting flock. It is not until early March that the first adults leave to return to their previous years' breeding territories. Breeding pairs which may have broken up during the moult are re-established, although any mates that are lost are replaced by new partners (Williams 1979b). Conversely, newly fledged young, together with juveniles of the previous year remain as a flock at the moulting site (Williams 1979b).

From April breeding pairs will defend their territories against neighboring pairs and newly paired birds who are attempting to establish a territory. Additionally, males will tenaciously guard their mates against any rival males. Meanwhile, the flock of young birds and failed breeders remaining at each moulting site, slowly break off into smaller groups and migrate to better nearby feeding areas, where they remain throughout the rest of the year. Although, from September through to November, some juvenile pairs will leave the flock temporarily and visit areas which are prospective breeding sites and some will even migrate more than 100km away (Williams 1979b). Williams (1981) found that paradise shelducks, banded near Taihape in North Island and several South Island sites in New Zealand, migrated within 20 km of the banding site 50% of the time, and within 60 km 90% of the time. Some individuals traveled over 200 km.

Starting in July, breeding pairs will begin to search for potential nesting sites typically in trees, hollow logs or holes in the ground (Williams 1979b). Pairs will spend a lot of their day away from their territories looking for a place to nest, which can be from 100m to 1km away from their territories. The first eggs are generally laid in August with a mean clutch size of 9.4 eggs (Williams 1979b). Williams (1979b) found that for paradise shelducks in the Gisborne-East Coast district, 5% of all eggs in a clutch were infertile and 87% of the fertile eggs hatched.

Ducklings first appear towards the end of September. The ducklings are taken from the nest to their parents' territory to fledge, where Williams (1979b) found only

approximately 60% of ducklings survived (Williams 1979b). During the first week, ducklings will feed frequently on aquatic insects but will subsequently change their diet to plant material (Williams 1979b). After fledging, the family group remains on the territory while the adults undergo most of their body moult. By December, breeding territories are abandoned and all birds start to return to their moulting sites to start the annual cycle once more (Fitzgerald 1966, McAllum 1966, Williams 1979b).

1.3.2 Distribution Patterns and Current Status

The paradise shelduck is one of the few birds, endemic to New Zealand, to have benefited from European settlement and the subsequent drastic alteration of the New Zealand landscape (Williams 1979b, Barker *et al.* 2005). Paradise shelducks were originally recorded by Captain James Cook and J. R. Forster on Cook's second voyage to New Zealand in 1773. However, the species was well known to Polynesians by this time and formed a part of their diet (Williams 1971). The distribution of paradise shelducks in the Pre-European era was restricted to lowland short-tussock grasslands and to a lesser extent, swamplands (Williams 1971). At that time this habitat type in New Zealand was limited to areas mainly in the north of the South Island. This suggests that paradise shelducks had a relatively low abundance at this time. However, Polynesians may have caused an increase in Paradise shelduck numbers and distribution, as a result of land clearance from forest burning (Williams 1971).

When Europeans settled in New Zealand, paradise shelduck numbers and their habitat range initially grew due to land clearance, but in some areas a significant decrease in numbers occurred. This was most likely caused by over-harvesting (Williams 1971, Barker 1990). In response, the first game laws came into being in 1899 where paradise shelducks became protected in a few selected areas (Williams 1971). From 1900, under inconsistent protection laws, there was a gradual increase in the paradise shelducks range and numbers (Williams 1971). This increase is also attributed to translocations of eight birds into the centre of the North Island in 1915 and 1917 and a further translocation of 15 birds in 1920-21 (Williams 1971). By the 1930s, when a considerable amount of native forest had been turned into agricultural land, numbers had increased rapidly and the range extended up through the North Island by way of additional translocations of South Islands birds (Williams 1971, Bisset 1976). Twelve

birds were translocated to Kapiti Island in 1931 and an unknown number was translocated to Lake Rotomahana some time prior to 1936 (Williams 1971).

In 1948 the species was placed on the game license (Williams 1971). Consequently, there was a dramatic decline in populations, especially in the South Island. This reduction was further fueled by an increase in shooting, due to a lengthening of the hunting season and high limits in the 1950's. By 1962 the species was given complete protection throughout Southland, which helped to reverse the decline (Williams 1971). As the result of further conversions of forest to pasture and additional translocations in Northland, their range continued to expand northward (Williams 1979a, b, Barker 1990). The Northland translocations were mainly birds from the middle of the North Island, but records of these translocations are incomplete and often inconsistent (Williams 1971).

Paradise shelducks adapted well to these new areas and now have a range that covers the entire country (Williams 1971, Bisset 1976). Additionally, the extensive construction of small watering ponds and troughs throughout agricultural land help create a habitat which the species has successfully exploited. Consequently, the introduced pasture grasses, originally intended for agricultural purposes, became this species main food (Bisset 1976, Williams 1979b). Again, this increase in population numbers caused a rise in human exploitation of this species (Williams 1979b). Since human settlement in New Zealand, paradise shelducks have at times been so over-harvested that either populations failed to recover or it has required a relatively long period of protection before numbers recover sufficiently for hunting to continue (Williams 1971, 1981). As a result, hunting became gradually more strictly controlled by limiting hunting to specific parts of districts, lower bag limits and shorter hunting seasons (Williams 1971). Furthermore, population trends are now monitored annually by counting paradise shelducks at their moulting sites (Williams 1971, 1979a, b). Over exploitation from hunting in the past is unlikely to occur again, although paradise shelduck population trends are still strongly related to the pressures of exploitation.

Currently, paradise shelducks are still managed for waterfowl hunting throughout New Zealand. The species is the second main game-bird species in New Zealand, with approximately 130,000 birds shot annually (Barker *et al.* 2005). Fish & Game New Zealand manages waterfowl species and upland game-birds on behalf of recreational hunters. Management of these birds includes setting rules for how many birds can be

taken by hunters and at what time of year. However some bird populations, such as paradise shelducks, are unable to be managed through traditional hunting. Reasons for this include the intelligence of the bird and the almost endless source of good quality food (Fish & Game New Zealand 2007). Special permits for paradise shelduck hunting outside the seasons are allocated to areas to allow culling and to disperse the birds after moult (Fish & Game New Zealand 2007). While it is unlikely that paradise shelducks are in danger of to extinction throughout New Zealand, local extinctions of this species may occur if they are perceived as a pest and a threat to New Zealand's agricultural economy.

1.3.3 Farmers and Public Perception of Paradise Shelducks

When New Zealand was first settled, paradise shelducks were relatively uncommon. Subsequently, due to the conversion of bush to pasture, and the creation of stock ponds and troughs (thousands of which were subsidised by hunters' licence fees) (Fish & Game New Zealand 2007), numbers of paradise shelducks have exploded. The paradise shelduck is well adapted to the open farmland of New Zealand and has become and remained a common species throughout this habitat. Fish & Game state that game-birds are hunted and harvested at a rate that is sustainable and in most cases at levels that are acceptable to all interested parties including farmers whose crops birds occasionally feed on (Fish & Game New Zealand 2007). Senior Fish & Game Officer Matthew McDougall reported that, since paradise shelducks enjoy eating grass, they do attract the attention and anger of farmers. With rapid increases in numbers, many hill country farmers regarded paradise shelducks as an agricultural pest and put pressure on government authorities to control any increasing populations. What is more, in the 1980s in particular, concerned farmers simply went out and illegally poisoned or slaughtered the birds as they congregated in flocks (Fish & Game New Zealand 2007). As a consequence, Fish and Game will now issue special permits to hunt paradise shelducks, to stop large flocks damaging farm pastures with their grazing. The New Zealand Herald reported that the President of the Federated Farmers, Charlie Pedersen has called for DOC to stop protecting paradise shelducks, which he said farmers found to be a nuisance because the ducks ate crops (Atkinson 2006). As a result, Conservation Minister Chris Carter says he is looking at whether some animals, including some

native birds, should continue to be protected from hunters by the Wildlife Act (Atkinson 2006).

Furthermore, Catherine Petrey, Executive Director, Policy of Federated Farmers, states that although farmers concern about paradise shelducks are generally about damage to crops and pasture, Mr. Pedersen, has stated that while there is no proof, some farmers are convinced that ducks are a source of *Salmonella* and are responsible for higher than expected losses of young lambs and calves (C. Petrey 2006, pers. comm., 24 March). The New Zealand Herald also reported that farmers have told Federated Farmers that they believe that game-birds are doing more to foul some waterways than their livestock (Burgess 2007). Frank Brenmuhl, who heads the Federated Farmers dairy section added to this by stating that *E. coli* contamination in Lake Ellesmere and other water bodies in Canterbury was not caused by livestock but by waterfowl (Burgess 2007). Brenmuhl went on further to say: "the run-off from cows is virtually zero into waters in particular in Canterbury and the input from birds is 100 per cent." (Burgess 2007).

On the other hand, Auckland Waikato Fish and Game Officer, John Dyer, states that paradise shelducks normally feed on good, clean pastures, and although they do sometimes get blamed for spreading *Salmonella*, this opinion is not always accurate (J. Dyer 2006, pers. comm., 14 March). Dyer goes on to state that "paradise shelduck are big and visible so when a vets eyes fall on them, that's what is blamed" and tests are not normally conducted to confirm this diagnosis. Because of this perception by farmers that paradise shelducks are reservoirs for diseases, farmers are still illegally killing them accurate (J. Dyer 2006, pers. comm., 14 March). Dyer concludes, that while some farmers may suffer significant losses, the idea that paradise shelducks spread salmonella is a prejudice of certain landowners. The potential of paradise shelduck for carrying diseases between stock animals has not been investigated, but suggestions of mechanical transmission are plausible.

1.4 Outline of the Present Study

The paradise shelduck is endemic to New Zealand (Barker *et al.* 2005) but only a few studies have been conducted on this species and little has been published since the 1970's. Due to the conversion of native forests into pasture by human settlers in New Zealand, the paradise shelduck has experienced an extensive range expansion and a

population increase, and they are now synonymous with agricultural land. Consequently, paradise shelducks compete directly with livestock for pasture. Additionally, it is a common perception among farmers that this species is a reservoir for certain pathogenic micro-organisms that are potentially harmful towards livestock and humans. As a result many farmers in New Zealand consider paradise shelducks to be a pest, but no research has been conducted to assist wildlife and game-bird managers and farmers on this issue. Therefore, the main aim for this study is to determine whether farmers should view the paradise shelduck as an agricultural pest, and if so to what degree?

The definition of “pest” is given as: a general term for organisms which may cause illness or damage or consume food crops and other materials important to humans. An organism that is considered a nuisance to man, and usually having pathogenic properties (Biology-Online.org 2007). To assess whether paradise shelducks are a pest to agricultural practices the following objectives were set for this study;

1. Determine the presence of selected bacteria and parasites in paradise shelduck faeces.
2. Determine the prevalence of bacteria and parasites in paradise shelduck faeces between seasons and between accumulated sample sizes.
3. Compare the presence of bacteria and parasites in fresh accumulated faeces deposited by paradise shelducks to those of sympatric species.
4. Evaluate the findings in terms of the relative risk of exposure for livestock and humans in association with faeces deposited by paradise shelducks.
5. Evaluate the possible transmission routes in an agricultural environment of pathogenic micro-organisms associated with paradise shelduck faeces.
6. Gain an accurate estimate of paradise shelduck density and their usage of managed pasture areas in the Tawharanui Regional Park.
7. Determine whether or not paradise shelduck have an affect on primary pasture production.

8. Determine whether or not paradise shelduck have an affect on pasture species composition.
9. Gain an accurate estimate of paradise shelduck daily food intake rates

The findings from the present study may have a significant impact on consumers, the food industry, health agencies, farmers, wildlife and game-bird managers. This information will provide an indication of the types of pathogens that may be encountered in paradise shelduck faeces and the subsequent risk of infection to agricultural livestock. Additionally, this information will increase the understanding of the impact of grazing by paradise shelducks on the community structure and composition of pastures associated with agriculture in New Zealand. Consideration of these findings will help to assess whether paradise shelducks are an agricultural pest, as well as assist wildlife mangers, health agencies, game-bird managers and farmers in management decisions.

To assess these objectives this study was divided into two sections; micro-organisms of paradise shelduck faeces and their effects on an agricultural environment (Chapter 2), and the effects of paradise shelducks on pastoral communities (Chapter 3). To examine the micro-organisms of paradise shelduck faeces and their effects on an agricultural environment, paradise shelduck faeces samples were collected from both a flock group and a breeding pair found on agricultural land. Samples were taken during four different seasons over a year long period and sent to New Zealand Veterinary Pathology Ltd. for analysis. Additionally, water trough samples and samples from other avian species associated with agricultural land were taken from within the paradise shelduck territories for analysis.

To examine the effects of paradise shelducks on pastoral communities, two enclosure were set up on agricultural land: a 'closed' enclosure to exclude all animals including paradise shelducks, and an 'open' enclosure to exclude livestock, but allow access for paradise shelducks. Pasture growth and species composition were measured for four weeks during four different seasons over a year long period. This allowed a comparison to be made between pastoral communities of grazed and un-grazed pasture plots by paradise shelduck. In order to estimate daily pasture intake rates of paradise shelducks, necropsies and observational research were conducted.

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CHAPTER 2: Micro-organisms of Paradise Shelduck Faeces and their Effects on an Agricultural Environment



Plate 2.1. Photo by M. Delaney 2006.

2.1 Abstract

The potential for the transport and dissemination of certain pathogenic micro-organisms by waterfowl is of general concern to farmers and conservation managers and is the subject of increased biosecurity vigilance. Previous studies have shown that waterfowl populations clearly carry micro-organisms potentially pathogenic to humans and livestock. However, the extent to which wild bird-vectored micro-organisms are being transmitted to mammalian hosts and the prevalence of such micro-organisms in New Zealand waterfowl populations is largely unknown. An understanding of pathogenic micro-organisms dynamics in an agricultural framework is essential to maintain the integrity of agriculture as an important industry.

The present study was undertaken to assess the extent to which paradise shelducks (*Tadorna variegata*) are acting as reservoirs for pathogenic micro-organisms and explore the possibility of cross-transmission of pathogenic micro-organisms to humans or livestock. No isolates of *Salmonella*, *Campylobacter* or *Yersinia* species were found in the paradise shelduck faeces at Tawharanui Regional Park. Relatively low prevalences of non haemolytic and alpha haemolytic *Streptococci*, *Enterococcus*, *Bacillus*, *Clostridium perfringens* and *Proteus mirabilis* were found. *E. coli* was consistently isolated from the faecal samples throughout the sampling period.

Additionally, no significant correlations were found between the number of accumulated faeces sampled and the presence or prevalence of the micro-organisms isolated. Furthermore, it appears that sampling during the driest times of the year will yield the highest presence of micro-organisms in paradise shelduck faeces.

Paradise shelducks may be acting as reservoirs for the micro-organisms isolated in this study, and these could potentially pose a threat to livestock, agricultural practices and human health. However, the serotypes of the micro-organisms were not determined, so no conclusions could be drawn in relation to their pathogenicity. Additionally, although a similar array of micro-organisms were found in pukekos (*Porphyrio melanotus*) and house sparrows (*Passer domesticus*) as well as high contamination levels of faecal indicators in troughs, no conclusive transmission routes for the micro-organisms were found.

2.2 Introduction

2.2.1 Pathogenic micro-organisms associated with waterfowl

It is well established that wild birds have the potential to disperse pathogenic micro-organisms (Clark 2003, Hubálek 2004). Birds can either serve as biological carriers when the pathogen multiplies in the avian body, or otherwise act as mechanical carriers when the pathogen does not multiply (Hubálek 2004). Internationally, there is an increasing awareness amongst biologist of the need to gather information on the diseases of wild birds (Cork 1994). Consequently, studies have concentrated on migratory and flocking bird species such as waterfowl (Fallacara *et al.* 2001, Ballweber 2004, Hubálek 2004, Clark & Hall 2006).

Waterfowl, whether wild or domestic, are hosts to a wide variety of internal micro-organisms (Hussong *et al.* 1979, Fleming *et al.* 2001, Clark 2003, Ballweber 2004). Internal micro-organisms are defined as an agent that passes through the digestive tract of a host and is still viable when excreted (Hubálek 2004). Such internal micro-organisms can occasionally be pathogenic. For example, *E. coli* is associated with the normal intestinal flora of birds and mammals (Ahmed *et al.* 2005), however it can cause infections under certain circumstances (Callaway *et al.* 2003).

There are unique characteristics in waterfowl that may enhance the conditions conducive to the development for micro-organisms and ultimately promote their transmission (Morishita 2004). Waterfowl tend to aggregate in flocks around staging and feeding areas. As a consequence, large numbers of birds are concentrated spatially and temporally. This causes an increased opportunity for infection by exposure to contaminated environments (Clark & Hall 2006). When congregation occurs, horizontal transmission of micro-organisms may occur between individuals from the same species, and even between species (Hubálek 2004). Additionally, the highly mobile behaviour of waterfowl and their utilisation of agricultural areas increases the possibility of cross-transmission of micro-organisms to other individuals or species, by direct contact or faecal contact. Certain environments, such as wetlands, may also promote disease manifestation. Because of their aquatic lifestyle, ducks may be exposed to, and consequently host, a diverse array of potentially pathogenic organisms such as

Campylobacter, *E. coli*, *Salmonella* spp., *Clostridium* spp., *Giardia*, *Yersinia* spp. and *Cryptosporidium* spp. (Cork 1994, Craven *et al.* 2000, Fallacara *et al.* 2001, Abbott 2003).

Despite the growing concern about the role waterfowl and their faeces may play in environmental contamination, very few studies have been conducted to determine the incidence of any of these micro-organisms in waterfowl populations. Recently more detailed studies on waterfowl have been published (Graczyk *et al.* 1998, Feare *et al.* 1999, Fallacara *et al.* 2001). Feare *et al.* (1999) screened waterfowl faeces for a range of bacteria and found a wide variety of *Enterobacteriaceae*, including *E. coli*, *Salmonella* spp., *Enterobacter aerogenes*, *Enterobacter clocae*, *Klebsiella pneumoniae* and *Proteus mirabilis*. The study also found that these bacteria can survive in the faeces for up to four weeks. In a survey of faecal shedding of selected bacterial pathogens from waterfowl in Ohio, Fallacara *et al.* (2001) isolated *Campylobacter jejuni*, *E. coli*, and *Salmonella*, from mallard ducks (*Anas platyrhynchos*), domestic hybrid ducks, and Canada geese (*Branta canadensis*). Prevalences of 67%, 50% and 0.2% were found for *E. coli*, *C. jejuni*, and *Salmonella*, respectively, for all waterfowl species. Graczyk *et al.* (1998) sampled Canada geese faeces collected from nine sites in Maryland, USA, and examined them for the presence of *Cryptosporidium parvum* and *Giardia* species. *Cryptosporidium* oocysts were found in faeces at seven of the nine sites, and *Giardia* cysts were found at all nine. These findings provide clear evidence that waterfowl can act as carriers of these organisms and disseminate them into the environment.

It must be noted that differences in the population biology and life history characteristics of wild birds, geographic location, time periods of sampling, study design and the sample size, make comparisons of results between studies problematic. However, these few examples clearly show that faeces from waterfowl populations are a rich source of relatively uncharacterised microbial diversity. Although less sensitive than some other pathogen survey techniques, faecal sampling does provide representative results for determining faecal micro-organisms of wild bird populations. Faecal sampling is also more reliable than cloacal samples since the latter can be variable due to the small amount of faecal material collected, and consequently a reduced chance of culturing the targeted organisms (Cork 1994).

2.2.2 Potential agriculture, livestock, economic and public health impacts

Many wildlife species are reservoirs of pathogens that threaten domestic animal and human health. Due to their great mobility, wild birds, such as waterfowl, may function as particularly effective spreaders of disease through faecal contamination of pastures, feed and water sources (Hussong *et al.* 1979, Kapperud & Rosef 1983). Hussong *et al.* (1979) screened faeces of Canada geese and whistling swans (*Olor columbianus*) in Maryland, Baltimore. A pathogenic strain of *E. coli* was isolated from the faeces, and was subsequently found to have contaminated local water sources. As a result of such studies, disease transmission by wild birds is of increasing concern in the areas of public health and agricultural production and is accordingly the subject of increased vigilance (Feare *et al.* 1999, Clark 2004).

Certain pathogens, such as *Yersinia pseudotuberculosis* (Cork 1994), have been isolated from apparently healthy wild birds. Furthermore, clinically affected wild birds can shed large numbers of micro-organism resulting in environmental contamination. *Yersinia* species are known to infect humans and livestock as well as birds (Cork 1994). This causes a potential risk for disease transmission. Equally important, waterfowl have been incriminated as the potential source of faecal indicators in the contamination of surface water (Luechtefeld *et al.* 1980, Graczyk *et al.* 1998, Murphy *et al.* 2005). A catchment study on the Island of Jersey (Wyer *et al.* 1995) found that waterfowl, such as ducks and swans, can significantly influence water quality compliance by increasing the total faecal coliforms, *E. coli*, and *Enterococci* concentrations. Furthermore, a study on the impact of Canada geese and whistling swans on aquatic ecosystems in Baltimore (Hussong *et al.* 1979) showed that large flocks of waterfowl can cause elevated faecal coliform densities in surface water. This can have a serious impact, as faecal contamination of water on farms can lead to potential disease transmission (Pyle 1974). For the most part micro-organism pathogen prevalences and transmission routes, detailed in Figure 2.1 are largely unknown. Additionally, the extent of the impact of disease transmission would depend principally on the numbers of faecal indicator bacteria discharged, accumulation of organic matter, and the presence or absence of pathogens in waterfowl faeces (Hussong *et al.* 1979).

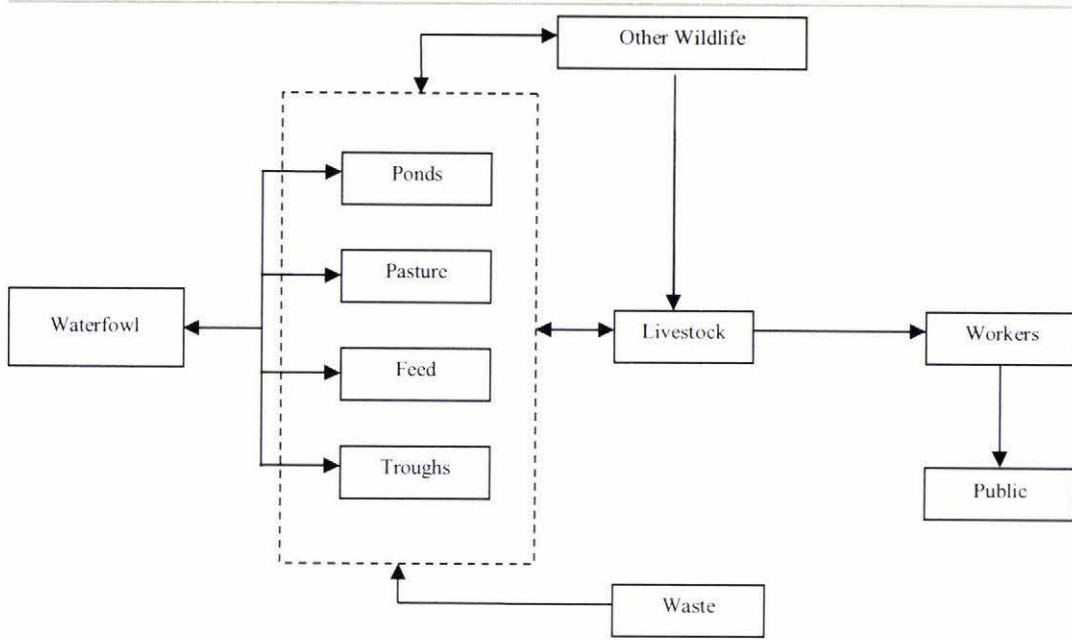


Figure 2.1. Possible transmission routes of exposure and dissemination of micro-organism pathogens between waterfowl and livestock.

Millán *et al* (2004) investigated *Salmonella* species in 205 wild birds and confirmed the importance of wild birds as a *Salmonella* reservoir and as a potential risk for humans and livestock. Waterfowl in New Zealand, specifically, are a potential reservoir of *Salmonella* and may introduce *Salmonella* into a farm environment, creating a risk for livestock (Robinson & Daniel 1968, Fossler *et al.* 2004). *Salmonella* infections are known to be a significant cause of mortality, morbidity and abortions in cattle (*Bos taurus*), sheep (*Ovis aries*) and horses (*Equus caballus*) (House & Smith 2000, Wray & Davies 2000, Wray & Linklater 2000). In the UK, *S. dublin* currently causes 400-500 incidents in cattle annually, and although *S. dublin* has been isolated from humans in New Zealand, it has not been detected in New Zealand livestock (Wray & Davies 2000). *Campylobacter* spp., *E. coli*, *Salmonella* spp., *Yersinia* spp., *Coccidia* and *Cryptosporidium* spp., can also all infect livestock and are similarly found in their faeces as well as waterfowl faeces. These micro-organisms have been associated with diarrhea and mortalities, particularly in neonatal livestock (Adesiyun & Kaminjolo 1994). Similarly, oocysts that pass through the gastrointestinal tract of waterfowl, retain their infectiousness (Graczyk *et al.* 1998) suggesting that waterfowl have the potential to serve as mechanical carriers and infect livestock. Fallacara *et al.*, (2001) concluded that waterfowl can serve as potential reservoirs for a variety of pathogens and that contact with these birds or their faeces can result in cross-transmission of the pathogens.

Tizard (2004) also concluded that cross-transmission can occur, as livestock may acquire infection from wild birds.

Cross-transmission of pathogenic micro-organisms on farms can dramatically affect agricultural practices by infecting livestock and causing a lower production rate. For example, livestock and wild birds may be acting as reservoirs of *Campylobacter* causing cross-transmission and serving as contaminators (Savill *et al.* 2003). Consequently, *Campylobacter fetus*, *C. jejuni* and *C. venerealis* are frequently associated with abortion, stillbirth and infertility in livestock (Luechtefeld *et al.* 1980, Varga 2001). In addition, intestinal parasitism, such as coccidiosis, is a major stress factor leading to malnutrition and lowered performance and production efficiency of livestock (Yun *et al.* 2000). Thus, infected livestock can have a significant impact on agricultural production and consequently the economy. This is of high concern for New Zealand as its economy is agriculturally based (Savill *et al.* 2003).

Micro-organisms that affect agriculture, such as milk production in dairy cows, can impact not only on agricultural economics but also public health. Food-borne bacterial pathogens directly affect consumers, the food industry, and are consequently a major concern for regulatory and health agencies. For example, *E. coli*, *Streptococcus* spp., *Salmonella* spp., *Clostridium* spp., *Enterobacter aerogenes*, *Enterobacter clocae*, *Klebsiella pneumoniae* and *Proteus miarblis* are just some of the micro-organisms, which can cause food-borne disease, isolated from human faeces (Stewart 2005). Consequently, pathogen contaminated faeces of animals and humans are the main source of bacteria contamination in foods. The role of *Campylobacter* as a leading cause of enteritis in people worldwide, has increased significantly over the past 20 years (Adhikari 2003). Additionally, the increasing trend in bacterial presence, particularly *Campylobacter jejuni*, manifesting on farms could result in a potential threat to the New Zealand's meat and milk industry.

Interventions, aimed at reducing the impact of food-borne pathogens on public health, that focus solely on minimising human exposure, without consideration of the environmental reservoirs of pathogenic micro-organisms, may only have limited success. A more effective approach may be to reduce the frequency with which the organism contaminates food and water at the source of the contamination, such as farms, thereby reducing the human exposure. Intervention strategies to stop the spread

of these pathogens to consumers include the appropriate animal husbandry practices on the farm. If the incidence of pathogenic micro-organisms can be reduced in livestock and their environment, it is likely that the incidence of these pathogenic micro-organisms in agricultural produce can be reduced or even eliminated. Controlling these pathogens on the farm requires knowledge of the ecology of the disease, including animal reservoirs. Besides veterinary solutions to herd health, limiting sources of infection by means of bio-security should be a high priority for producers.

2.3 Background on targeted pathogenic micro-organisms

2.3.1 Bacteria

2.3.1.1 *Salmonella*

Salmonella is a genus of rod-shaped Gram-negative enterobacteria, and is among the most common and costly causes of food-borne illness in humans. Additionally *Salmonella* can also cause disease and occasionally death in livestock (Fossler *et al.* 2004, Millán *et al.* 2004, Tizard 2004). *Salmonella* serotypes that are potentially pathogenic in humans and animals include; *S. brandenburg*, *S. agona*, *S. stanley*, and *S. typhimurium*. These serotypes have also been isolated in waterfowl faeces (Robinson & Daniel 1968, Levesque *et al.* 1993, Hubálek 2004, Tsai & Hsiang 2005). Although the prevalence of *Salmonella* in waterfowl is well recognised internationally, the degree to which the waterfowl population itself suffers as a consequence, appears to be minimal (Henry 2000, Morishita 2004).

Salmonella bacteria, especially *S. typhimurium* are commonly found in the intestines of wild birds (Tizard 2004). The prevalence of *Salmonella* in wild birds appears to have greatly increased worldwide over the past 40 years (Tizard 2004). Mortality due to salmonellosis has rarely been reported in birds in New Zealand, although sporadic mortalities in house sparrows and other passerines are not uncommon during winter months. In particular, *S. typhimurium* DT160 was not recorded in New Zealand prior to 1998 or in animals prior to 2000. Subsequently, there has been a rapid rise in the

frequency of outbreaks during winter and spring in birds and livestock. Wild birds have been identified as asymptomatic carriers of *S. typhimurium*, and this genetic type now appears to be endemic in New Zealand (Alley *et al.* 2002, Tizard 2004). *S. typhimurium* are considered to be non-host specific, since they are capable of infecting an enormous diversity of species, including cattle, pigs (*Sus* spp.), rodents (*Rattus* and *Mus* spp.) and birds (Tizard 2004). Because of its rapid spread and wide distribution throughout New Zealand, the organism must now be considered a serious zoonotic risk. Additionally, an outbreak of *S. brandenburg* during 1999 and 2000 in New Zealand caused abortions in sheep flocks (New Zealand Food Safety Authority). No conclusive transmission routes were found. But, one out of five ducks (species not identified), found on a farm where an outbreak occurred, tested positive for *S. brandenburg*, and it was thought the sheep picked up the pathogen from contaminated pasture or water and thus reflects environmental contamination.

2.3.1.2 *Campylobacter*

Campylobacter is a genus of Gram-negative bacteria, and is the greatest cause of bacterial gastrointestinal infections worldwide (Murphy *et al.* 2006). The reported numbers of human *Campylobacter jejuni* infections have increased considerably in many countries during the last few years and the reason for this is largely unknown (Petersen *et al.* 2001). In New Zealand, the annual incidence rate (302.5 cases/1000 000) of human campylobacteriosis in 2003 was higher than that of any other notifiable disease, and exceeds the incidence of campylobacteriosis reported by other developed countries (Adhikari 2003, Savill *et al.* 2003). Campylobacteriosis occurs more than twice as often in New Zealand as in England, and more than three times as frequently as in Australia and Canada (Hearnden *et al.* 1998).

Campylobacter, especially *C. jejuni*, is regularly found in ducks and geese. These species can be important reservoirs for this bacteria and can shed *Campylobacter* into water sources (Yogasundram *et al.* 1989, Altekruise *et al.* 1999, Craven *et al.* 2000, Adhikari 2003, Savill *et al.* 2003, Murphy *et al.* 2006). Moreover, overlap is reported between serotypes of *C. jejuni* found in humans, livestock and wild birds (Altekruise *et al.* 1999). For instance, *C. jejuni*, which causes acute diarrhoea in humans, was isolated in the caeca 35% (n=445) of ducks killed by hunters in Colorado (Luechtefeld *et al.* 1980). Additionally, during banding in Washington, Pacha *et al.* (1988) collected swabs

from ducks and recovered *Campylobacter* from 73% (n=133) of samples. The commonality of *C. jejuni* serotypes in ducks and geese with those of humans signals the zoonotic potential of these birds in relation to human campylobacteriosis.

2.3.1.3 *Yersinia*

Yersinia is a genus of Gram-negative bacteria, which can cause disease resulting in malaise or diarrhoea in both animals and humans. Yersiniosis in mammals and birds is generally caused by *Y. pseudotuberculosis* or *Y. enterocolitica*. It is rarely caused by other species of *Yersinia*, except in exceptional cases where the host is severely debilitated (Cork 1994). *Yersinia* tends to cause disease in cooler months and in populations or individuals under nutritional or management stress, or with concurrent disease. *Yersinia* species can infect humans, livestock and birds, including waterfowl. Furthermore, the clinical signs of yersiniosis are very similar in both wild birds and livestock (Mackintosh & Henderson 1984, Fukushima & Gomyoda 1991, Cork 1994). This suggests that mammals and wild birds, in New Zealand, may be reservoir hosts for *Yersinia* species and a potential source of infection on farms.

2.3.1.4 *Escherichia coli*

E. coli is an enteric Gram-negative bacteria species that is not normally pathogenic as it is part of the normal intestinal flora of birds and mammals necessary for the proper digestion of food (Callaway *et al.* 2003, Ahmed *et al.* 2005). Accordingly, *E. coli* presence in groundwater is a common indicator of faecal contamination (Russo & Johnson 2003). However, *E. coli* can at times be pathogenic to humans and animals, and some strains such as, *E. coli* 0157:H7 are the cause of large scale outbreaks of human diseases such as hemorrhagic colitis (Callaway *et al.* 2003). *E. coli* 0157:H7 have also previously been isolated from healthy and diseased wild birds (Hubálek 2004). For example, Samadpour *et al.* (2002) isolated *E. coli* 0157:H7 from duck faecal samples in an outbreak in Vancouver. Consequently, the authors were unable to ascertain if the resident population of ducks was the source of the contamination. They suggest that the ducks may have been transiently infected by contaminated water and may have helped to sustain contamination levels at the lake over a period of time.

2.3.1.5 *Bacillus*

The genus *Bacillus* includes Gram-positive and Gram-variable rod-shaped bacteria. Several *Bacillus* species, such as *B. thuringiensis* and *B. cereus*, are known for their pathogenicity and are a significant cause of food-borne disease (Castagnola *et al.* 2001, Ehling-Schulz *et al.* 2004, Schoeni & Wong 2005). *Bacillus* is widespread in nature and can be commonly isolated from dairy products, meat, chicken and vegetables (Ehling-Schulz *et al.* 2004, Schoeni & Wong 2005). However, there are very few studies concerning the transmission routes of *Bacillus* in a farm environment.

2.3.1.6 *Streptococci*

There are many species within this genus which are responsible for significant levels of disease in domestic, farm and aquatic animals (Hardie & Whitey 1997). *S. pyogenes* and *S. pneumoniae* are well recognised as major human pathogens and many others are capable of causing disease under appropriate conditions. Additionally, *Streptococci* species are also associated with infection of livestock (Hardie & Whitey 1997). However, in most cases the streptococcal involved with animal infections are different from those responsible for human disease. Although, in a few case some *Streptococci* species, such as *S. agalactiae*, *S. bovis* and *S. dygalactiae*, do cause infections in both animals and humans (Hardie & Whitey 1997). Bovine mastitis is one disease of considerable economic significance to agricultural production, which can be caused by several streptococcal species including *S. canis*, *S. agalactiae*, *S. parauberis*, *S. uberis* and *S. dygalactiae* (Watts 1988, Forsman *et al.* 1997). In spite of this, there are very few studies concerning the transmission routes of *Bacillus* in an agricultural environment.

2.3.1.7 *Enterococcus*

Enterococcus is a genus of Gram-positive bacteria, which were originally classified with the group *Streptococcus* until 1984. *Enterococcus* species are a part of the normal intestinal flora and faeces of birds and mammals, but are also important pathogens responsible for serious infections such as endocarditis and bacteremia. There are many species within this genera which are responsible for significant levels of disease in domestic, farm and aquatic animals (Hardie & Whitey 1997). Unfortunately, once again

there are very few studies concerning the transmission routes of *Enterococcus* in a farm environment.

2.3.1.8 *Clostridium*

Clostridium is a large genus of Gram-positive bacteria, with some of its species, such as *C. botulinum* and *C. perfringens*, being pathogenic. *C. botulinum* causes botulism by the ingestion of a toxin produced by the bacteria. Both ducks and geese can succumb to botulism and perpetuate the botulism cycle. *C. perfringens* is commonly encountered in infections and as an agent of food poisoning (Schotte *et al.* 2004, Songer & Miskimmins 2004). It is an important cause of enteric disease in domestic animals (Schotte *et al.* 2004, Songer & Miskimmins 2004). Additionally, these bacteria and their spore can survive in the environment for an extended period of time (Morishita 2004).

2.3.2 Faecal parasites

2.3.2.1 *Cryptosporidium*

Cryptosporidium is a coccidian parasite that has traditionally been considered a strictly animal pathogen. In a survey by Chilvers *et al.* (1998), large numbers of animal reservoirs for *Cryptosporidium* have been identified among wild animals on farms in New Zealand. *Cryptosporidium* oocysts were detected in three out of six mammalian species and three out of seven passerine species sampled. *Cryptosporidium* can cause coccidiosis, which is an intestinal infection that can lead to malnutrition and lowered performance and production efficiency in livestock. Furthermore, *Cryptosporidium* is now recognised as an important human pathogen, as it is a leading cause of persistent diarrhoea in developing countries (Abbott 2003).

2.3.2.2 *Giardia*

Giardia is a flagellated protozoan parasite that colonises the intestine of many mammals and birds. *Giardia* is recognised as the most common human intestinal parasite in the world and is a major cause worldwide of waterborne diseases in humans (Abbott 2003). Their infectious stage, the cyst, is transmitted via water and faecal-oral contamination.

Cross-transmission of avian isolates of *Giardia* to mammals may have serious implications for contamination of water sources (Graczyk *et al.* 1998, Heitman *et al.* 2002). In New Zealand large numbers of animal reservoirs for *Giardia* have been identified among wild mammals and birds surveyed on farms (Marino 1993, Chilvers *et al.* 1998). Chilvers *et al.* (1998) detected *Giardia* cysts in faecal samples from six mammalian species and six out of nine passerine species; no cysts were detected in any of the five duck samples tested.

2.3.2.3 *Ascarid*

Ascarid roundworms are usually found in the lumen of the small intestines of animals. They have a simple and direct life-cycle. The eggs are discharged on the faeces and develop into the infective form after about two weeks. The infective eggs will remain viable under suitable conditions for up to a year. Following ingestion by a susceptible host, the larvae are liberated from the egg and take about four weeks to become adults and produce eggs (Reece 1989). All parasites may inflict pathological and physiological disorders on the host resulting in impaired metabolic efficiency and absorbance of nutrients (Hakkarainen *et al.* 2006).

2.4 Objectives

The study of wildlife disease from an agricultural management perspective focuses on four areas; (1) the role that wildlife has in the dissemination and transmission of pathogens with zoonotic potential, (2) the role that wildlife has in the dissemination and transmission of pathogens that affect livestock, (3) the economic consequences of wildlife disseminated and transmitted disease, and (4) possible management options to disrupt dissemination and transmission of pathogens.

The general objective of this chapter was to determine if specific micro-organisms that can cause disease in livestock or humans are present in faecal material deposited by resident populations of paradise shelducks (*Tadorna variegata*) in an agricultural environment. Specifically, the objectives in this chapter are:

1. Determine the presence of selected bacteria and parasites in fresh faeces deposited by paradise shelduck.

2. Determine the prevalence of bacteria and parasites in fresh faeces deposited by paradise shelduck between seasons and between accumulated sample sizes.
3. Compare the presence of bacteria and parasites in fresh faeces deposited by paradise shelduck to those of two other sympatric wild avian species: pukeko (*Porphyrio melanotus*) and the house sparrow (*Passer domesticus*).
4. Evaluate from these results, the relative risk of exposure for livestock and humans in contact with faeces deposited by paradise shelducks.
5. Evaluate the possible transmission routes in an agricultural environment of pathogenic micro-organisms associated with faeces deposited by paradise shelduck.

This information will provide an indication of the types of pathogens that may be encountered in paradise shelduck faeces and the subsequent risk of infection to agricultural livestock. Consideration of these interactions could be used to predict the outcome of future infection, and assist in agricultural management decisions.

2.5 Methods

2.5.1 Study Site

This study was based at Tawharanui Regional Park (Figure 2.2), situated 90 km north of Auckland on a peninsula in the Hauraki Gulf. Tawharanui Regional Park is a 588 hectare ‘mainland island’ consisting of coastal lowland environments, such as, dunelands, coastal forest, wetlands, streams and open agricultural pasture (TOSSI 2007). A 2.5 km long predator-proof fence across the base of the peninsula from coast to coast completed in 2004 made Tawharanui Regional Park New Zealand's first integrated open sanctuary where farming, public recreation and conservation of native species are combined. Currently, Tawharanui Regional Park has no introduced mammals except for livestock, rabbits and mice, which are all controlled. Tawharanui Regional Park was chosen for this study as it contains typical North Island hill-country farmland, which is the characteristic habitat for North-Island paradise shelducks. The

area has a combined total of 150 hectares of agricultural pastures of mixed ryegrass, kikuyu and white clover, farmed with sheep and cattle (ARC 2007). This is the preferred pasture of paradise shelducks, who actively seek out mixed pastures with clover species (Bisset 1976). Additionally, Tawharanui Regional Park has hosted a population of paradise shelducks for decades (Ward 2006). However, this population suffered a substantial loss of 32 paradise shelducks from a population of 43.4, after two aerial poison drops were conducted in 2004 (Lovegrove & Ritchie 2005). Consequently, this population recovered to its initial size in the following year (Lovegrove & Ritchie 2005). During this study (May 2006 to March 2007) there was only one flock present within the Tawharanui Regional Park, which included between 44.92 and 77.17 individual birds (Table 3.2). In addition, there were approximately 20 breeding pairs within the park.

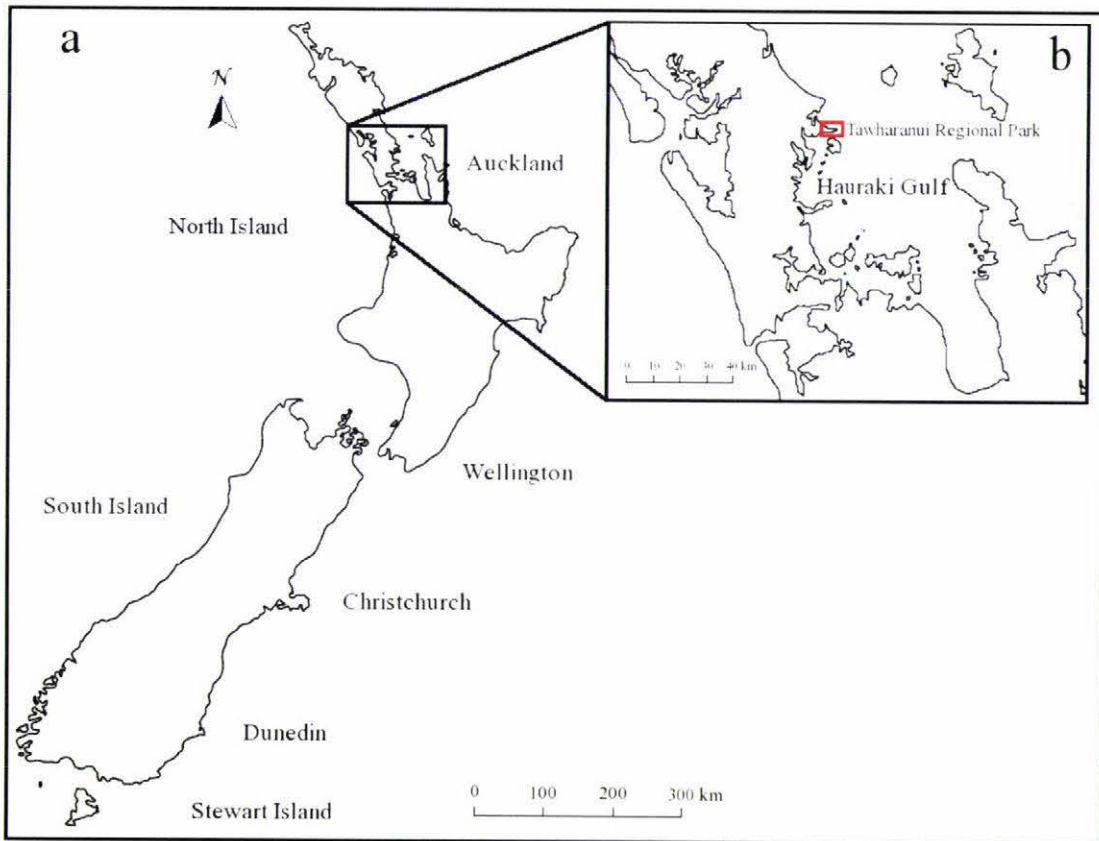


Figure 2.2. (a) Map of New Zealand outlining the Hauraki Gulf. (b) Enlarged map of Auckland showing the Hauraki Gulf and Tawharanui Regional Park.

2.5.2 Faecal sampling

Paradise shelduck faecal samples were collected from four sites within the Tawharanui Regional Park (Figure 2.3). Samples were taken at different times of the year between 2006 and 2007 (Table 2.1). Each sample set consisted of six samples (*i – vi*) collected as follows:

(*i – iii*) *Breeding pairs on permanent territories*: The same pairs were always used and identified by colour bands. One sample consisted of two combined samples (one from each individual of two pairs at different locations).

(*iv – vi*) *Flock samples from flocking territory*: these samples were obtained from different individuals from the flock within the flocking territory (Figure 2.3). Sample *iv* consisted of five individual faecal samples combined, sample *v* consisted of 10 individual faecal samples combined, sample *vi* consisted of 25 individual faecal samples combined (Table 2.1).

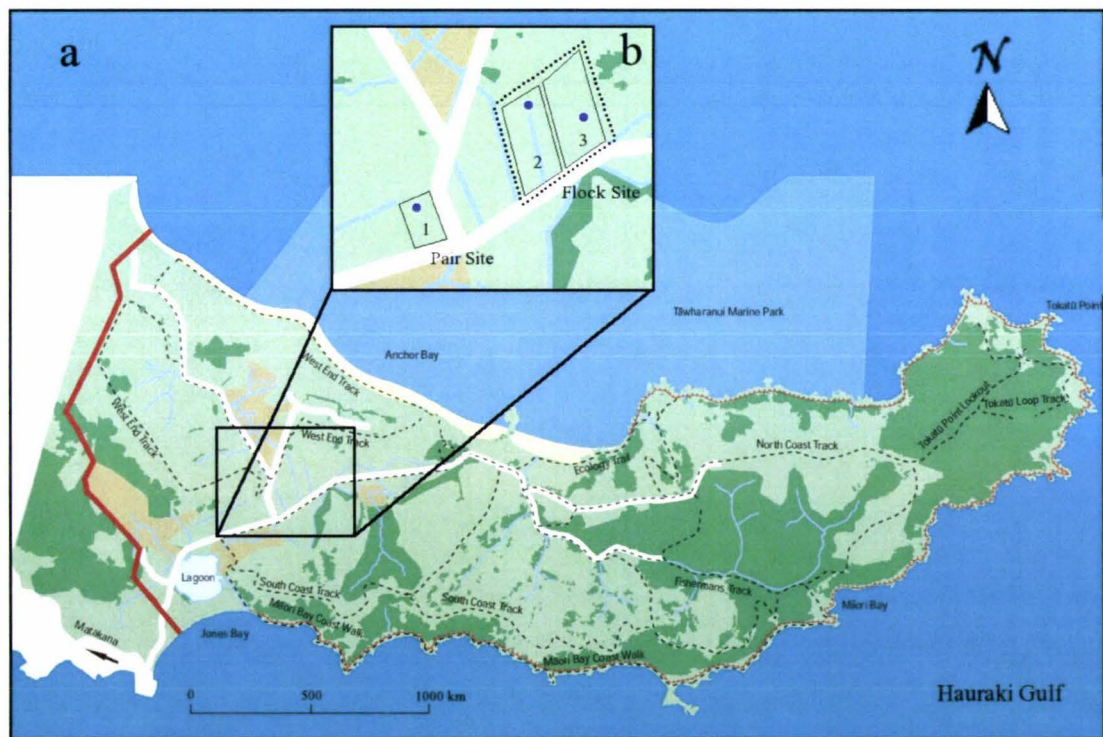


Figure 2.3. (a) Map of Tawharanui Regional Park outlining the study area. (b) Enlarged map of study area showing Sites 1 (Pair Site), 2 and 3 (Flock Site) and (●) trough locations. (Altered from ARC 2007).

Only fresh paradise shelduck faeces were collected, using sterile swabs, and placed in sterile pottles. Twenty grams of each sample was placed on ice packs in a chilly bin and transported within six hours to the NZVP laboratory (New Zealand Veterinary Pathology Ltd.) to test for the presence of targeted bacteria and parasitic species.

Two further species were sampled (samples *vii* - *viii*) on the 13/06/2007, using the same methodology and from the same area as the flock site. Sample *vii*, consisted of five combined samples of pukeko (*Porphyrio porphyrio*) faeces and sample *viii*, consisted of 20 combined house sparrow (*Passer domesticus*) faeces samples (Table 2.1).

Table 2.1. Samples sent to NZVP for analysis.

Sample Set	Date	Sample	Sample Type	No. of Faeces Included in Sample
1	26/04/2006	1.i	Pair	2
		1.ii	Pair	2
		1.iii	Pair	2
		1.iv	Flock	5
		1.v	Flock	10
		1.vi	Flock	25
2	26/07/2006	2.i	Pair	2
		2.ii	Pair	2
		2.iii	Pair	2
		2.iv	Flock	5
		2.v	Flock	10
		2.vi	Flock	25
3	28/11/2006	3.i	Pair	2
		3.ii	Pair	2
		3.iii	Pair	2
		3.iv	Flock	5
		3.v	Flock	10
		3.vi	Flock	25
4	30/03/2007	4.i	Pair	2
		4.ii	Pair	2
		4.iii	Pair	2
		4.iv	Flock	5
		4.v	Flock	10
		4.vi	Flock	25
5	13/06/2007	5.vii	Pukeko	5
		5.viii	Sparrow	20

2.5.2.1 *Methods used by NZVP*

All bacteria isolated from faecal samples by NZVP were quantified by a growth value (Table 2.2).

Table 2.2. Quantitative growth values of bacteria isolates.

Growth Value	Description
1	Present, but in small numbers
2	Light to moderate growth of bacteria isolates
3	Moderate to heavy growth of bacteria isolates
4	Heavy to extremely high growth of bacteria isolates

2.5.2.1.1 *Bacteria isolation*

2.5.2.1.1.1 *Aerobic culture method*

Swabs of the faecal samples were inoculated onto Sheep Blood agar, MacConkey agar and Columbia CAN agar plates. The Sheep Blood agar and the Columbia CAN agar plates were incubated in 10% CO₂ at 37°C for 48 hours, while the MacConkey agar plates were incubated in O₂ at 37°C for 48 hours. After incubation, all agar plates were checked for presence of bacteria.

2.5.2.1.1.2 *Anaerobic culture method*

Swabs of the faecal samples were inoculated onto Sheep Blood agar and Fastidious Anaerobic agar plates. The Sheep Blood agar plates were incubated in 10% CO₂ at 37°C for 48 hours. The Fastidious Anaerobic agar plates were incubated anaerobically at 37°C for 48 hours. After incubation, all agar plates were checked for presence of bacteria.

2.5.2.1.1.3 *Enteric screen culture method*

2.5.2.1.1.3.1 *Salmonella culture method*

Faeces samples were directly inoculated onto XLD agar plates and a small proportion inoculated into Tetrathionate, Rappaport and Selenite broth. The XLD agar plates were incubated in O₂ at 37°C for 48 hours, while the Rappaport broth was incubated in O₂ at 42°C for 24 hours. This was subbed after 24 hours onto XLD agar plates, before being

incubated for a further 24 hours. The Tetrathionate broth and the Selenite broth were incubated in O₂ at 37°C for 24 hours. These were also then incubated for a further 24 hours. After the final incubation, all agar plates were checked for presence of bacteria.

2.5.2.1.1.3.2 *Yersinia* culture method

Faeces samples were directly inoculated onto *Yersinia* Selective agar plates and incubated in O₂ at 30°C for 48 hours. The plates were checked for the presence of suspicious colonies after incubation.

2.5.2.1.1.3.3 *Campylobacter* culture method

Faeces samples were directly inoculated onto Blood Free *Campylobacter* agar plates and incubated micro-aerophilically at 37°C for 72 hours. The plates were checked for the presence of suspicious colonies after incubation.

2.5.2.1.1.4 *Antibiotic sensitivity testing*

Waterfowl can serve as important indicator species with respect to trends in antimicrobial susceptibility patterns in wildlife and in the transfer of antibiotic resistance to other susceptible host (Fallacara *et al.* 2001). Therefore, the antimicrobial susceptibility of the bacterial isolates found in the paradise shelduck faeces in this study were determined. If a bacteria culture was isolated on one of the agar plates, then a series of antibiotic sensitivity tests were performed on the culture;

Cultures were inoculated onto Sensitivity Test agar, plain agar and blood enriched agar plates to form an even, confluent bacterial layer. A series of antibiotic paper disks were placed on agar plates. The antibiotics used were: Ampicillin, Amox and CLav Acid, Amikacin, Clindamycin, Enrofloxacin, Trimeth/ Sulpahm and Tetracycline. The agar plates were then incubated to allow growth of the bacteria and the time for the antibiotics to diffuse into the agar plates. The plain agar plates were incubated in O₂ at 37°C for 24 hours as were the blood enriched agar plates. If an organism is susceptible to an antibiotic a clear zone appears around the disk where growth has been inhibited. The size of this zone of inhibition depends on the sensitivity of the bacteria to the specific antibiotic and the antibiotic's ability to diffuse through the agar. Refer to Appendix 2.10.1 for the antibiotic sensitivity testing of bacterial isolates.

2.5.2.1.1.5 *Ziehl-Neelsen stain*

Faecal samples were smeared onto slides to create a thin layer before being flooded with Ziehl-Neelsen Carbol fuchsin for five minutes and then gently heated until steaming. After heating, the slides were rinsed and excess water drained, then flooded with decolouriser for 1-2 minutes. The slides were then rinsed and excess water drained before being flooded with the counter stain, Malachite Green, for 30 seconds. Lastly the slides were rinsed, drained and then examined for red/pink rods with a green background to confirm a positive result for mycobacteria.

2.5.2.1.2 *Faecal parasite counts*

2.5.2.1.2.1 *Cryptosporidium*

Small representative samples of the mixed faeces were placed on slides to dry, before being fixed in 96% methanol for 2-5 minutes. The slides were then stained with carbol fuchsin for 20-30 minutes and then rinsed and drained. After staining, the slides were decolourised with 10% Sulphuric Acid for 30-60 seconds and then rinsed and drained. A counterstain, with 5% Malachite Green was then used to flood the slides for 5 minutes. The slides were then rinsed, drained, dried and examined under an oil immersion lens. *Cryptosporidium* appear as dark red round bodies 4-5 μ in diameter against a blue/green background.

2.5.2.1.2.2 *Giardia*

The centrifugation flotation technique was used for the isolation of Giardia Cysts (Egwang & Slocombe 1981, 1982). Five grams of faeces was taken from each sample and mixed with 12ml of water and strained through a tea strainer. The container in which the original mixing was done was rinsed with 2-3ml of water and this material was also strained. The wet faecal debris on the strainer was pressed until it was very dry to remove as much of the liquid as possible and then discarded. The strained faeces water mixture was placed in a 25ml centrifuge tube and centrifuged at 264 x g for three minutes. After the centrifuge, the supernatant was discarded and the centrifuge tube completely filled with saturated sucrose solution and the sediment mixed well with the flotation medium. A coverslip was placed on the meniscus and the material centrifuged at 264g for five minutes. The coverslip was then removed and placed onto a slide and

examined at 100 x magnification. The number of cysts was counted and divided by five to determine the eggs per gram (epg).

2.5.2.1.2.3 *Faecal egg count*

The McMaster Egg counting Technique was used to demonstrate and count parasitic eggs in the faecal samples. The method was used to determine the number of nematode eggs per gram of faeces in order to estimate the worm burden in the animals. Two grams of faeces per sample was weighed out. Each sample was then sieved into a dish containing 60ml of saturated salt solution. The sample was then mixed vigorously, and then a sample is taken using a pipette and transferred into the chambers of a McMaster slide. After a 30 second interval, the total number of eggs under the etched area of the slide was counted. The total number of eggs in the two chambers was then multiplied by 100; giving the epg value.

2.5.3 Trough water samples

Water samples were collected from three water troughs (Trough 1, 2 and 3 (Figure 2.3) within the Tawharanui Regional Park in one litre sterile glass bottles, 0.3 metres below the water surface. Four sets of samples were taken at different times of the year between 2006 and 2007 (15.05.2006, 17.07.2006, 07.12.2006 and 29.03.2007).

Samples were placed on ice packs in a chilly bin and transported to the Watercare Services Ltd. Laboratory, within six hours, to test for the presence of *E. coli*, salmonella and fecal coliforms.

2.5.3.1 *Methods used by Watercare Services Ltd.*

2.5.3.1.1 *Escherichia coli isolation and counts*

Water samples were filtered through a membrane filter, and the filter then placed on mTEC (membrane Thermotolerant *E. coli*) agar plates, containing bromocresol purple and bromophenol red. The agar plate was then incubated at 35°C for two hours to rejuvenate injured or stressed bacteria, and then incubated at 44.5°C for 22 hours. After incubation, the filter was then transferred to a filter pad saturated with urea substrate (2.0g urea, 10g phenol red, 100ml reagent-grade water). After 15 minutes cultured *E.*

coli colonies are counted, using a fluorescent lamp and magnifying lens. Colonies that remain yellow or yellow-brown are positive for *E. coli*.

2.5.3.1.2 Fecal coliform isolation and counts

Water samples were filtered through a membrane filter, and the filter then placed on mFC agar plates, containing aniline blue as an indicator. The agar plate was then incubated at 44.5°C for 22-24. After incubation, cultured fecal coliforms colonies were counted. Colonies that are various shades of blue colour are positive for fecal coliforms. The blue colour indicates the capability to ferment lactose to acid.



Plate 2.2. Paradise shelduck pair on water trough. Photo by M. Delaney 2006.

2.5.3.1.3 Salmonella isolation

A 3-tube most probable number (MPN) technique was used using buffered peptone water (BPW) as a pre-enrichment broth. Ten millilitres were taken from each sample and placed into sterile test tubes, and then one millilitre of sample was transferred to triplicate 9ml BPW dilution tubes followed by serial dilution in triplicate tubes of BPW. All tubes were then incubated at 37°C for 18-24 hours before transferring 0.1mL of the appropriate dilutions to triplicate tubes containing 10ml of Rappaport-Vassiliadis (RV)

broth for selective enrichment. All RV broth tubes were incubated at 42°C for 24 hours. After incubation, one loopful from each tube was streaked for isolation onto modified lysine iron agar plates and incubated at 37°C for 24 hours. Presumptive positive *Salmonella* colonies were confirmed by agglutination using poly-O antiserum.

2.5.4 Statistical analysis

A one way ANOVA was used to determine the differences between seasons of mean bacterial growth values in paradise shelduck faecal samples separately for each category of ducks sampled. In addition, a Tukey test was performed to distinguish the mean differences which were significantly different. A Spearman's rank correlation test was used to test the significance of the correlation between bacterial growth values in paradise shelduck faecal samples and the number of accumulated faeces per sample separately for each season.

2.6 Results

2.6.1 Faecal micro-organisms

A significant positive correlation was found between mean total number of micro-organisms isolated in the combined paradise shelduck faecal samples, and the month of sampling (Spearman rank correlation; $r_s = 0.45$, $P = 0.03$) (Figure 2.4). Although there was a positive trend between mean total number of micro-organisms isolated in the faeces samples for pairs of paradise shelducks and the month of sampling, the correlation was not significant (Spearman rank correlation; $r_s = 0.48$, $P = 0.12$) (Figure 2.4). This was also true for the correlation between mean total number of micro-organisms isolated in the faeces samples of paradise shelduck flock birds and the month of sampling (Spearman rank correlation; $r_s = 0.428$, $P = 0.18$) (Figure 2.4). No isolates of *Salmonella*, *Campylobacter*, *Yersinia*, *Cryptosporidium* or *Giardia* were found in the paradise shelduck faeces at Tawharanui Regional Park.

2.6.1.1 *E. coli*

E. coli isolates were established in 87.5% of the 24 paradise shelduck faecal samples. Figure 2.6 suggests a positive relationship between the growth values of *E. coli* in paradise shelduck faecal samples and the sampling dates, especially in relation to the paradise shelduck pairs.

Likewise, we see this relationship in Figure 2.7, where it is shown that there are significant differences between the sampling dates and the different sampling groups. The mean *E. coli* growth value for the combined sampling group was found to be significantly different (one way ANOVA; $F_{3,20} = 18.12$, $P < 0.0001^6$) between seasons. May and August had significantly lower *E. coli* growth values of 1.17 and 1.33, respectively, than November and March, which had *E. coli* growth values of 3.33 and 3.83, respectively. Similarly, the mean *E. coli* growth value for the pairs and flock sampling groups showed a significant difference (one way ANOVA; $F_{3,8} = 57.83$, $P < 0.0001$ and $F_{3,8} = 17.22$, $P = 0.0007$, respectively).

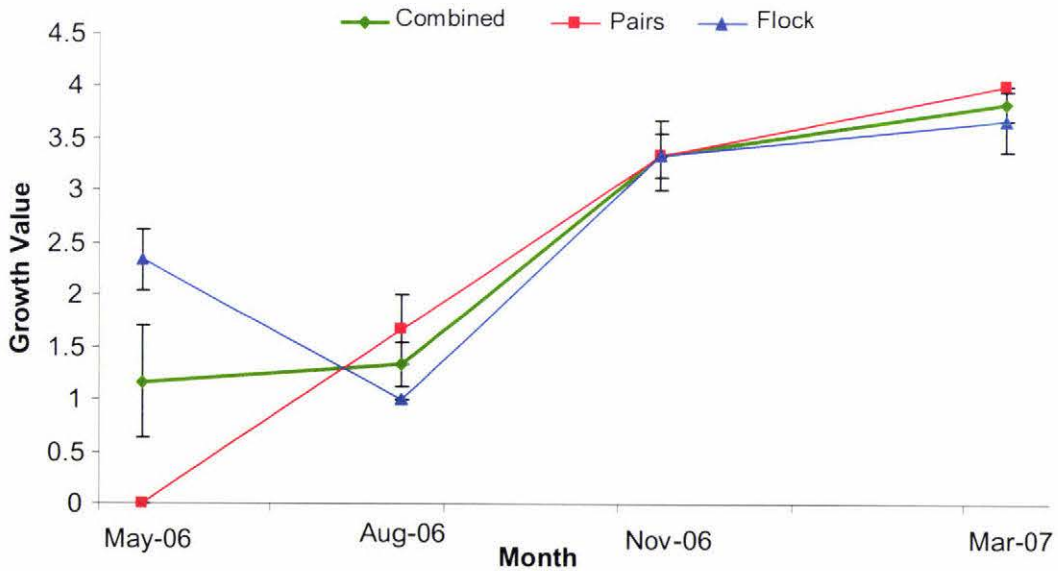


Figure 2.6. *E. coli* growth values in paradise shelduck faecal samples to sampling date. Data points represent means ± SE.

No significant correlation was found between the *E. coli* growth values and the number of accumulated faeces per sample (Spearman rank correlation; $r_s = 0.12$, $P = 0.58$) over the entire sampling period (Figure 2.8a). From Figure 2.7, we can divide the sampling dates into two groups; the low season (May and August 2006) and the high season (November 2006 and March 2007). Figure 2.8b and c, once again, both show no significant correlation between *E. coli* growth values and the number of accumulated faeces per sample for the low and high season (Spearman rank correlation; $r_s = 0.44$, $P = 0.15$ and $r_s = -0.05$, $P = 0.87$, respectively).

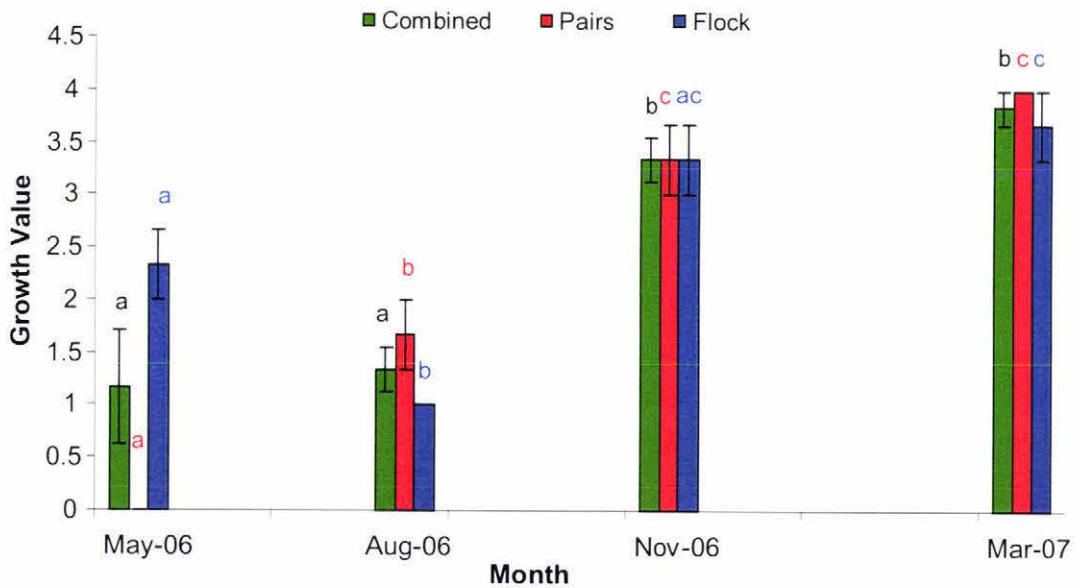


Figure 2.7. Mean *E. coli* growth values in paradise shelduck faecal samples to sampling date. Letters represent significantly different means at a 0.05 level (Tukey test).

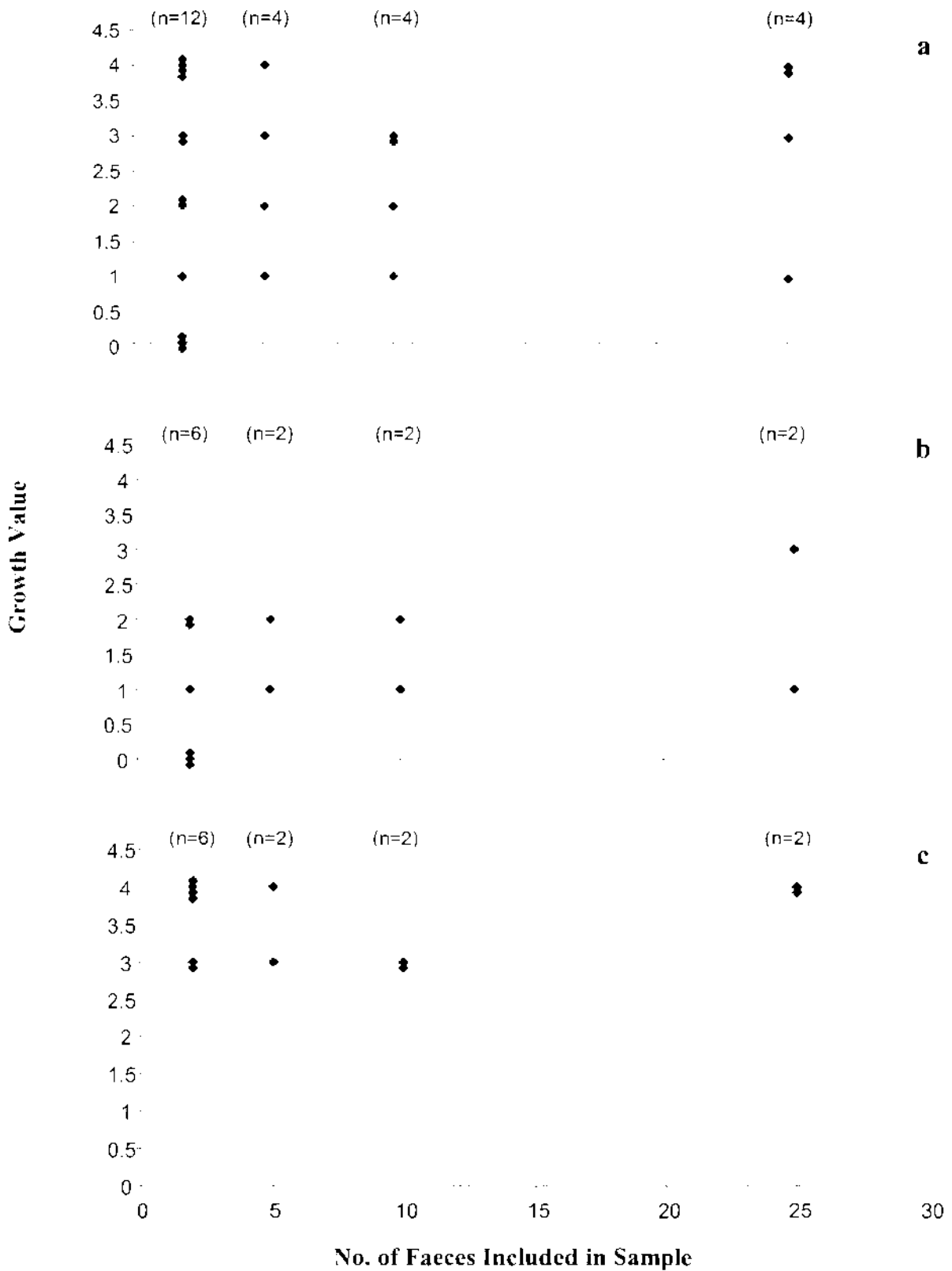


Figure 2.8. *E. coli* growth values in paradise shelduck faecal samples to number of accumulated faeces per sample for a) all sampling dates, b) samples in the low season (May & August 2006) and c) samples in the high season (November 2006 & March 2007). Data points may represent more than one sample.

2.6.1.2 Non haemolytic *Streptococci*

Non haemolytic *Streptococci* isolates were established in 29.2% of the 24 paradise shelduck faecal samples. Growth values of non haemolytic *Streptococci* found in paradise shelduck faeces were very low during the sampling period. Additionally, faecal samples from pairs had non haemolytic *Streptococci* growth more often than the flock samples (Figure 2.9).

A significant difference was found between the mean growth of non haemolytic *Streptococci* in the combined sample group (one way ANOVA; $F_{3,20} = 3.67$, $P = 0.03$) (Figure 2.10). For the combined sample group, August 2006 was significantly different to May 2006 and March 2007. However, the mean non haemolytic *Streptococci* growth value for the pairs and flock sampling groups showed no significant difference (one way ANOVA; $F_{3,8} = 1.33$, $P = 0.33$ and $F_{3,8} = 1.33$, $P = 0.45$, respectively) (Figure 2.10).

Furthermore, no significant correlation was found between the non haemolytic *Streptococci* growth values and the number of accumulated faeces per sample (Spearman rank correlation; $r_s = 0.12$, $P = 0.62$) over the entire sampling period (Figure 2.11).

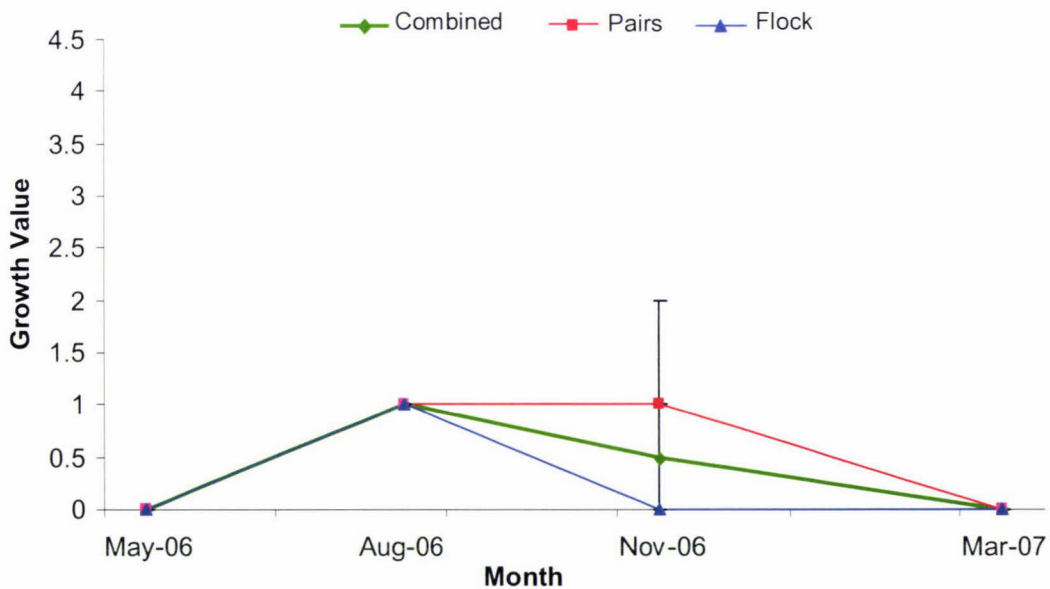


Figure 2.9. Non Haemolytic *Streptococci* growth values in paradise shelduck faecal samples to sampling date. Data points represent means \pm SE.

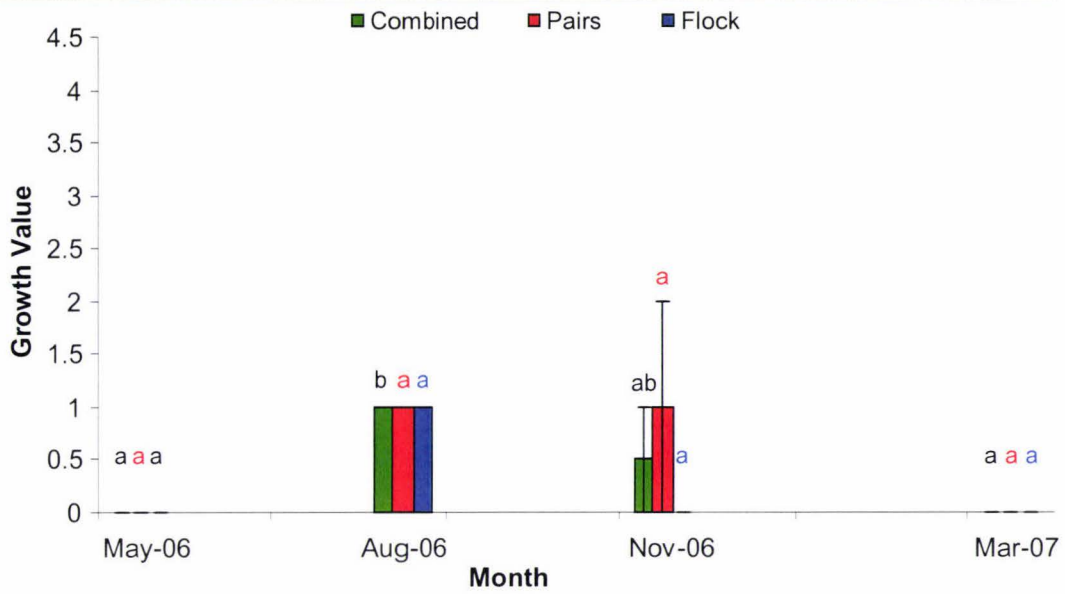


Figure 2.10. Mean Non Haemolytic *Streptococci* growth values in paradise shelduck faecal samples to sampling date. Letters represent significantly different means at a 0.05 level (Tukey test).

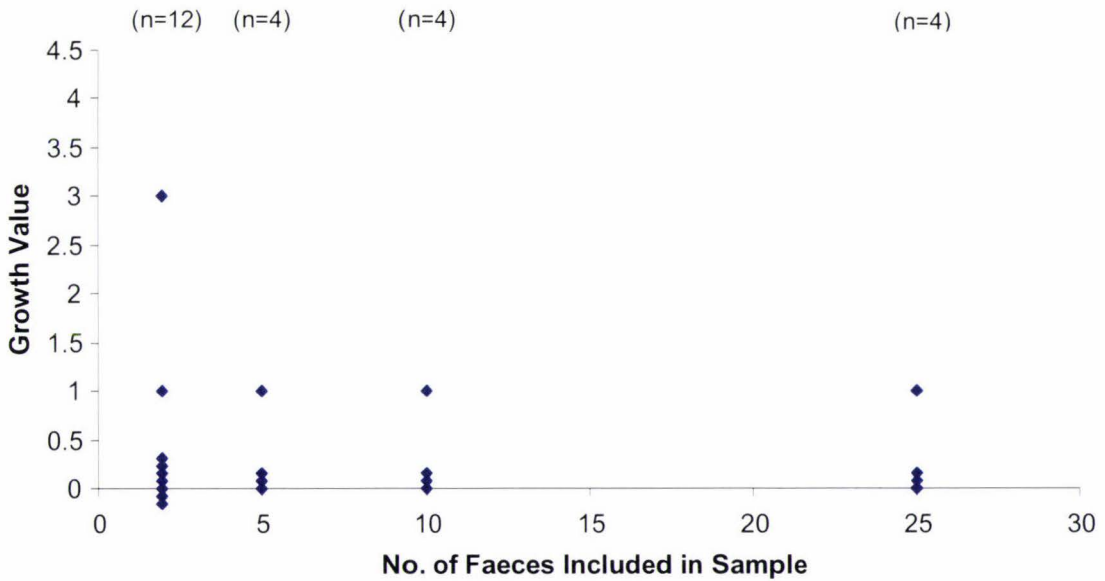


Figure 2.11. Non Haemolytic *Streptococci* growth values in paradise shelduck faecal samples to number of accumulated faeces per sample.

2.6.1.3 *Alpha haemolytic Streptococci*

Alpha haemolytic *Streptococci* isolates were established in 33.3% of the 24 paradise shelduck faecal samples. During the sampling period alpha haemolytic *Streptococci* growth values in paradise shelduck faecal samples showed a considerable increase during November 2006 and March 2007 (Figure 2.12).

Figure 2.13 shows that only the November 2006 mean alpha haemolytic *Streptococci* growth values was significantly different to May and August (2006), for the combined

and flock samples (one way ANOVA; $F_{3,20} = 7.51$, $P = 0.001$ and $F_{3,8} = 7.31$, $P = 0.01$, respectively). Alternately, no significant difference was found between any of sampling dates for the pair samples (one way ANOVA; $F_{3,8} = 1.6$, $P = 0.26$).

No significant correlation was established between the alpha haemolytic *Streptococci* growth values and the number of accumulated faeces per sample (Spearman rank correlation; $r_s = 0.1$, $P = 0.65$) over the entire sampling period (Figure 2.14).

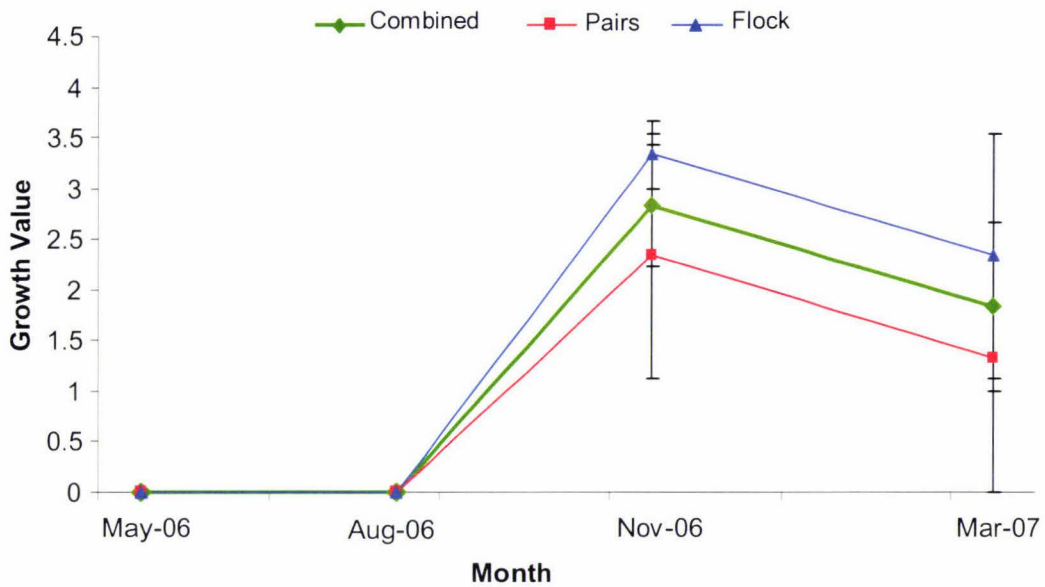


Figure 2.12. Alpha Haemolytic *Streptococci* growth values in paradise shelduck faecal samples to sampling date. Data points represent means \pm SE.

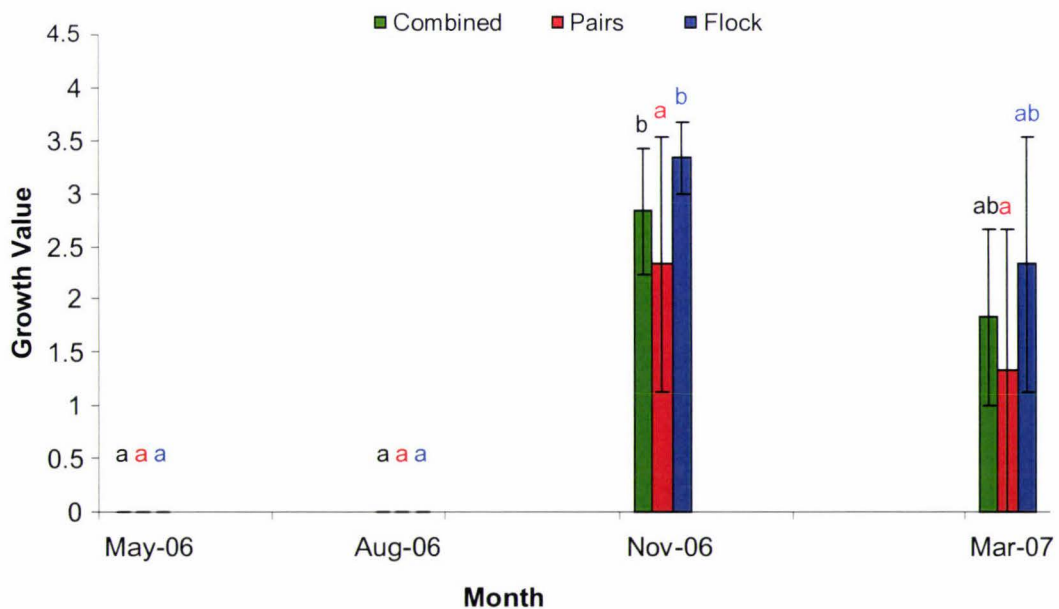


Figure 2.13. Mean Alpha Haemolytic *Streptococci* growth values in paradise shelduck faecal samples to sampling date. Letters represent significantly different means at a 0.05 level (Tukey test).

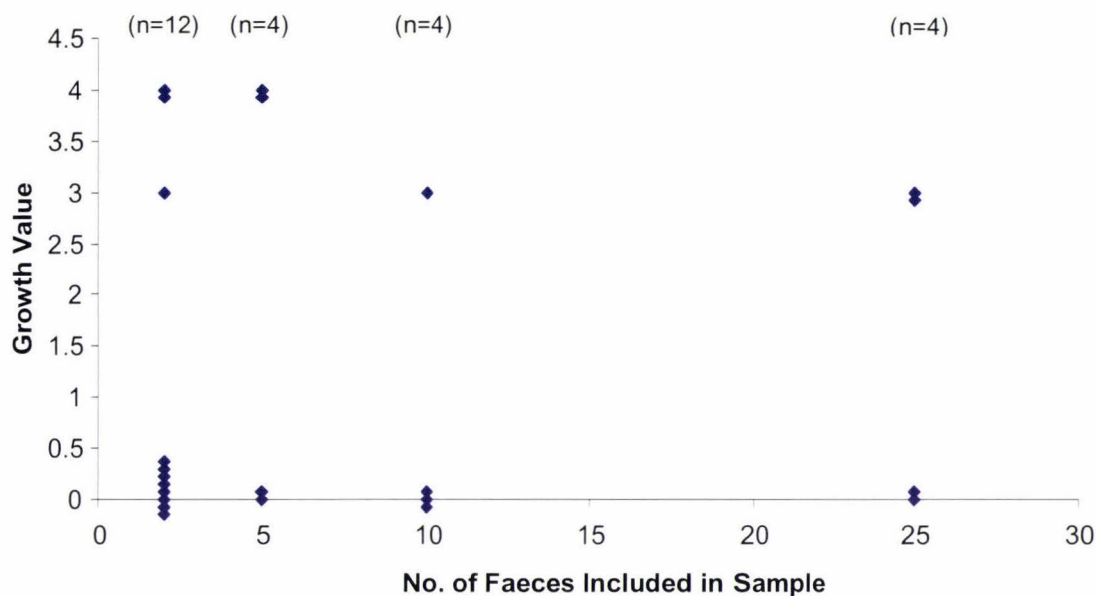


Figure 2.14. Alpha Haemolytic *Streptococci* growth values in paradise shelduck faecal samples to number of accumulated faeces per sample. Data points may represent more than one sample.

2.6.1.4 *Enterococcus*

Enterococcus isolates were established in 16.7% of the 24 paradise shelduck faecal samples. *Enterococcus* growth only occurred in faecal samples from May 2006. What is more, the *Enterococcus* growth was very light with the highest mean growth value of 2 occurring in the pairs sampling group (Figure 2.15).

Similarly, the only significant difference found between the sampling dates and the mean *Enterococcus* growth values, was in May 2006, for the combined sampling group (one way ANOVA; $F_{3,20} = 10$, $P = 0.003$) (Figure 2.16). There were no significant differences established with the pairs and flock sample groups (one way ANOVA; $F_{3,8} = 4$, $P = 0.052$).

The number of accumulated faeces per sample did not affect the *Enterococcus* growth values (Spearman rank correlation; $r_s = 0$, $P = 1$) over the entire sampling period (Figure 2.17).

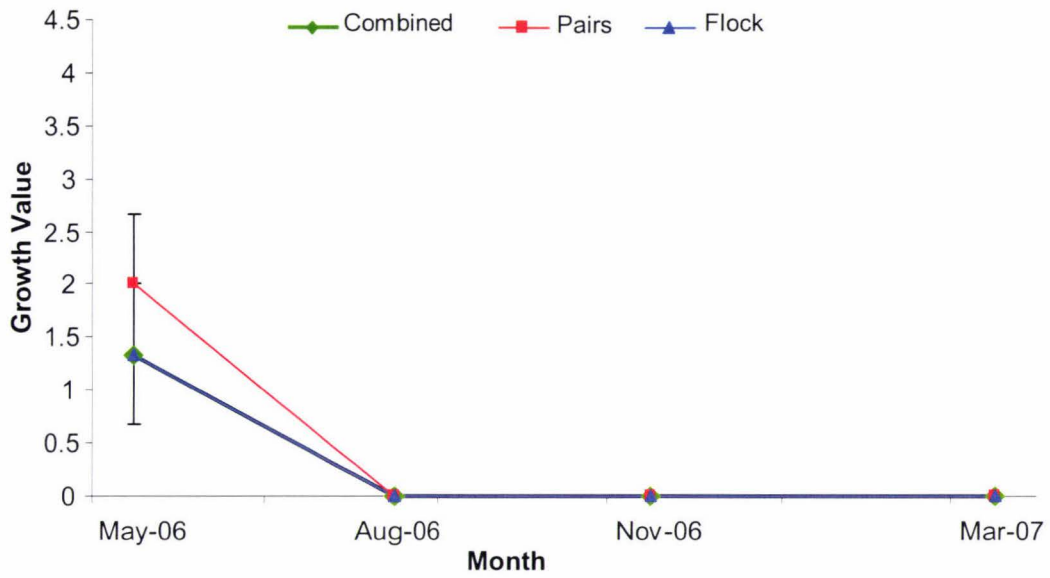


Figure 2.15. *Enterococcus* growth values in paradise shelduck faecal samples to sampling date. Data points represent means ± SE.

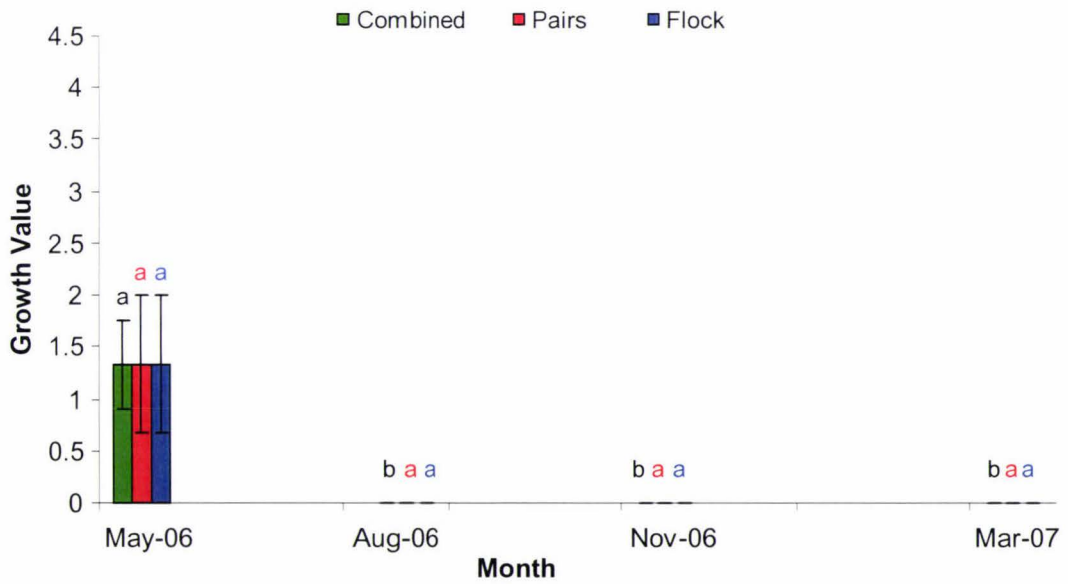


Figure 2.16. Mean *Enterococcus* growth values in paradise shelduck faecal samples to sampling date. Letters represent significantly different means at a 0.05 level (Tukey test).

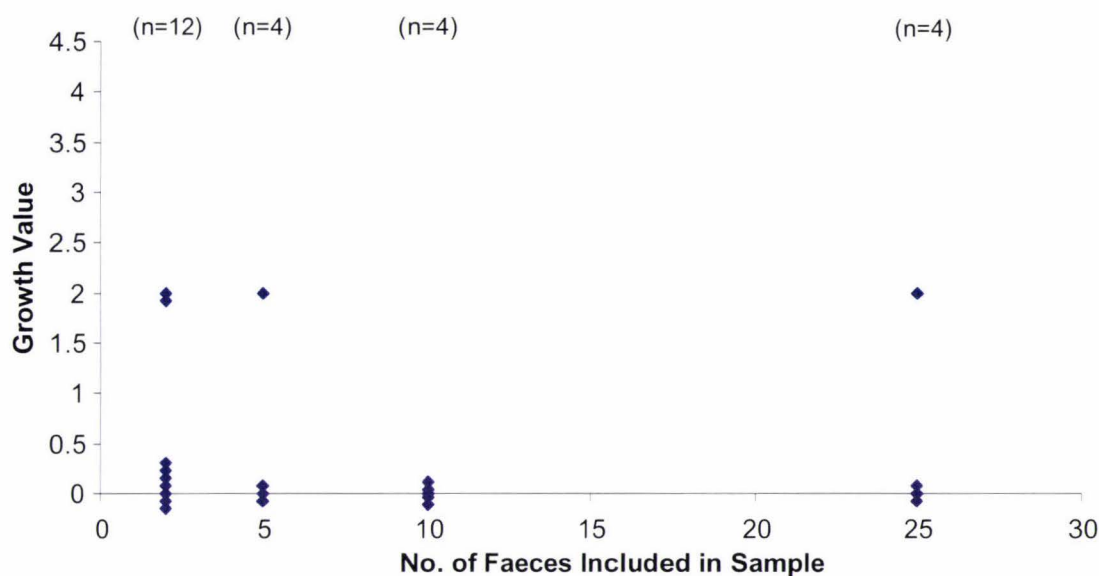


Figure 2.17. *Enterococcus* growth values in paradise shelduck faecal samples to number of accumulated faeces per sample.

2.6.1.5 *Bacillus*

Bacillus isolates were established in 50% of the 24 paradise shelduck faecal samples. *Bacillus* growth occurred in paradise shelduck faeces throughout the sampling period except in November 2006. In August, *Bacillus* growth only took place in faecal samples from pairs of paradise shelduck. Conversely, in all the other sampling months, the flock sample group had higher mean *Bacillus* growth values (Figure 2.18).

No significant differences were established between sampling dates for the mean *Bacillus* growth values in the pairs sampling group (one way ANOVA; $F_{3,8} = 2.57$, $P = 0.13$). In contrast, there were significant differences found between the mean *Bacillus* growth values for May 2006 and both August 2006 and November 2006, in the combined sampling group. Furthermore, the sampling period of March 2007 was found to have a significantly different mean growth value to November 2006. Also, there were significant differences found between the mean *Bacillus* growth values for May 2006 and both August 2006 and November 2006, in the flock sampling group (Figure 2.19).

Once again, no significant correlation was found between the *Bacillus* growth values and the number of accumulated faeces per sample (Spearman rank correlation; $r_s = 0.05$, $P = 0.82$) over the entire sampling period (Figure 2.20).

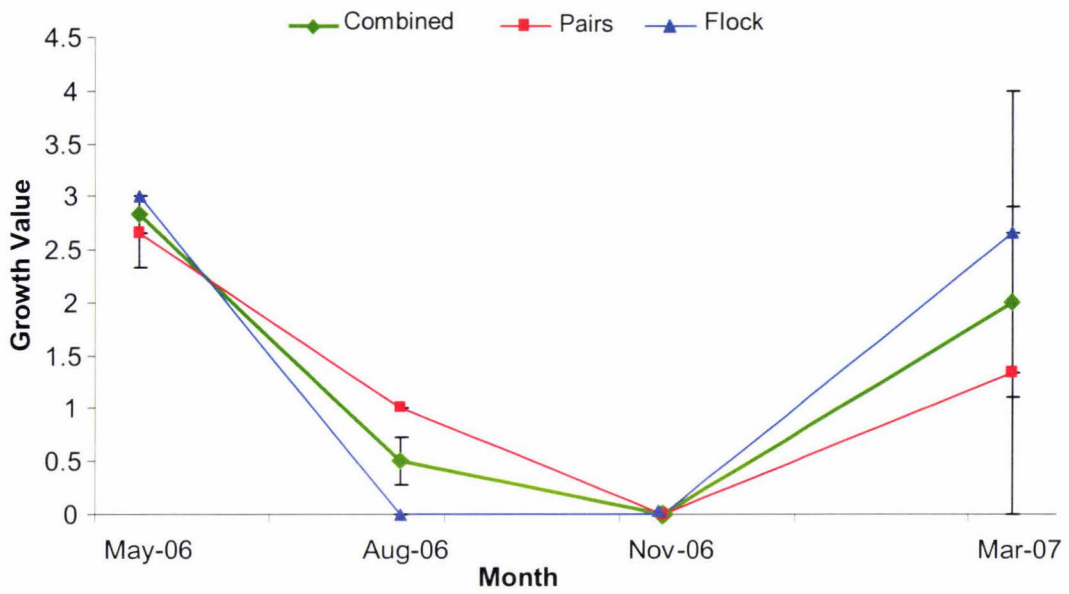


Figure 2.18. *Bacillus* growth values in paradise shelduck faecal samples to sampling date. Data points represent means ± SE.

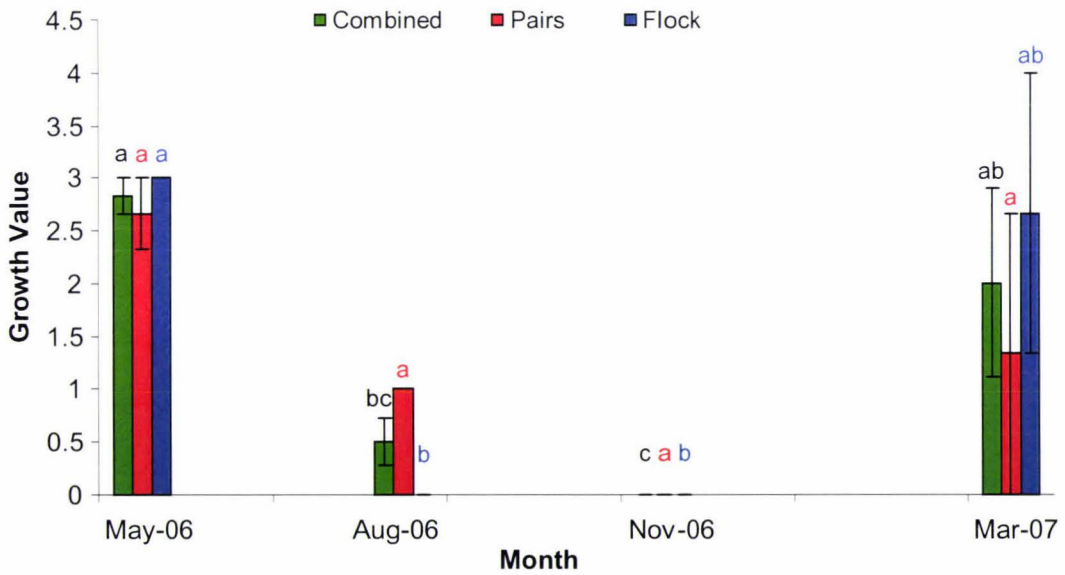


Figure 2.19. Mean *Bacillus* growth values in paradise shelduck faecal samples to sampling date. Letters represent significantly different means at a 0.05 level (Tukey test).

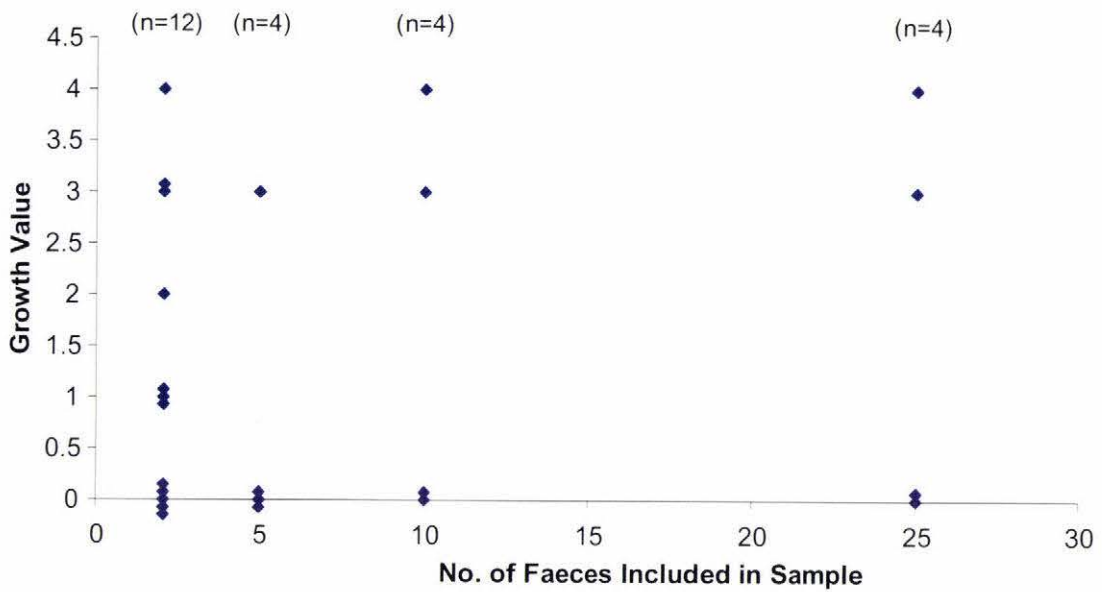


Figure 2.20. *Bacillus* growth values in paradise shelduck faecal samples to number of accumulated faeces per sample.

2.6.1.6 *Proteus mirabilis*

Proteus mirabilis isolates were established in 41.7% of the 24 paradise shelduck faecal samples. Figure 2.21, suggests a positive relationship between the growth values of *Proteus mirabilis* in paradise shelduck faecal samples and the sampling dates, for all the sampling groups.

Similarly, there is evidence of a relationship between the growth values of *Proteus mirabilis* in paradise shelduck faecal samples and the sampling dates in Figure 2.22. There is a significant difference of mean *Proteus mirabilis* growth values between November 2006 and March 2007 in the combined sampling group. Additionally November 2006 and March 2007 are significantly different to May and August 2006 (one way ANOVA; $F_{3,20} = 31.75$, $P = < 0.0001^8$). Furthermore, in both the pair and flock sampling groups, the mean *Proteus mirabilis* growth value for March 2007 is significantly different to all other sampling dates (one way ANOVA; $F_{3,8} = 14.67$, $P = 0.001$ and $F_{3,8} = 11.3$, $P = 0.003$, respectively).

No significant correlation was found between the *Proteus mirabilis* growth values and the number of accumulated faeces per sample (Spearman rank correlation; $r_s = -0.07$, $P = 0.74$) over the entire sampling period (

Figure 2.23 a). From Figure 2.7, we can divide the sampling dates into two groups; the low season (May and August 2006) and the high season (November 2006 and March 2007).

Figure 2.23b, once again, shows no significant correlation between *Proteus mirabilis* growth values and the number of accumulated faeces per sample for the low and high season (Spearman rank correlation; $r_s = -0.18$, $P = 0.58$).

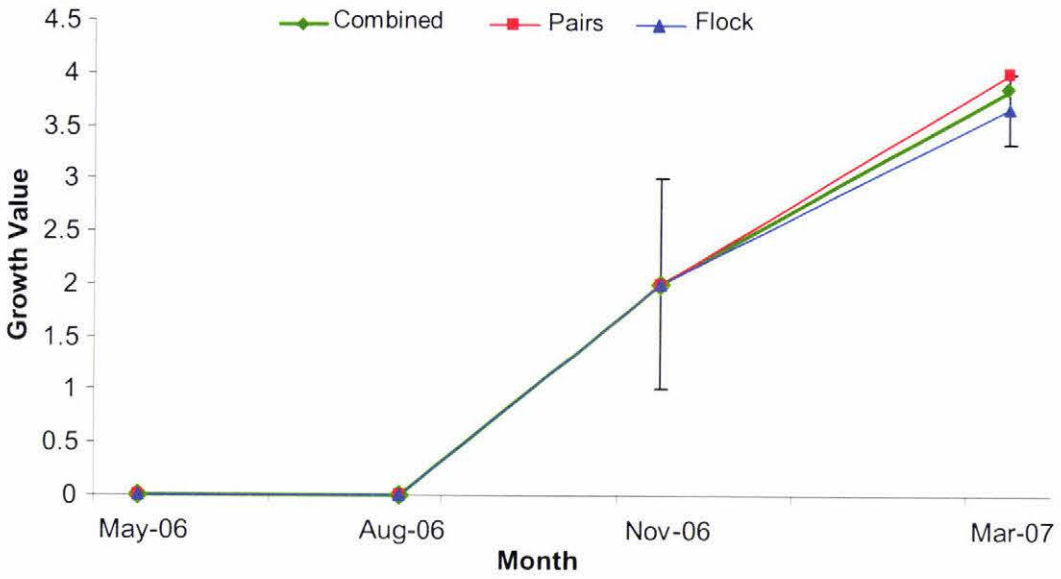


Figure 2.21. *Proteus mirabilis* growth values in paradise shelduck faecal samples to sampling date. Data points represent means \pm SE.

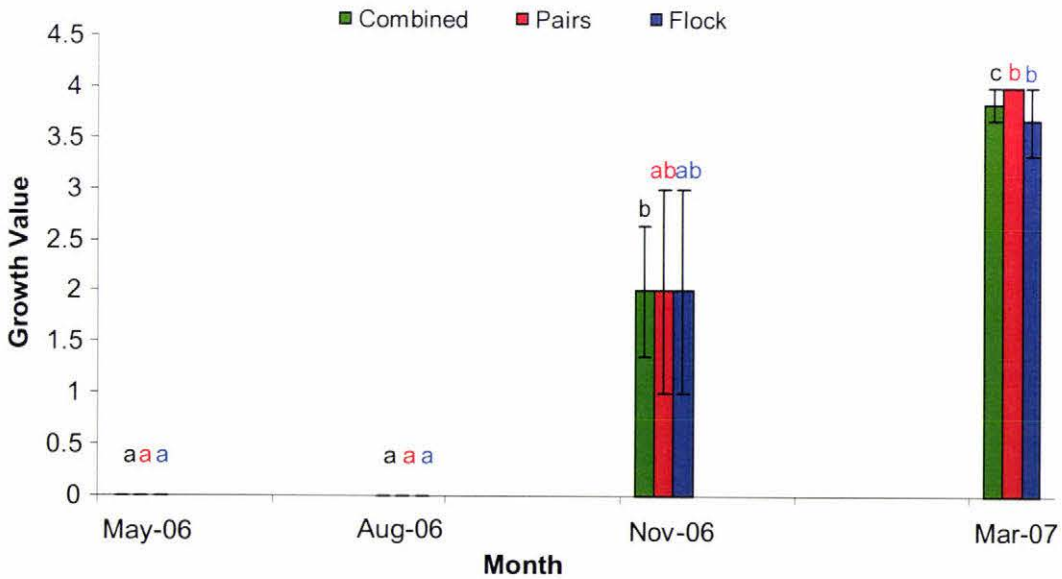


Figure 2.22. Mean *Proteus mirabilis* growth values in paradise shelduck faecal samples to sampling date. Letters represent significantly different means at a 0.05 level (Tukey test).

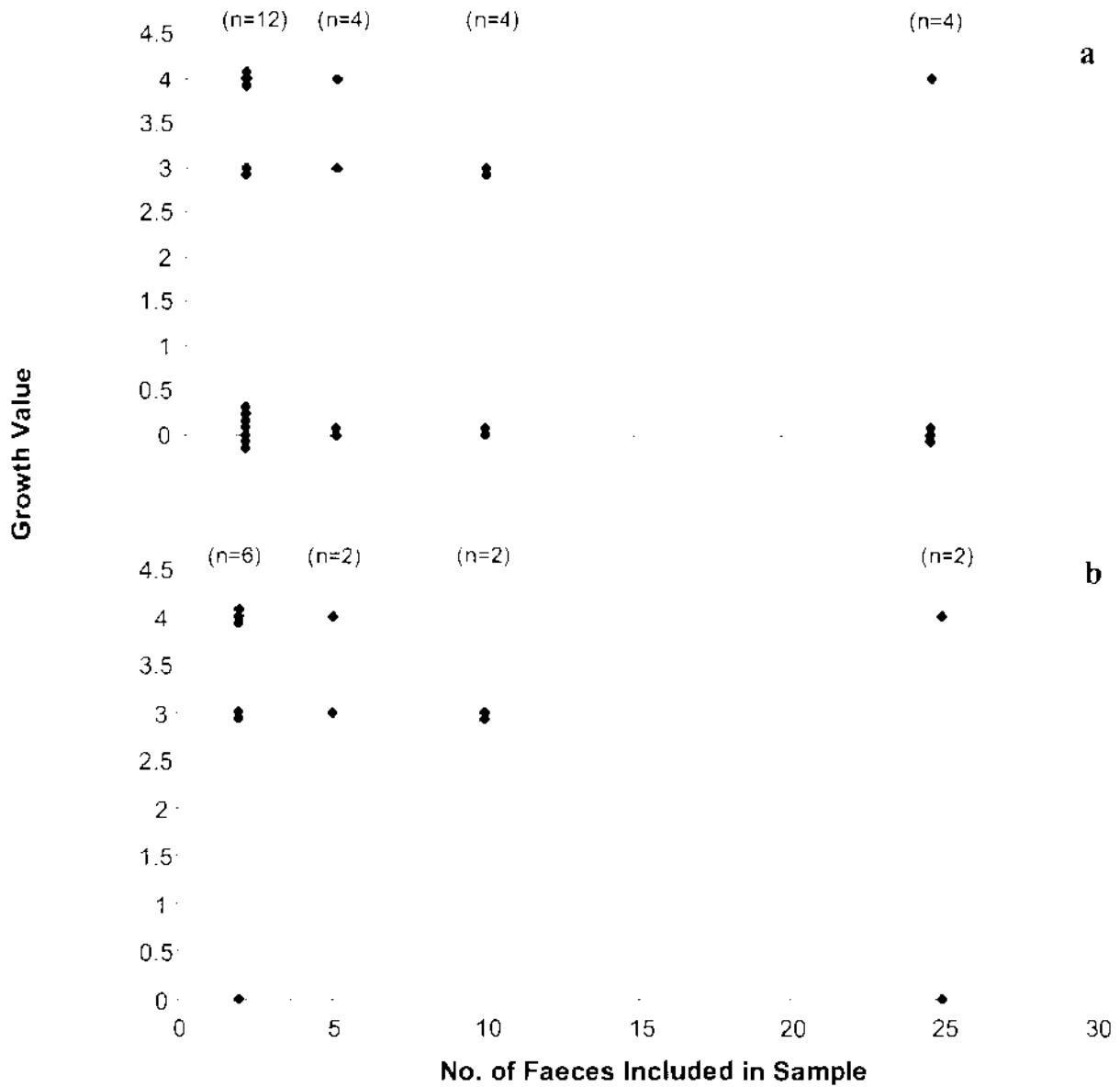


Figure 2.23. *Proteus mirabilis* growth values in paradise shelduck faecal samples to number of accumulated faeces per sample for a) all sampling dates, b) samples in the high season (November 2006 & March 2007).

2.6.1.7 Additional faecal micro-organisms

Other micro-organisms found in paradise faecal samples, but infrequently and generally in low numbers, include: *Clostridium perfringens*, *Coccidia* and *Strongyle* species (Table 2.3).

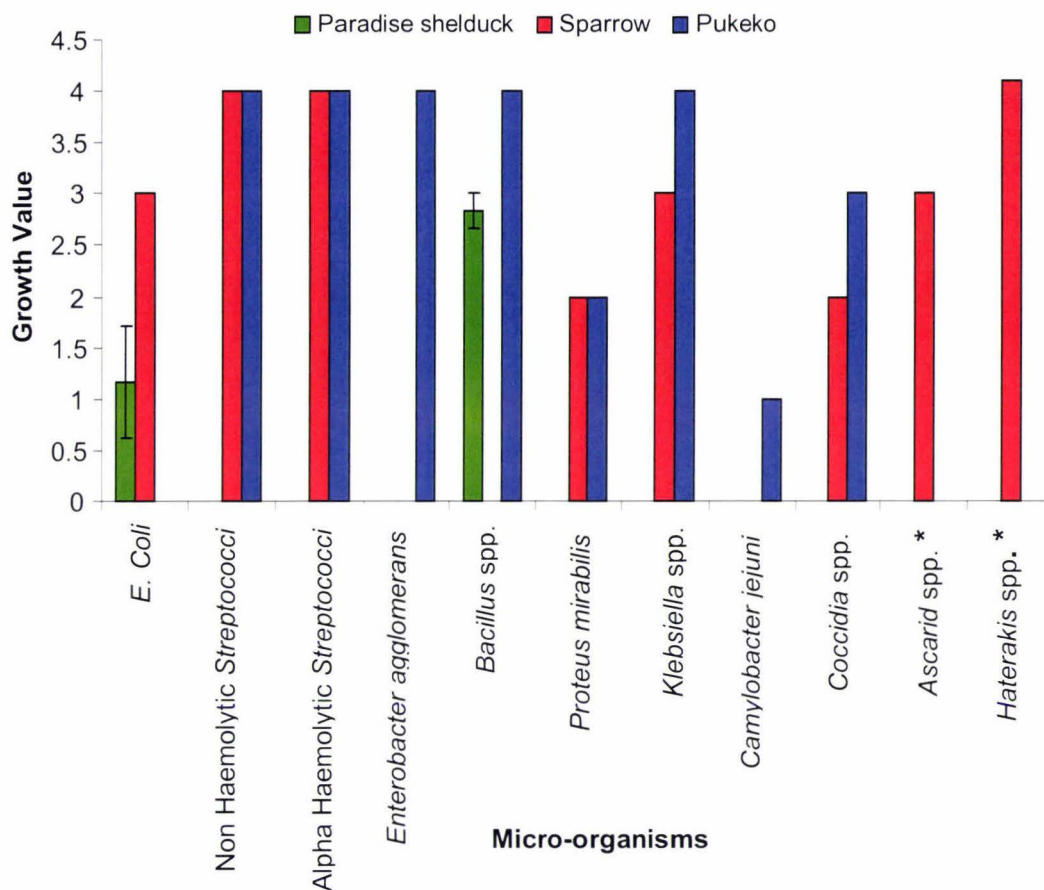
Table 2.3. Growth values for micro-organisms found in paradise shelduck faeces.

		No. Accumulated Faeces per Sample					
		Pair Samples			Flock Samples		
		2 (Site a)	2 (Site b)	2 (Site c)	5	10	25
03/05/2006	<i>Clostridium perfringens</i>	-	-	-	-	-	-
	<i>Coccidia</i>	-	-	-	-	-	-
	<i>Strongyle</i>	-	-	-	-	-	-
04/08/2006	<i>Clostridium perfringens</i>	-	-	2	-	-	-
	<i>Coccidia</i>	-	-	-	-	-	2
	<i>Strongyle</i>	-	-	-	-	-	-
28/11/2006	<i>Clostridium perfringens</i>	-	-	-	-	-	-
	<i>Coccidia</i>	-	-	1	-	-	-
	<i>Strongyle</i>	-	-	-	-	-	-
28/03/2007	<i>Clostridium perfringens</i>	-	-	-	-	-	-
	<i>Coccidia</i>	-	-	-	-	-	-
	<i>Strongyle</i>	-	-	4*	-	-	-

Growth value based on EPG

2.6.1.8 Pukeko and house sparrow comparison

Both the pukeko and the house sparrow faecal samples contained a total of eight different micro-organism species, including five species that were not present in any of the paradise shelduck faeces samples. These five species were; *Klebsiella*, *Enterobacter agglomerans*, *Campylobacter jejuni*, *Ascarid*. and *Heterakis*. (Figure 2.24).



* Growth value based on EPG

Figure 2.24. Growth values of micro-organisms found in faecal samples of paradise shelducks, pukekos and house sparrows. Note: The paradise shelduck figures are the mean growth values of all the sampling groups for the May 2006 sampling date.

2.6.2 Water troughs

E. coli was present in all three water troughs and all the water troughs showed similar levels of prevalence over the entire sampling period. There was a large variation in the concentration of *E. coli* for each trough between the sampling periods, with Trough 2 having a high of 63 000 cfu/100ml in May 2007 and only 400 cfu/100ml in December 2006. Trough 3 had the highest concentration of *E. coli* in May (340 000 cfu/100ml) compared to all the other samples. Trough 1 consistently had the lowest concentration of *E. coli* over the entire sampling period (Figure 2.25).

Likewise, faecal coliforms were present in all three water troughs and all three showed a similar trend over the entire sampling period. Once again, there was a large variation in the concentration of faecal coliforms for each trough between sampling periods. Trough three had the lowest and the highest faecal coliforms concentrations (10 and 840 000 cfu/100ml, respectively) (Figure 2.26).

The presence of *Salmonella* was only detected once out of all the samples. This was found in Trough 3 during the May sampling period (Table 2.4).

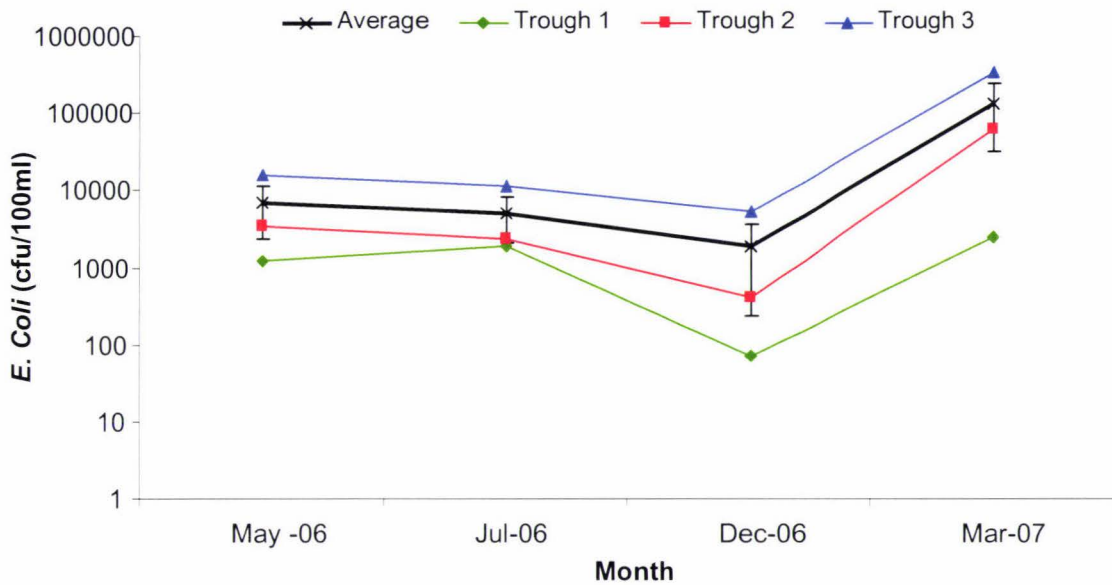


Figure 2.25. Concentration of *E. coli* (cfu/100ml) found in water samples taken from water troughs at Tawharanui Regional Park.

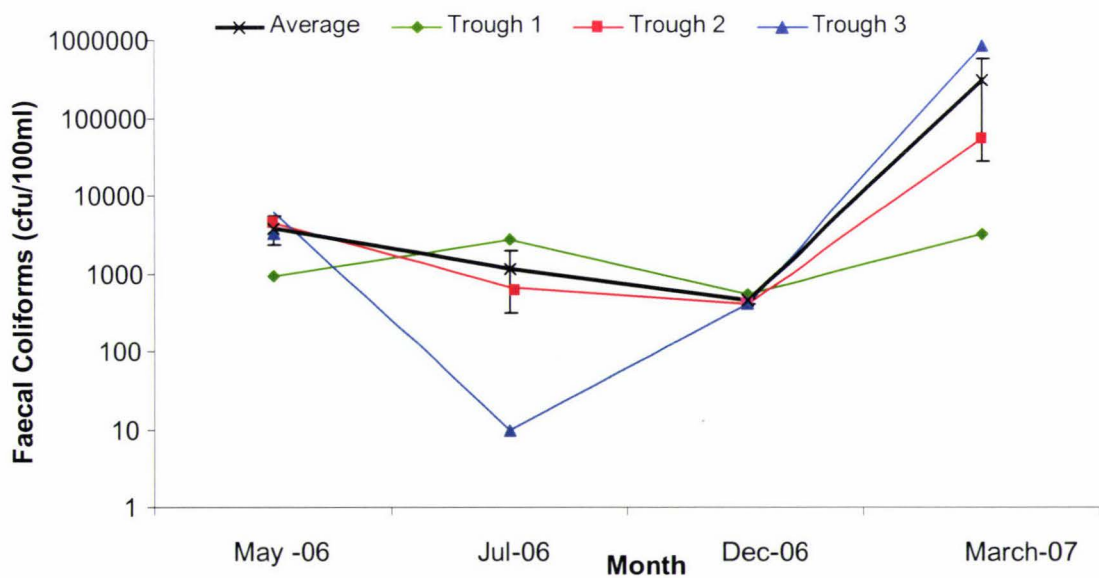


Figure 2.26. Concentration of faecal coliforms (cfu/100ml) found in water samples taken from water troughs at Tawharanui Regional Park.

Table 2.4. *Salmonella* presence in water troughs at Tawharanui Regional Park. + represents a positive result and – represents a negative result.

	<i>Salmonella</i>			
	15/05/2006	17/07/2006	07/12/2006	29/03/2007
Trough 1	-	-	-	-
Trough 2	-	-	-	-
Trough 3	+	-	-	-

2.7 Discussion

No isolates of *Salmonella*, *Campylobacter*, *Yersinia*, *Cryptosporidium* or *Giardia* were found in the paradise shelduck faeces at Tawharanui Regional Park. Relatively low prevalences of non haemolytic and alpha haemolytic *Streptococci*, *Enterococcus*, *Bacillus*, *Clostridium perfringens*, *Proteus mirabilis*, strongyle eggs and *Coccidia* eggs were found. *E. coli* was consistently isolated from the faecal samples throughout the sampling period.

Both the house sparrow and pukeko samples contained non haemolytic *Streptococci*, alpha haemolytic *Streptococci*, *Proteus mirabilis* and *Coccidia*. Additionally, both the pukeko and the house sparrow faecal samples contained micro-organism species that were not present in any of the paradise shelduck faeces samples. These species were; *Klebsiella*, *Enterobacter agglomerans*, *Campylobacter jejuni*, *Ascarid* and *Heterakis*. No *Campylobacter* or *Salmonella* were detected in the house sparrow faeces in this survey, but *Campylobacter jejuni* was detected in the pukeko sample. Extremely high levels of faecal coliforms and *E. coli* were detected in all three troughs throughout the sampling period, but *Salmonella* was only detected once.

2.7.1 *Salmonella*

This survey detected no *Salmonella* isolations from any of the paradise shelduck faeces, which, indicates that paradise shelducks at Tawharanui are not carriers or reservoirs for *Salmonella*. Yet, *Salmonella* is shed intermittently (Cork 1994), and intermittent shedding of salmonellae by infected wild birds makes the interpretation of prevalence surveys for salmonellae, difficult where faecal isolation alone is used to determine the

level of infection (Barrow 1993). Therefore, this survey may not be a true measure of prevalence for *Salmonella* in paradise shelduck faeces. Similarly, a study of free-living Canada geese and mallard ducks in metropolitan parks in Ohio did not demonstrate a high prevalence of salmonellosis (0.2% of 449 faecal samples) in free living waterfowl (Fallacara *et al.* 2001). Hussong *et al.* (1979) detected no *Salmonella* in 44 Canada geese and whistling swans in Baltimore. They concluded that only a minority of the birds, if any, were carrying *Salmonella* species. Likewise, only one out five ducks, found on a farm in New Zealand, where an outbreak occurred, tested positive for *S. brandenburg*. Moreover, it was thought this duck picked it up from contaminated pasture or water and thus reflects environmental contamination by the organism (New Zealand Food Safety Authority).

Conversely, *Salmonella* a common occurrence in wild birds that feed on the ground or on food subject to faecal contamination, and among those that live or feed in contaminated water (Tizard 2004). Additionally, high animal densities favour transmission of *Salmonella* in other animals (New Zealand Food Safety Authority). These characteristics are common in waterfowl, and thus, waterfowl are not uncommonly infected with *Salmonella*, but in spite of this waterfowl are only very rarely diseased (Henry 2000). Since *Salmonella*-infected birds shed these organisms in their faeces, *Salmonella* can be spread to other individuals, and consequently, many investigators have surveyed avian faecal samples for the presence of these organisms (Tizard 2004). *Salmonella* may be present in wild birds for two reasons. One possibility is that the organism is adapted to the host and establishes itself as a part of the intestinal flora on a permanent basis. A second scenario is that the *Salmonella* may only be present in faeces for a short time, as a result of environmental contamination (Murray 2000, Tizard 2004). In New Zealand *Salmonella* have been isolated from aquatic birds, such as pukekos and waterfowl, caught close to an outbreak of salmonellosis in domestic stock. Nevertheless, it is possible that water supplies can become temporarily contaminated by livestock with salmonellae, rather than by local aquatic birds (Robinson & Daniel 1968). It appears that waterfowl are not effective carriers of *Salmonella* species, and it is more likely that waterfowl are exposed to a contaminated environment and may then become accidentally infected (Robinson & Daniel 1968, Tizard 2004). Accordingly, isolation rates of *Salmonella* are usually low in waterfowl (Hussong *et al.* 1979, Henry 2000, Fallacara *et al.* 2001).

2.7.2 *Campylobacter*

No *Campylobacter* isolates were found in any of the paradise shelduck faeces. This suggests that paradise shelduck at Tawharanui are not carriers or reservoirs of *Campylobacter*. This result is in contrast to previous studies which have shown high prevalences of *Campylobacter* in waterfowl; 35% of migrating ducks tested in Colorado harboured *Campylobacter jejuni* (Luechtefeld *et al.* 1980), Fallacara *et al.* (2001) surveyed free-living waterfowl and found a prevalence of 50% *C. jejuni* in Canada geese and mallard ducks. Additionally, Pacha *et al.* (1988) collected swabs from Canada geese and migratory ducks (*Aythya collaris*, *Anas carolinensis*, *Aythya americana*, and *Anas platyrhynchos*) and recovered *Campylobacter* species from 73% (n=133) of the samples.

Campylobacter is the highest recorded cause of bacterial gastrointestinal infections worldwide (Murphy *et al.* 2006). The direct cost of campylobacteriosis to New Zealand is estimated to be \$4.48 million per annum (Withington & Chambers 1997). Up to 20% of campylobacteriosis cases are attributable to infections via horizontal transmission from environmental contaminants, for which domestic and wild animals are suspected as the source of the pathogen (Jacobs-Restsma *et al.* 1995, Clark 2003). Furthermore, Pacha *et al.* (1988) suggested migratory waterfowl should be considered high risk species for environmental contamination by *Campylobacter*. However, traditionally it has been thought that *Campylobacter* does not survive well outside the host. Hence, human health risks associated with contact with faeces, or contaminated pasture, are presumed to be low. Conversely, Clark (2003) showed that *Campylobacter* survival is adequate in faecal samples up to 24 hours post deposition, suggesting a moderate level of environmental contamination risk. Thus, since no *Campylobacter* was isolated from fresh paradise shelduck faeces at Tawharanui Regional Park it is assumed that they are not carriers or reservoirs of *Campylobacter*.

2.7.3 *Yersinia*

No *Yersinia* isolates were detected in any of the paradise shelduck faeces. This is in contrast to a study by Mackintosh and Henderson (1984), who found the prevalence of *Y. pseudotuberculosis* to be 5.3% from 75 ducks on a farm on the southern end of the

South Island of New Zealand, an area which was known to be contaminated. Elsewhere, *Yersinia* species have been isolated from the faeces of healthy birds, including waterfowl, and mammals, which can infect humans and livestock (Mackintosh & Henderson 1984, Fukushima & Gomyoda 1991, Cork 1994). This suggests that wild birds may be reservoir hosts for *Yersinia* and a potential source of infection on farms. Subsequently, potentially pathogenic species of *Yersinia* could be transmitted between different species through contaminated feed or water supplies (Cork 1994). It is generally recognised that yersiniosis is a disease which requires a predisposing factor, such as, extreme cold weather, nutritional stress, management stress or concurrent disease. In this survey, there was no evidence of predisposing factors enabling yersiniosis to prevail. Furthermore, in relation to *Salmonella*, *Campylobacter* and *Yersinia*, the inability to detect micro-organisms in faecal samples can be attributed to a number of factors: a true absence of the micro-organisms in the population at the time of sampling, limitations of bacteriologic culture or intermittent shedding in individuals. Because micro-organisms in faecal samples can be shed intermittently, it was not unexpected to have negative faecal bacteria cultures results, given the frequency of sampling used. Ultimately, only with long term monitoring and the presence of predisposing factors, can paradise shelducks be identified as possible carriers or reservoirs of *Yersinia*.

2.7.4 *E. coli*

This survey detected *E. coli* isolates in 87.5% of the paradise shelduck faeces samples. Similarly, in a survey of faecal shedding of selected bacterial pathogens from waterfowl in Ohio, Fallacara *et al.* (2001) isolated *E. coli* from 89% of 82 mallard duck faeces and 63% of 357 Canada goose faeces. This result is much lower than a previous survey by Fallacara and Morishita, who isolated *E. coli* from 87% of 69 Canada goose faeces (Fallacara *et al.* 2001). Limited information exists as to the prevalence of *E. coli* shedding in waterfowl (Fallacara *et al.* 2001). Samadpour *et al.* (2002) investigated an *E. coli* O157:H7 outbreak, associated with a lake in Vancouver, Washington. Although *E. coli* was recovered from duck faecal samples near the lake, it was not clear if the resident population of ducks at the lake, was the source of contamination. It was quite likely that the ducks were transiently infected by contaminated water. The high

prevalence of *E. coli* detected in this study implies that the population of paradise shelducks at Tawharanui are healthy carriers of *E. coli*.

However, the serotypes of the *E. coli* isolates detected in this study were not determined in this investigation, so no conclusions could be made in relation to their pathogenicity. *E. coli* is not normally pathogenic. However, *E. coli* can cause infections, and some strains such as, *E. coli* 0157:H7 are the cause of large scale outbreaks (Callaway *et al.* 2003). Generally, the concern regarding *E. coli* isolations, particularly in relation to its presence in faeces, lies in the potential presence of other more serious pathogens, such as *Salmonella*, rather than the concern over the inherent *E. coli* pathogenicity (Converse *et al.* 1999). Accordingly, *E. coli* is used as an indicator of environmental contamination by faeces. Livestock are also known to harbour *E. coli* and act as reservoirs, and furthermore, it is not unusual to find high carrying levels of Stx genes (A gene associated with *E. coli* 0157:H7) in livestock (Samadpour *et al.* 2002, Callaway *et al.* 2003). However, Hussong *et al.* (1979) isolated seven enterotoxin-producing *E. coli* from a random selection of 75 *E. coli*, which were isolated from Canada geese and whistling swans in Baltimore. (Ahmed *et al.* 2005). Additionally, *E. coli* 0157:H7 have previously been isolated from healthy and diseased wild birds (Hubálek 2004).

2.7.5 Additional bacteria

Non haemolytic and alpha haemolytic *Streptococci*, *Enterococcus*, *Bacillus*, *Clostridium perfringens* and *Proteus mirabilis* isolates were all detected in the paradise shelduck faeces sampled in this survey. The prevalences for these bacteria in the paradise shelduck faeces were; 29.2%, 33.3%, 16.7%, 50%, 4.7% and 41.7%, respectively. All of these bacteria can pose a threat to livestock and human health (Hardie & Whitey 1997, Castagnola *et al.* 2001, Ehling-Schulz *et al.* 2004, Schotte *et al.* 2004, Songer & Miskimmins 2004, Schoeni & Wong 2005). However, the serotypes of these bacteria isolates were not determined in this investigation, so no conclusions could be drawn in relation to their pathogenicity. Also, there are very few studies concerning prevalences and transmission routes of these bacteria in waterfowl faeces, to compare with.

2.7.6 Huia database

The New Zealand Wildlife Centre, maintain a database (Huia database) of all wildlife that go through their practice. The Huia database, has recorded only nine paradise shelduck cases that have been sent to the New Zealand Wildlife Centre since 1996 (Appendix 2.10.2). Of these nine cases only one was diagnosed with a possible infection of bacteria which lead to its death (Appendix 2.10.3). This suggests that there is a low incidence of diseased paradise shelduck. However, this can not be taken as a true indication, as it is unlikely that most dead or dying paradise shelduck would be sent to the New Zealand Wildlife Centre for diagnosis.

2.7.7 Faecal parasites

Although *Giardia* and *Cryptosporidium* are widespread in wild animals on New Zealand farms (Chilvers *et al.* 1998), no *Cryptosporidium* oocysts or *Giardia* cysts were detected in any of the paradise shelduck faecal samples from this study. Abbotts (2003) results were similar to this survey, where no *Cryptosporidium* oocysts or *Giardia* cysts were detected in any of the 279 screened duck faecal samples from New Zealand. Conversely, in a survey of wild ducks on the Rio Grande River in New Mexico, Kuhn *et al.* (2002) found 49%, of the 69 faecal samples, tested positive for *Cryptosporidium* and 26% for *Giardia*. Avian isolates of *Giardia* cysts can contaminate waterways and are a potential danger to humans, livestock and native animals (Graczyk *et al.* 1998). Despite this, little is known about the cross-transmission and it is suspected that wildlife infection of *Giardia* and *Cryptosporidium* has limited direct impact on the cause or maintenance of infection in humans (Chilvers *et al.* 1998).

In contrast to *Giardia* and *Cryptosporidium*, strongyle eggs were detected in 4.2% of all the paradise shelduck faeces sampled, while *Coccidia* eggs were detected in 12.5% of the samples. *Eimeria*, which is a genus of coccidian parasites, are generally highly host specific. Rarely does one species of *Eimeria* complete an infectious cycle in more than one host species (Yun *et al.* 2000, Ballweber 2004). Therefore, with few exceptions, coccidiosis in free-living waterfowl is not a primary health concern because of host specificity and the self-limiting nature of their infections (Ballweber 2004).

It must be remembered, that when interpreting the McMaster results, a number of factors can influence the occurrence and recognition of parasitic eggs found in a faecal sample. In particular, the daily output of eggs by fertile female parasites is influenced by the hosts' physiological factors such as stress. Additionally, the concentration of egg is influenced by the daily volume of faeces being produced by the host, the rate of passage through the intestine, and the distribution of eggs throughout the faecal mass.

2.7.8 Flock size

In general, infectious disease are transmitted more efficiently at relatively high host population densities (May 1995). There are two distinct levels at which host density may influence the transmission of micro-organism: an increased risk of transmission starting as the density of a susceptible host population increases, as well as a higher frequency of transmission in a more dense host populations (Botzler 1991).

Throughout this survey, four types of 20 g accumulated faeces samples were analysed independently. These were: faeces combined from pairs that were not associated with the flock, faeces combined from five individual birds from the flock, faeces combined from 10 individual birds from the flock and faeces combined from 25 individual birds from the flock (Table 2.1). This was done to simulate different host densities and to test whether flock size influences the prevalence of some bacteria associated with paradise shelduck faeces. This survey found no correlation between the number of accumulated faeces per sample and the prevalence of any of the bacteria isolated from paradise shelduck faeces from Tawharanui. This indicates that there is no relationship between the prevalences of bacteria and flock size of paradise shelducks. As a result, this implies that only a few individuals of a population are needed to be surveyed in order to gain an indication of the bacterial flora present in that particular population. However, the method of pooling faecal samples from individual birds in a flock that consists of a mix of infected and non-infected birds may dilute the concentrations of pathogens and therefore lower the sensitivity of the analyses to detect the pathogens. Additionally, it must be noted that, sample size can also explain the variation in prevalence in some of the results: large numbers of samples would have resulted in less variation.

2.7.9 Seasonal effect

Environmental conditions are important in the maintenance, promotion and transmission of micro-organisms in mammals and birds (Fukushima & Gomyoda 1991, Hubálek 2004, Morishita 2004), with more outbreaks of transmission and infection occurring, following cool, wet weather, especially in winter (Mackintosh & Henderson 1984, Morishita 2004). This survey sampled paradise shelduck faeces at four different times of the year, to determine if there was any seasonal effects on the prevalences of the bacteria isolated in the faecal samples.

All the bacteria isolated from the samples in this survey showed a significant seasonality difference in their prevalences, albeit, the high prevalence seasons were not all the same between the different isolated bacteria. *E. coli* had a distinct high season in November and March (Figure 2.7). These months are generally warmer months, which is in contrast to the assumption that higher prevalences occur in the cooler months (Mackintosh & Henderson 1984, Morishita 2004). Non haemolytic *Streptococci* had a higher prevalence in August (Figure 2.10), while alpha haemolytic *Streptococci* had a higher prevalence in November and March (Figure 2.13), as well as *Proteus mirabilis* (Figure 2.22). Once again, these high prevalences were in the warmer months. *Enterococcus* had a higher prevalence in May (Figure 2.16) and *Bacillus* had a higher prevalence in May and March (Figure 2.19). Overall, the highest number of different potentially pathogenic micro-organisms isolated in paradise shelduck faeces was during March (Figure 2.4), which is one of the warmest months in New Zealand. This may be a result of March being a fairly dry month, so consequently more individuals and different species congregate around water sources, such as a trough, where there will be a higher chance of transmission and cross-transmission. This suggests that it is best to survey a paradise shelduck population for pathogenic micro-organisms in the warmer, drier months of the year.

2.7.10 Host species comparison

To be of maximum usefulness, bacteriological surveys of wildlife diseases should include concurrent sampling of the species of interest, other species and the environment in the chosen location of the survey (Cork 1994). This study included

faecal samples from two other common ground foraging species found sympatrically with paradise shelducks: pukekos and house sparrows, during May 2007. *E. coli* was isolated from house sparrow samples during the same time of year as *E. coli* was isolated in paradise shelduck faeces. Both the house sparrow and pukeko samples contained non haemolytic *Streptococci*, alpha haemolytic *Streptococci*, *Proteus mirabilis* and *Coccidia*, which were also all isolated from paradise shelduck faeces during the survey. Additionally, both the pukeko and the house sparrow faecal samples contained micro-organism species that were not present in any of the paradise shelduck faeces samples. These species were; *Klebsiella*, *Enterobacter agglomerans*, *Campylobacter jejuni*, *Ascarid* and *Heterakis*. This implies that the environment is contaminated with non haemolytic *Streptococci*, alpha haemolytic *Streptococci*, *Proteus mirabilis* and *Coccidia*, and that cross-transmission of some of these micro-organisms may occur.

Adhikari (2003) found that 40% of 53 house sparrows had a high isolation rate of *Campylobacter* and were important reservoirs. House sparrows are also known carriers of *Salmonella* in New Zealand (Alley *et al.* 2002, Connolly *et al.* 2006). No *Campylobacter* or *Salmonella* were detected in the house sparrow faeces in this survey, but *Campylobacter jejuni* was detected in the pukeko sample. While no Canada geese were present in Tawharanui Regional Park, this species is known to share the same habitat as paradise shelducks (White 1986, Harris *et al.* 1987, Spurr & Coleman 2005). Furthermore, Canada geese are known to carry some of the same species of micro-organisms carried by paradise shelducks and this species is considered a greater potential health risk than other waterfowl (Hussong *et al.* 1979, Feare *et al.* 1999, Clark 2003, Bönner *et al.* 2004, Clark 2004, Spurr & Coleman 2005).

Additionally, livestock are also known to harbour *E. coli* and act as reservoirs (Samadpour *et al.* 2002, Callaway *et al.* 2003). The number of bacteria shed by livestock, defecating approximately 25 kg of fresh faeces per day (Matsuzaki 1975), should greatly exceed the faecal bacteria found in paradise shelducks faeces. Higher concentrations of organisms and volume of livestock faecal matter could affect their significance as a source of environmental contamination. Thus, livestock may be maintaining infections on farms. Consequently, the transmission route of *E. coli* is not clear, as the livestock could be acting as a reservoir for the pathogen, which is allowing

cross-transmission to the paradise shelduck, or vice-versa. Thus, conclusive evidence for certain transmission routes was not found in this survey.

2.7.11 Troughs

Analysis of water samples for each individual type of micro-organism was not practical, due to the expense and time-constraints. Since most water-borne pathogenic organisms are usually present in low numbers and are difficult to cultivate, organisms which are characteristic of faecal material and which can normally survive for longer periods, in water are relied on as indicators (Pyle 1974, Abbott 2003). The most common of these are coliform organisms. Pyle (1974) concluded in his study that faecal coliforms were good indicators of animal pollution in pond water associated with farms. Faecal coliforms have been widely used as an indicator of the microbiological quality of surface and ground water, but recently it has been suggested that *E. coli* are much better indicators of faecal contamination (Ahmed *et al.* 2005).

Water sources, such as troughs for livestock, supplied by farmers, are necessary to increase carrying capacity of the land and improve the well-being of livestock. These water sources are also used by other species, such as pukekos and paradise shelducks, and consequently, have become a source of disease for livestock (Pyle 1974). In waterborne infections, the micro-organisms can be shed by infected hosts, resulting in contamination of water with faecal bacteria (Hubálek 2004, Ahmed *et al.* 2005). Troughs located in the same area as the paradise shelduck surveyed in this study were sampled and tested for faecal contamination. Multiple indicator organisms were targeted for satisfactory detection.

Extremely high levels, well above the Auckland Regional Councils water quality limit of 1000 cfu/100ml, of faecal coliforms and *E. coli*, were detected in all three troughs throughout the sampling period. The highest levels were detected in March 2007, which is during the hottest and driest time of the year. This may be due to higher numbers of animals using and congregating around troughs at this time of year. Pyle (1974) also showed in his study, that the concentrations of indicator bacteria in water holes for livestock were low in spring, rising sharply in the summer as stock begin to drink at water sources. Trough 1 consistently had lower levels of *E. coli* contamination throughout the sampling period. This may be due to trough 1 being located in the

territory of a pair, while the other two troughs were in the flock territory, so a higher number of paradise shelducks had access and congregated at these troughs. Throughout the sampling period *Salmonella* was only detected once, but since *Salmonella* may be emitted intermittently from a diseased host, the testing programme may have missed detection on the other occasions. However, the results do illustrate that *Salmonella* was present in the same environment and at the same time as the paradise shelducks were in this survey. This implies that the paradise shelduck had direct contact with *Salmonella*, but they were not infected, thus paradise shelducks seem to be resistant to *Salmonella* and are potentially not reservoirs for this pathogen.

Domestic and wild animal defecation is known to be a source of such contamination. Ahmed *et al.* (2005) found that, from 27 water samples from five different sites in Maroochydoore, Australia, 9% of the contamination was from ducks and 7% from livestock. Although, a study by Abbott (2003) found no correlation between the number of ducks and either total coliforms or *E. coli* counts in surface water. Faecal contamination of water on farms has led to potential disease transfer (Pyle 1974). It is not clear whether paradise shelducks are contaminating the troughs or if they are being infected by contaminated trough water. The initial source may have been other animals that reside in the same vicinity. The presence of the shelducks, however, may have helped sustain contamination levels.

2.7.12 Paradise shelduck as reservoirs

‘Wildlife reservoir’ is defined as a population of wild animals which is able to maintain an infectious organism through successive generations without the need for re-infection from an external source (Schurrenberger *et al.* 1987). Cork (1994) states, that to be an effective ‘wild life reservoir’ it would be expected that either: the host population would not be severely affected by the potential pathogen and would shed the pathogen over a long period of time either continuously or intermittently; or individuals in the host population may be susceptible to the disease but would shed large numbers of organisms infecting other individuals in the population before they died. The first option is possibly more common, where the species could act as amplifier hosts or mechanical carriers, but the latter could be effective if the bacteria were shed for sufficient periods of time or the infective dose was low. In the second option the spread of disease is

dependent on the population dynamics of the species being conducive to the spread of infection, for example birds which gather in flocks and migrate out, and thus spread the infection.

In the case of paradise shelducks at Tawharanui, it seems that the second option is not a possibility, as the population does not appear susceptible to any of the diseases that can occur from the bacteria that they harbour. However, the first option appears to apply to paradise shelducks, more specifically in relation to *E. coli*. The paradise shelducks at Tawharanui appear to harbour *E. coli* over a long period of time, shed the bacteria regularly and are not severely affected by the pathogen. This implies that paradise shelducks at Tawharanui, are reservoirs for *E. coli*. However, *E. coli* is not normally pathogenic, and only a few strains such as, *E. coli* 0157:H7, are infectious. It also needs to be remembered, that the serotypes of the *E. coli* isolates were not determined in this investigation, so no conclusions could be made in relation to their pathogenicity.

As for the other micro-organisms isolated from paradise shelduck faeces, their prevalences were much lower than the prevalences of *E. coli*. This suggests that paradise shelducks are not likely to be reservoirs for these micro-organisms, as their circumstances do not meet Cork's requirements. The low prevalence of some of the organisms in the paradise shelduck surveyed, suggests that this population would need a continual re-infection from environmental sources to maintain these micro-organisms in their intestinal flora. There was no consistent distribution of positive samples over time within the sampling periods or between the number of accumulated faeces per sample. The low frequency of positive cultures indicates that the risk of infection through contact with paradise shelduck faeces appears to be minimal.

Not all host species are important reservoirs for pathogenic micro-organisms. Some may experience only short term infection and some may be intermittent or poor excretors (Mackintosh & Henderson 1984). Additionally, even if paradise shelducks are shedding pathogenic micro-organisms into the environment, it is not known if the strains in New Zealand wildlife are able to infect humans or livestock, as most strains recovered from animals and environmental sources probably lack clinical significance.

Like this study, many recent surveys have shown the prevalence of micro-organisms in the faeces of wild birds has been found to be relatively low for some species. However, faecal surveys may give an underestimate of the prevalence of infection due to the

possibility of intermittent shedding which would not be detected in a single sample. Additionally, it must be noted, that factors such as transmission route, infective dose and the sensitivity of culture techniques must be considered when evaluating the role of 'reservoir' populations. The sensitivity of faecal culture is not known for paradise shelducks and possibly gives an underestimate of the true prevalence of the organism (Barrow 1993, Fossler *et al.* 2004, Davison *et al.* 2005). So, although the prevalence of some of the micro-organism was low, this study does not rule out the possibility that paradise shelduck may serve as a reservoir for the micro-organisms isolated in this survey.

The power of many of the comparisons presented here was low because of the small sample size. In addition these isolates were collected from a small number of samples, which may not sufficiently represent the diverse faecal bacteria found in paradise shelducks. Due to the limitations of faecal surveys, serological screening for disease surveillance in wild populations could be a more reliable method. Additionally, the diversity, quantity and pathogenicity of micro-organisms may not only differ among species of birds, but also in different populations of the same species (Ballweber 2004). As is the case in this study, the findings shown may not reflect those of other waterfowl species or even other populations of paradise shelducks.

The extent of transmission from wild bird-vectored organisms to mammalian hosts and the importance of these parasites in avian species are largely unknown (Kuhn *et al.* 2002, Millán *et al.* 2004). Although the isolation of these bacteria does not directly implicate paradise shelduck as a source of transmission to livestock or as a reservoir, it does indicate they are carriers and pose a risk for transmission. While no direct link between contact with paradise shelduck faeces and livestock illness has been made, there is increasing evidence that micro-organism pathogenic to livestock are present in waterfowl faeces. However as in so many cases cause and effect are difficult to untangle.

2.8 Conclusions

The role of paradise shelducks as host/reservoir species for pathogens is of concern to the agricultural community. An understanding of pathogenic micro-organisms dynamics in agricultural sources is important to maintain the integrity of agriculture as an

important industry. The patterns and use of pastures and water by paradise shelducks, the degree of environmental contamination by pathogens, and how these pathogens might make their way to livestock need to be considered. It seems that the population of paradise shelducks, at Tawharanui, are not reservoirs or carriers of *Salmonella*, *Campylobacter* or *Yersinia*, as no isolations were detected in the faecal samples, even though they were potentially exposed to environmental contamination of *Salmonella* and *Campylobacter*.

Paradise shelducks may be reservoirs of *E. coli*, since there was high prevalence in the faecal samples throughout the sampling period, which could be a source of infection to the environment and other species. Although the route of the contamination transmission is unclear, as the paradise shelducks may be contracting *E. coli* themselves from other species, such as house sparrows, or from environmental contaminations, like the contaminated water troughs.

The prevalences of Non haemolytic and alpha haemolytic *Streptococci*, *Enterococcus*, *Bacillus*, *Clostridium perfringens* and *Proteus mirabilis* in the faecal samples taken from the paradise shelducks at Tawharanui were relatively low. Intermittent shedding or latent carriage of pathogens could explain the low rate of isolation of these micro-organisms in this study. However, this seems unlikely considering the consistently low numbers of isolates recovered throughout the sampling period and the prevalence of the micro-organisms in the environment. Additionally, the serotypes of the micro-organisms isolated in this study were not determined, so no conclusions can be drawn in relation to their pathogenicity.

The micro-organism isolated from the paradise shelducks may only be relevant for the Tawharanui Regional Park population. In addition, the micro-organism flora found in the Tawharanui Regional Park population may vary over time. Differences in micro-organisms diversity and abundance within and between populations may be caused by changes in climate, habitat, host immunity or pathogen evolution. Accordingly, it can not be assumed that other populations of paradise shelducks have similar micro-organisms associated with their faeces. Additional studies, similar to this one, are needed to provide a comprehensive micro-organism profile for paradise shelducks.

Identification of the presence and prevalence of micro-organisms from a population involves many tests and can be expensive and time consuming. To save money and

time, the results from this study suggest that the best time of year for sampling a paradise shelduck population for potentially pathogenic micro-organisms is during the hottest/driest periods and that there is no apparent need to sample a large number of birds from within a population.

In conclusion, this study illustrates that paradise shelducks do harbour potentially pathogenic micro-organisms. Therefore, paradise shelducks can serve as possible reservoirs, and contact with these birds or environments which have resident paradise shelduck can potentially result in cross transmission of pathogens.

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CHAPTER 3: Paradise Shelducks as Grazers in Pastoral Communities



Plate 3.1. Photo by M. Delaney 2006.

3.1 Abstract

Damage to agricultural crops and pasture consumption by grazing waterfowl has been reported in many parts of the world. In New Zealand, paradise shelducks (*Tadorna variegata*) have established a firm foothold in the agricultural environment. As a result of their feeding habits and habitat use, paradise shelducks compete directly with livestock for pasture. Consequently, paradise shelducks are considered a pest by many farmers in a agricultural setting. Despite this perception, there have been no studies to date that have tried to quantify and evaluate the effects that paradise shelducks may be having on agricultural pastures.

The present study was undertaken to evaluate the level of impact paradise shelducks have on pastoral communities, and whether potential impacts could have negative consequences for agricultural practices in New Zealand. To investigate this objective, two exclosure were set up on agricultural land at Tawharanui Regional Park: a 'closed' exclosure to exclude all animals including paradise shelducks, and an 'open' exclosure to exclude livestock, but allow access for paradise shelducks. A significant difference in pasture growth was found between the open and closed exclosures. In contrast, no significant differences were found for ryegrass (*Lolium perenne*) or kikuyu (*Pennisetum clandestinum*) composition between the two exclosure types. However, a significant difference was found between the two exclosures for white clover (*Trifolium repens*) composition, with open exclosures consistently having lower percentages of white clover cover. Although, it should be noted that these variations could be due to light intensity differences between the two exclosure treatments. Furthermore, it was estimated that the paradise shelducks at Tawharanui Regional Park had a foraging intake rate of 104 ± 15 g/day of pasture dry matter. In conclusion, this study suggests that paradise shelducks can have a significant negative impact on pasture production and seem to selectively graze white clover.

3.2 Introduction

Cereals and pasture grasses are economically the most important agricultural plants in the world (Langer 1979). Pasture grasses in many different climates and countries are predominately used for livestock production (Radcliffe 1974a, b, Langer 1979). This is the case in New Zealand, where agricultural practices are largely based on temperate pastures (Butler 1986) which are primarily used for the feeding of livestock and consequently for the production of meat, milk, wool and other animal products (Radcliffe 1974a, b, Langer 1979). It is well known that herbivores, such as livestock, influence the primary production of plant and pastoral communities (Olofsson *et al.* 2007). Fortunately, the grasses used for livestock production are extremely well adapted to being grazed. Before the flowering stage in grasses is reached, leaf formation continues during and after defoliation. This is because during the vegetative stage, the meristematic zones are located close to the soil surface, beyond the reach of livestock (Langer 1979). But the act of grazing is a complex process far beyond the simple removal of leaves. It involves physiological changes in all parts of the plant. Grazing can change the microclimate of the pasture, such as light intensity, moisture and temperature (Scofield 1970, Langer 1979). Grazing can also alter the soil environment through the trampling action of livestock as well as nutrient leeching from the faeces and urine of livestock (Scofield 1970, Langer 1979). All these factors have variable effects on pasture production and species composition, depending on the severity of the grazing in relation to the stage of growth of each pasture species (Scofield 1970, Langer 1979). As a result, considerable research has been done to explain the responses of pasture to management applications, especially with respect to the intensity and frequency of defoliation (Boswell 1977, Butler 1986).

Butler (1986) states that, the objective of grazing management is to obtain high feed intakes of livestock so that per hectare performance and income is optimised. Accordingly, control over the frequency and severity of defoliation has long been advocated as a means by which the productivity of pastures can be increased, for example, by decreasing the frequency of defoliation, production from pastoral communities is generally improved (Boswell 1977, Butler 1986). Consequently, grazing management practices try to reduce any negative impacts on the productivity of pasture,

such as pasture damage or competition for pasture by other competing species, like grazing waterfowl.

Damage to agricultural crops and pasture consumption by waterfowl has been reported in many parts of the world (Gillespie 1985). Grazing waterfowl are generally classified as foragers that retain food for a short period of time in their alimentary tract, and digest food only superficially (Prop & Vulink 1992). As a result grazing waterfowl tend to select high quality plants within their foraging range and graze continuously to meet their daily energy requirements (Summers & Grieve 1982, Prop & Vulink 1992). The level of damage to crops and the amount of pasture consumed by waterfowl is variable and widespread (Gillespie 1985). It has been estimated that some waterfowl can consume about 80% of the net above-ground primary production in particular environments (Cargill & Jefferies 1984). Within New Zealand, it is known that Canada geese (*Branta canadensis*) compete directly with livestock for pasture (Leathers & Costello 1986, Win & Hickling 2000). Likewise, paradise shelducks (*Tadorna variegata*) could potentially have a negative impact on agricultural practices. Paradise shelducks show a strong preference for pasture, almost exclusively inhabiting farmland, and as a result, like Canada geese, they may compete directly with livestock. Bisset (1976) found that paradise shelduck flocks selected pastures where grasses and clovers were the dominant ground cover and relied on the pasture for the majority of their food. These feeding habits have brought them into direct conflict with farmers, who consider the birds to be a pest, although, the perceived impacts of paradise shelducks on agricultural land may be an inflated estimate of true loss. Livestock utilisation of available pasture is commonly less than 100% (White 1986), hence paradise shelduck pasture intake may not imply a direct competition with livestock for a limited resource. In contrast, it has been suggested that waterfowl such as paradise shelducks may actually stimulate grass growth, by accelerating the turnover of organic matter and nutrients (White 1986). Despite the controversy, the impact of paradise shelduck flocks on pasture growth, species composition, and consequently their economic impact, is unknown.

3.3 Objectives

Grazing management and research for agricultural purposes principally focuses on the intensity and frequency of defoliation as well as changes in species composition of pastoral communities. Grazing animals can affect pasture attributes such as species composition and dry matter production (Milton *et al.* 1994). Thus, control over the defoliation and change in species composition by livestock and other competitive grazing animals have long been advocated as a means by which the productivity of pastures can be increased.

The general objective of this chapter was to evaluate the level of impact paradise shelducks have on pastoral communities, and whether this impact could have negative consequences on agricultural practices in New Zealand. Specifically, the objectives in this chapter are:

1. Estimate the density of paradise shelduck and their usage of managed pasture areas in the Tawharanui Regional Park.
2. Determine whether or not paradise shelduck have an affect on pasture primary production.
3. Determine whether or not paradise shelduck have an affect on pasture species composition.
4. Estimate the daily food intake rates of paradise shelduck.

This information will increase the understanding of the impact of grazing by paradise shelducks on the community structure and composition of pastures associated with agricultural practices in New Zealand. Consideration of these findings could be used in grazing management decisions as well as paradise shelduck population management decisions.

3.4 Methods

3.4.1 Pasture trials

The total effect on pasture biomass accumulation and species composition can be determined by excluding the target grazer experimentally (Mitchell & Wass 1996). Therefore, to investigate the effects of paradise shelducks on pastoral communities, two exclosures were designed (1): a ‘closed’ exclosure to exclude all animals, and (2) an ‘open’ exclosure to exclude livestock but allow access to paradise shelducks (Plate 3.2).



Plate 3.2. Showing a sampling site containing a set of exclosures; two closed exclosures (a), and two open exclosures (b). Photo by M. Delaney 2006.

Each exclosure measured 4m x 4m, and stood approximately 1.5m high. The closed exclosures consisted of four metal warratah posts enclosed by bird mesh. The open exclosures consisted of a perimeter of portable electric fencing to ward off livestock but allow paradise shelducks access to the area from above and below.

Three different sites were used; Sites 1, 2 and 3 within the study site location (See section 2.5.1). Sites 2 and 3 were chosen for this study because the combined area formed the flock territory of the Tawharanui Regional Park population. Consequently, Site 1 was chosen because it contained the same habitat type as Site 2 and 3 and additionally, was the territory of a breeding pair of which comparisons could be made to the flock territory. At each site two open and two closed exclosures were set up and left erect for four weeks (sampling period) on four consecutive occasions (May, August, November and March). Each exclosure, was erected in areas which were selected for similar aspect, gradient, altitude as these factors can affect some pasture species growth (Radcliffe 1982). Additionally, similar pasture composition and density were selected and all exclosures were at least 5 m apart. Care was taken to avoid plots with patchy pasture growth and high levels of cow faeces.

At the start of each sampling period, the areas within exclosures were mowed to a two cm height to give an initial even distribution of pasture growth between each exclosures. To measure primary pasture production, a Ravensdown sward stick was used to measure the pasture height and estimate dry matter. During each sampling period the pasture height was measured weekly in each exclosure. In each exclosure four points were measured; 0.5m due north, south, east and west from the centre. This gave a total of 16 weekly measurements at each site, and a total of 48 readings for the whole study area. Pasture height measurements were then converted into dry matter (kg/ha). The change in pasture composition was also recorded, by estimating the relative proportions of pasture species within each exclosure on a weekly basis, over all four sampling periods. Pasture species were grouped into six categories: kikuyu (*Pennisetum clandestinum*), ryegrass (*Lolium perenne*), white clover (*Trifolium repens*), *Plantago* species, *Ranunculus* species and 'other' species (including *Oxalis* species, *Epilobium ciliatum*, *Conyza albida*, *Cirsium* species, and *Solanum nigrum*). At the end of each sampling period, the exclosures were dissembled and removed from the sites to allow stock to be reintroduced the areas.

Additionally, bird counts were conducted weekly during each sampling period from one vantage point, at 10:00 hours. The study area was scanned for all bird species, three times, at five minute intervals, using 8 x 42 binoculars.

3.4.2 Estimation of daily pasture intake

Geese and shelducks are generally classified as foragers that retain food for a short amount of time in their alimentary tract, and hence digest their food only superficially (White 1986, Prop & Vulink 1992). Vegetation generally clears the gut in waterfowl within 2-4 hours (Prop & Vulink 1992, Gloutney *et al.* 2001). During May 2006, 28 fresh paradise shelducks were obtained from hunters and farmers within the Auckland region. Necropsies were performed on all the birds and the oesophageal contents, plus un-ground vegetation in the gizzard were removed, dried and weighed. It was assumed that all food from previous foraging bouts would have been ground in the gizzard and so only un-ground vegetation in the gizzard was included in the food intake analysis. Total food intake for foraging bouts was calculated as total dry mass of oesophageal contents plus un-ground vegetation in the gizzard. Additionally, 20 foraging behaviour observations of paradise shelducks were made at Tawharanui Regional Park during August. The paradise shelducks were observed with 8 x 42 binoculars from a distance of 100-300 metres. Foraging bout times were recorded as well as time spent feeding within a bout. Intake rates of food for paradise shelducks (adapted from Gloutney *et al.* 2001) were calculated as follows:

$$\text{intake rate (g/h)} = \text{total dry mass ingested (g)} / \text{time foraging (h)}$$

Where time foraging is the number of minutes that the paradise shelducks were observed foraging during a bout. Using an estimate of daily foraging time obtained from Williams (1979a, b), total daily food intake rates were calculated as follows:

$$\text{estimated daily intake (g/day)} = \text{intake rate (g/h)} \times \text{daily foraging time (h/day)}$$

3.4.3 Environmental conditions

To test for any significant differences in environmental conditions between the two types of exclosures, onset HOBO[®] U12 data loggers were used inside all exclosures. Temperature, relative humidity, dew point, absolute humidity and light intensity were measured every 30 minutes during the first pasture trial from 08:00 – 16:30 hours.

Additionally, soil nutrient levels within the exclosures were determined to test for any significant differences between the two types of exclosures. Twenty, 75mm core soil samples were taken from each exclosure during the first pasture trial. These samples

were sent to NZLABS (New Zealand Laboratory Services LTD.) for soil nutrient level testing (Table 3.1).

Table 3.1. Testing methods for soil nutrient levels by NZLABS.

Nutrient	Test Methodology
Acidity/Alkalinity (pH)	1:2.1 V/W Water Slurry
Calcium (MAF QT)	Ammonium Acetate Extraction: AA determination
Phosphorus ($\mu\text{g/ml}$)	Olsen Extraction: Colorimetry
Potassium (MAF QT)	Ammonium Acetate Extraction: AA determination
Sulphur (ppm)	Potassium Phosphate Extraction: ICP
Magnesium (MAF QT)	Ammonium Acetate Extraction: AA determination
Sodium (MAF QT)	Ammonium Acetate Extraction: AA determination

3.4.4 Statistical analysis

It is clear that the environmental factors that are constraining the pasture growth and affecting species composition are acting together and are interrelated. Generally, however, environmental conditions are studied separately. In order to obtain a better understating of their action over pasture species composition and growth, both multivariate (repeated measures) and univariate (ANOVA) statistical analysis were used on the data.

Two types of general linear models were used when analysing the data; a repeated measures analysis of variance (Pillai's Trace) and a three-way ANOVA. The repeated measure Pillai's Trace was used to examine the effects that the variables; time (weeks), flock size, enclosure type and season has on pasture growth and composition, as well as the 2nd and 3rd order interactions between the variables. A full factorial three-way ANOVA test was performed to examine the effects that the variables; flock size, enclosure type and season have on pasture growth and composition, separately for each week of the pasture trial. Additionally, one-way ANOVAs were used to test for significant differences in the environmental conditions between the enclosure types. All statistical tests were performed using the statistical program SAS 9.0[©] and a significance level of $\alpha=0.05$ was used for all tests. For all ANOVAs the errors were checked for normality and heterogeneity of variance and transformed when necessary.

3.5 Results

3.5.1 Bird species counts

The bird species survey conducted in the study area (Figure 2.3) showed that over the entire research period, paradise shelducks were the most abundant bird species within its habitat (Table 3.2). Their mean numbers ranged from 45, in August to 79 in May, which represent 69% and 83% of the total number of birds counted, respectively. Figure 3.1, illustrates that site 1 (pair site) within the study area had no more than two paradise shelducks over the entire sampling period. While, site 2 and 3 (flock site) always had a combined total of 44 or greater. Additionally, site 2 consistently had higher numbers of paradise shelducks compared to the other two sites

Table 3.2. Mean \pm SE (n=4) number of birds observed in all three study sites combined (Figure 2.3) at Tawharanui Regional Park over the entire sampling period.

Species	2006			2007
	May	August	November	March
Paradise ducks (<i>Tadorna variegata</i>)	79.17 \pm 5.33	44.92 \pm 1.36	66.75 \pm 5.88	77.42 \pm 3.70
Pukekos (<i>Porphyrio melanotus</i>)	9.33 \pm 2.19	12.13 \pm 2.95	5.00 \pm 0.89	10.08 \pm 1.41
Plovers (<i>Vanellus miles novaehollandiae</i>)	4.83 \pm 0.44	3.54 \pm 0.52	3.92 \pm 1.21	4.5 \pm 0.22
Oyster Catchers (<i>Haematopus ostralegus finschi</i>)	2.58 \pm 1.61	4.46 \pm 1.40	2.00 \pm 1.15	–
Pied Stilts (<i>Himantopus himantopus leucocephalus</i>)	–	0.50 \pm 0.50	2.08 \pm 1.49	–
Mallards (<i>Anas platyrhynchos</i>)	–	0.25 \pm 0.25	0.50 \pm 0.50	–

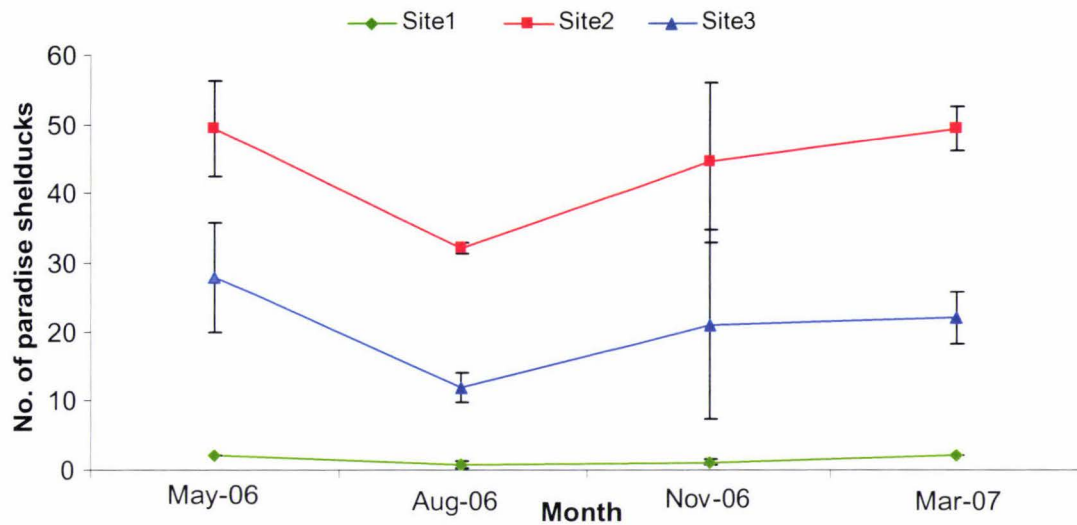


Figure 3.1. Number ($\bar{x} \pm SE$) of paradise shelducks observed at each of the three study sites (Figure 2.3) at Tawharanui Regional Park over the entire sampling period.

3.5.2 Environmental conditions

No significant differences for temperature, relative humidity, dew point and absolute humidity were found between the open and closed exclosures (Table 3.3). A significant difference was found in the light intensity levels between the exclosures, where the open exclosures had a consistent higher level of light intensity. No significant differences for soil nutrient levels of; acidity/alkalinity, calcium, phosphorus, potassium, sulphur, magnesium or sodium were found between the open and closed exclosures.

Table 3.3. Mean $\pm SE$ (range) and ANOVAs (df) for environmental measures inside open and closed exclosures at Tawharanui Regional Park.

Environmental Measure	Closed Exclosure	Open Exclosure	F	P Value
Temperature ($^{\circ}C$)	18.05 ± 0.62 (8.23-24.01)	17.75 ± 0.56 (10.21-24.79)	0.13 _(1,70)	0.72
Relative Humidity (%)	52.65 ± 1.67 (38.7-84.30)	56.83 ± 2.24 (36.9-91.7)	2.14 _(1,70)	0.15
Dew Point ($^{\circ}C$)	7.95 ± 0.39 (4.98-13.69)	8.70 ± 0.46 (3.98-14.16)	1.55 _(1,70)	0.22
Absolute Humidity (gm/M3)	8.03 ± 0.22 (6.70-11)	8.50 ± 0.27 (6.20-11.80)	1.82 _(1,70)	0.18
Light Intensity (lum/sqf)	787.53 ± 7.85 (737-839)	964.75 ± 22.13 (839-1103)	56.97 _(1,70)	<0.01
Acidity/Alkalinity (pH)	5.64 ± 0.10 (5.3-6.0)	5.74 ± 0.11 (5.4-6.2)	0.48 _(1,14)	0.51
Calcium (MAF QT)	6.75 ± 0.31 (6-8)	7.00 ± 0.73 (6-12)	0.10 _(1,14)	0.76
Phosphorus ($\mu g/ml$)	51.38 ± 10.60 (7-86)	59.38 ± 7.96 (26-84)	0.01 _(1,14)	0.93
Potassium (MAF QT)	10.38 ± 1.51 (4-16)	10.00 ± 2.12 (3-21)	0.02 _(1,14)	0.89
Sulphur (ppm)	4.38 ± 0.73 (2-8)	4.25 ± 0.49 (2-6)	0.02 _(1,14)	0.89
Magnesium (MAF QT)	37.13 ± 2.86 (26-50)	38.75 ± 2.71 (27-49)	0.17 _(1,14)	0.69
Sodium (MAF QT)	7.25 ± 0.56 (5-10)	7.00 ± 0.73 (5-11)	0.07 _(1,14)	0.79

3.5.3 Pasture primary production

For all pasture trials, no significant differences were found in 3 way interactions for either the Pillai's Trace or the three-way ANOVAs. Consequently, they were removed from subsequent models.

As was expected, there was a significant difference of accumulated dry matter over time (Table 3.4), where week one and week four have the lowest and highest dry matter accumulation values, respectively (Figure 3.2). No significant difference was found between flock sizes for accumulated dry matter. Significant differences were found for the values of accumulated dry matter between seasons, as well as between exclosures. August consistently had the lowest accumulated dry matter and November the highest. Additionally, the open exclosures generally had the lower accumulated dry matter when compared to the closed exclosures. No significant differences were found for the 2 way interactions, implying that the main effect differences (time, flock size, season and exclosure) were simple.

Table 3.4. Repeated measures analysis of variance (Pillai's Trace) for the effects of time, flock size (flock or pair sites), season and exclosure type (open or closed) on the net accumulated dry matter production.

Model Factor	F _(df)	P Value
Time (weeks)	2395.34 _(3,177)	<0.01
Flock Size	1.9 _(3,177)	0.13
Season	27.07 _(9,537)	<0.01
Exclosure	6.27 _(3,177)	<0.01
Flock Size * Season	0.29 _(9,537)	0.98
Flock Size * Exclosure	1.68 _(3,177)	0.17
Exclosure * Season	0.9 _(3,537)	0.53

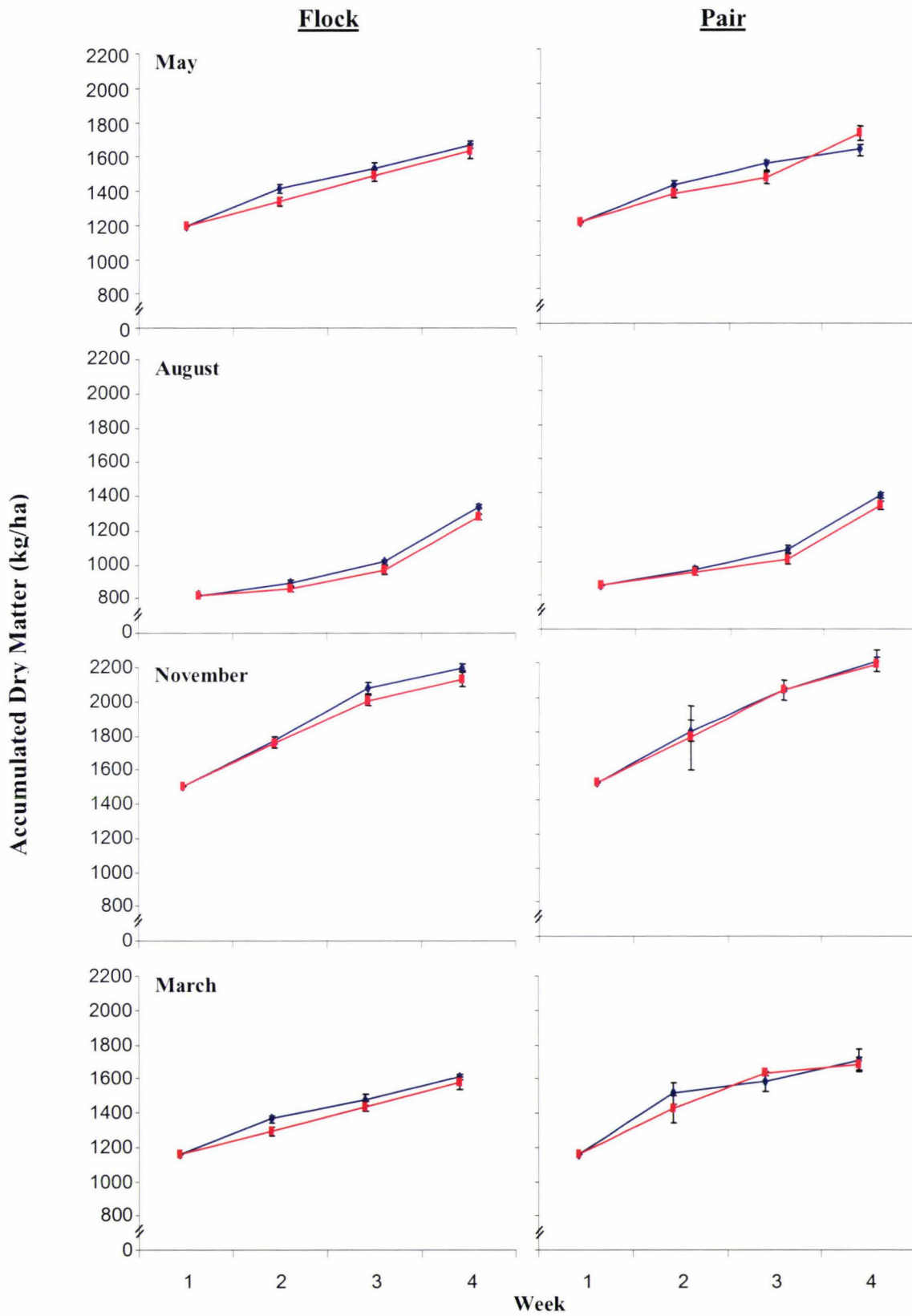


Figure 3.2. Accumulated pasture dry matter ($\bar{x} \pm SE$ kg/ha) for both closed (\blacklozenge) and open (\blacksquare) enclosures over a four week growth period in each sampling month for flock and pair treatments.

A significant seasonal difference for accumulated dry matter was found across all the weeks when each period was analysed separately (Table 3.5). Additionally, no significant differences were found for accumulated dry matter between flock sizes. Since all the experimental pasture plots were mowed to an even height at the start of the trials, no significant differences were found for accumulated dry matter between enclosure types for the first two weeks. But, in subsequent weeks of the trials, a significant difference of accumulated dry matter was found, where closed enclosures had a higher accumulated dry matter compared to the open enclosures (Figure 3.2). No significant interactions were found for week three. This implies that significant main effects for enclosure and season are consistent. In the last week of the trials (week four), there was a significant interaction between flock size and enclosure. This suggests that the differences in accumulated dry matter found between the enclosure types vary with the number of paradise shelducks. More specifically, there was a greater difference of accumulated dry matter between the open and closed enclosures in the flock site than the pair site.

Table 3.5. Three-way analysis of variance (ANOVA) for the effects of flock size (flock or pair sites), season and enclosure type (open or closed) on the net accumulated dry matter production for each week of the trial.

Model Factor	Week 1		Week 2		Week 3		Week 4	
	F _(6,179)	P Value	F _(6,179)	P Value	F _(6,179)	P Value	F _(6,179)	P Value
Flock Size	-	-	2.40	0.12	1.10	0.3	2.57	0.11
Season	∞	<0.01	237.13	<0.01	671.92	<0.01	581.55	<0.01
Enclosure	-	-	3.00	0.08	4.97	0.03	5.05	0.03
Flock Size * Season	-	-	0.30	0.83	0.52	0.67	0.35	0.79
Flock Size * Enclosure	-	-	0.06	0.81	0.61	0.44	4.22	0.04
Enclosure * Season	-	-	0.15	0.93	0.28	0.84	1.56	0.20

3.5.4 Pasture species composition

Kikuyu was the dominant plant species found in all the pasture trial plots, followed by ryegrass then white clover (Figure 3.3). *Plantago*, *Rannunculus* and other pasture species were also found, but these made up only a small percentage of the pasture species composition.

No significant differences were found in the pasture plots for the percentage of ryegrass between weeks, flock size or enclosure types (Table 3.6), although, a significant

difference was found between the seasons. November and March had the highest and lowest ryegrass cover, respectively (Figure 3.3). There was also a significant interaction between flock size and season; (Figure 3.3) there is a smaller seasonal difference in ryegrass cover within the flock site compared to the pair site. No other interactions were significant.

Table 3.6. Repeated measures analysis of variance (Pillai's Trace) for the effects of time, flock size (flock or pair sites), season and enclosure type (open or closed) on the pasture composition (%) of ryegrass.

Model Factor	F _(df)	P Value
Time (weeks)	2.58 _(3,33)	0.07
Flock Size	1.55 _(3,33)	0.22
Season	2.24 _(3,105)	0.02
Enclosure	1.2 _(3,33)	0.33
Flock Size * Season	1.95 _(3,105)	0.05
Flock Size * Enclosure	0.86 _(3,33)	0.47
Enclosure * Season	0.64 _(3,105)	0.76

When weeks were analysed separately, there were no significant differences found for pasture ryegrass cover between enclosure types (Table 3.7). However, there was a consistent significant difference between seasons over the four weeks, again with November and March had the highest and lowest kikuyu cover, respectively. Additionally, a significant difference was also found between the flock sizes during the first week, where the flock site had a higher percentage of ryegrass cover. Furthermore, there was a significant flock size * season interaction in the first two weeks. This was evident in March when there was a lesser difference of ryegrass cover between the flock site and pair site compared to the other seasons. Consequently, this implies that only for the first two weeks did flock size have an influence on the seasonal effect of ryegrass cover. No other interactions were significant.

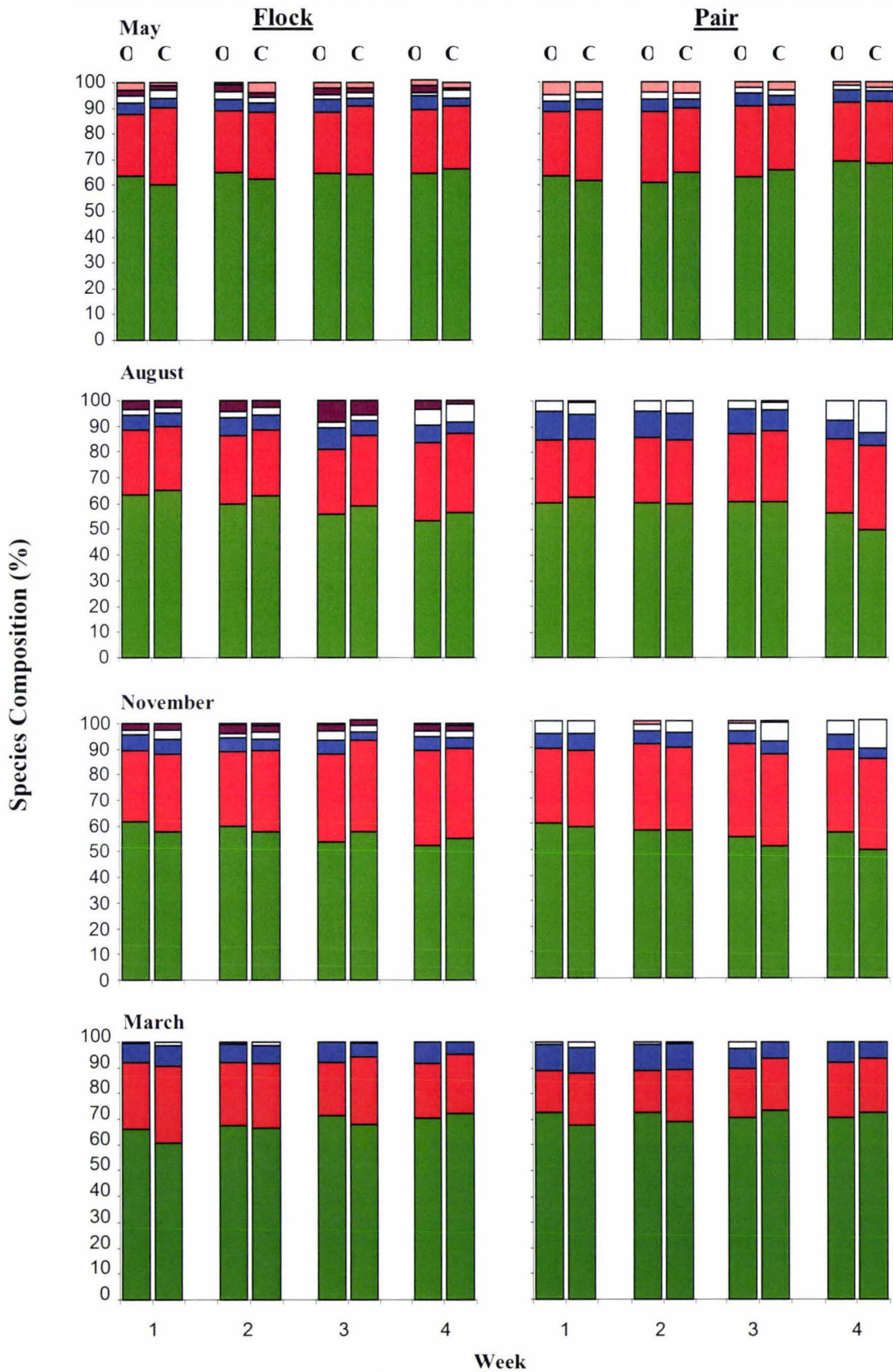


Figure 3.3. Total mean pasture species composition (%) for both closed (C) and open (O) enclosures over a four week growth period in each sampling month for flock and pair treatment types. Where ■ kikuyu, ■ ryegrass, ■ white clover, □ *Plantago* spp., ■ *Ranunculus* spp., ■ other species.

Table 3.7. Three-way analysis of variance (ANOVA) for the effects of flock size (flock or pair sites), season and enclosure type (open or closed) on the pasture composition (%) of ryegrass, for each week of the trial.

Model Factor	Week 1		Week 2		Week 3		Week 4	
	$F_{(6,35)}$	<i>P</i> Value	$F_{(6,35)}$	<i>P</i> Value	$F_{(6,35)}$	<i>P</i> Value	$F_{(6,35)}$	<i>P</i> Value
Flock Size	4.66	0.04	0.91	0.35	0.10	0.75	0.65	0.43
Season	4.62	0.01	18.53	<0.01	23.89	<0.01	25.88	<0.01
Enclosure	2.92	0.10	0.39	0.54	1.35	0.25	0.65	0.43
Flock Size * Season	3.19	0.04	4.62	0.01	1.00	0.41	0.16	0.92
Flock Size * Enclosure	0.49	0.49	0.39	0.54	1.35	0.25	0.92	0.34
Enclosure * Season	1.3	0.29	0.33	0.81	0.61	0.61	0.15	0.93

The change in percentage kikuyu cover over the pasture trials, shows a similar pattern to ryegrass. No significant differences were found for the composition percentage of kikuyu in the pasture plots between weeks, flock size or enclosure types (Table 3.8). However, a significant difference was found between the seasons. March and November had the highest and lowest kikuyu cover in the pasture plots, respectively (Figure 3.3). A significant difference was also found for the flock size * season interaction, showing that kikuyu cover varied differently between the flock sizes in the different seasons. There was, like ryegrass, a smaller seasonal difference in kikuyu cover within the flock site compared to the pair site. No other interactions were significant.

Table 3.8. Repeated measures analysis of variance (Pillai's Trace) for the effects of time, flock size (flock or pair sites), season and enclosure type (open or closed) on the pasture composition (%) of kikuyu.

Model Factor	$F_{(df)}$	<i>P</i> Value
Time (weeks)	0.98 _(3,33)	0.41
Flock Size	0.23 _(3,33)	0.88
Season	2.82 _(3,105)	0.01
Enclosure	1.47 _(3,33)	0.24
Flock Size * Season	2.84 _(3,105)	0.01
Flock Size * Enclosure	1.62 _(3,33)	0.20
Enclosure * Season	0.71 _(3,105)	0.70

When weeks were analysed separately, there were no significant differences found for the kikuyu cover in the pasture between flock sizes or between enclosure types (Table 3.9). However, there was a consistent significant seasonal difference in kikuyu cover and a significant interaction between flock size and season during the first week of the experiment. Once again, March and November were found to have the highest and lowest kikuyu cover in the pasture plots, respectively.

Table 3.9. Three-way analysis of variance (ANOVA) for the effects of flock size (flock or pair sites), season and enclosure type (open or closed) on the pasture composition (%) of kikuyu, for each week of the trial.

Model Factor	Week 1		Week 2		Week 3		Week 4	
	F _(6,35)	P Value	F _(6,35)	P Value	F _(6,35)	P Value	F _(6,35)	P Value
Flock Size	0.93	0.34	0.07	0.79	0.78	0.38	0.07	0.80
Season	7.23	<0.01	30.01	<0.01	44.11	<0.01	39.31	<0.01
Enclosure	3.51	0.07	0.17	0.68	0.34	0.56	0.07	0.80
Flock Size * Season	3.00	0.04	2.18	0.11	1.67	0.19	0.60	0.62
Flock Size * Enclosure	0.39	0.54	0.17	0.68	0.01	0.91	3.54	0.07
Enclosure * Season	2.02	0.13	1.22	0.32	0.69	0.56	0.12	0.95

The largest effects on the pasture species composition from these pasture trials, were found for white clover cover. Significant differences were found for clover cover between the weeks, flock sizes, seasons and enclosure types (Table 3.10). Overall clover cover declined as time progressed and there was less clover cover found in the flock sites and open enclosures compared to the pair sites and closed enclosures, respectively (Figure 3.4). A significant difference was also found between the seasons. May had the lowest clover cover, while August and March had the highest values, with March being slightly higher. A significant difference flock size * season interaction was found, where there was a lesser seasonal difference in clover cover within the flock site compared to the pair site. No interactions flock size * enclosure and enclosure * season were found. Hence the differences found in clover cover between the open and closed enclosures were consistent over the flock sizes and seasons.

Table 3.10. Repeated measures analysis of variance (Pillai's Trace) for the effects of time, flock size (flock or pair sites), season and enclosure type (open or closed) on the pasture composition (%) of clover.

Model Factor	F _(df)	P Value
Time (weeks)	22.87 _(3,33)	<0.01
Flock Size	9.57 _(3,33)	<0.01
Season	2.73 _(3,105)	<0.01
Enclosure	4.06 _(3,33)	0.01
Flock Size * Season	4.72 _(3,105)	<0.01
Flock Size * Enclosure	2.33 _(3,33)	0.09
Enclosure * Season	1.44 _(3,105)	0.18

When looking at each week separately, the effect of the enclosure type on clover cover only becomes significant after week one (Table 3.11). This was not unexpected because, at the start of the trials (week one), plots were chosen with similar species composition. Furthermore, all enclosure type interactions were not significant. Hence, the clover cover in open enclosures were consistent lower than in closed enclosures. There was also a significant difference between the pair and flock treatments where clover cover was lower in the pair site than in the flock site for all weeks, except week four. Likewise, there was a consistent significant difference between seasons for all the weeks. August and March had higher clover cover compared to May and November. Finally, a significant difference was also found for the interaction flock size * season, for all weeks, except week four.

Table 3.11. Three-way analysis of variance (ANOVA) for the effects of flock size (flock or pair sites), season and enclosure type (open or closed) on the pasture composition (%) of clover. for each week of the trial.

Model Factor	Week 1		Week 2		Week 3		Week 4	
	F _(6,35)	P Value	F _(6,35)	P Value	F _(6,35)	P Value	F _(6,35)	P Value
Flock Size	22.97	<0.01	71.37	<0.01	12.17	<0.01	1.53	0.22
Season	39.88	<0.01	97.40	<0.01	56.39	<0.01	17.02	<0.01
Enclosure	0.43	0.51	5.93	0.02	48.68	<0.01	43.97	<0.01
Flock Size * Season	11.05	<0.01	18.12	<0.01	4.15	0.01	0.01	0.99
Flock Size * Enclosure	0.01	0.93	1.66	0.21	2.59	0.12	0.62	0.44
Enclosure * Season	0.72	0.54	1.68	0.19	1.30	0.29	1.99	0.13

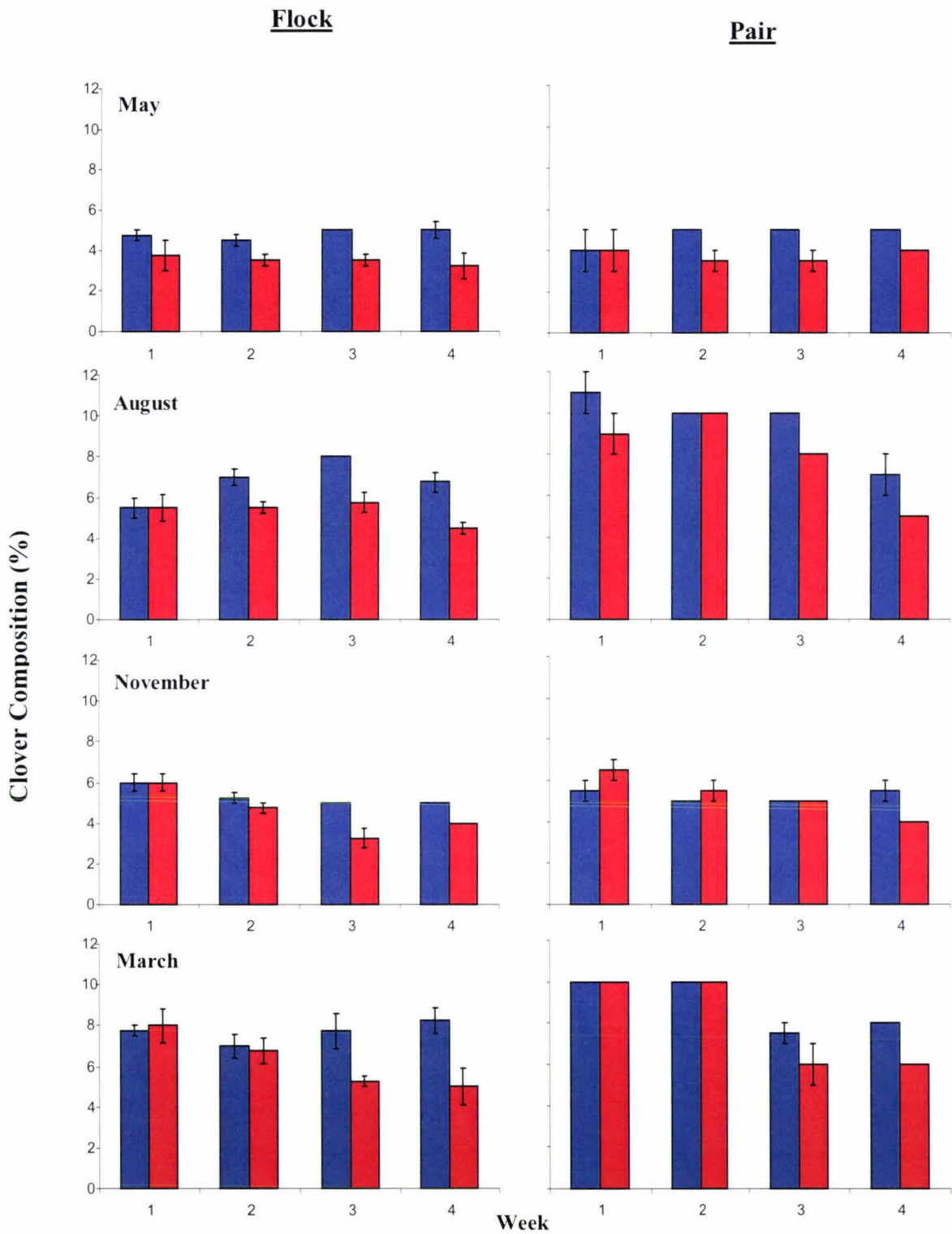


Figure 3.4. Total mean pasture clover composition (%) for both closed (■) and open (■) enclosures over a four week growth period in each sampling month for flock and pair treatment types.

3.5.5 Pasture intake rate

From the 28 paradise necropsies performed in May, a mean of 3.52 ± 0.22 g of dry matter was found inside the oesophagus and gizzard per individual bird (Table 3.12). From the 20 paradise shelduck foraging behaviour observations at Tawharanui Regional Park during August, a mean foraging bout time of 26.33 ± 2.26 min was found. Additionally, a mean time of 12.12 ± 1.77 min was spent foraging during each bout. Consequently, an estimated daily food intake rate of 104.04 ± 15 g/day of dry matter was calculated for paradise shelducks at Tawharanui.

Table 3.12. Mean \pm SE (range) amount of food ingested by paradise shelducks shot in the Auckland Region, mean \pm SE (range) foraging data for paradise shelducks at Tawharanui Regional Park and the estimated daily food intake for paradise shelducks. (n = sample size).

Total dry mass (g)	3.52 ± 0.22 (0.85-5.37)	(n=28)
Foraging bout (min)	26.33 ± 2.26 (12.36-46.11)	(n=20)
Time spent foraging (min)	12.12 ± 1.77 (2.24-35.17)	(n=20)
Food intake (g/h)	17.34	
Daily foraging time (h)*	6	
Daily food intake (g/day)	104.04 ± 15.49	

* Obtained from Williams 1979

3.6 Discussion

3.6.1 Pasture primary production

The response of pasture growth to external factors has been thoroughly investigated. A number of variables are known to affect the rate of pasture primary production, such as: aspect, gradient, altitude, light intensity, temperature, moisture and soil nutrients (Boswell 1977, Langer 1979, Radcliffe 1982, Devkota 2000, Dodd *et al.* 2005, Guevara-Escobar *et al.* 2007). Hence, there are considerable differences in pasture production between seasons as environmental conditions change (Langer 1979, Barker *et al.* 1985, McKenzie *et al.* 2006a). This was shown in the present study where significant differences were found between seasons. Likewise, these environmental variables can cause inconsistencies between plots in pasture trials (Butler 1986). For

this reason, the areas for the pasture trial plots were selected for similar aspect, gradient, and altitude. Additionally, tests were performed to evaluate whether the environmental conditions within the open and closed exclosures were similar, so valid comparisons could be made. Consequently, no significant differences were found for soil nutrients between the two types of exclosures. Also, no significant differences were found for temperature, relative humidity, absolute humidity or dew point. Although, it was found that the closed exclosures had a significantly lower light intensity reading than the open exclosures. It is known that low light intensity or shading severely limits the rate of pasture primary production (Langer 1979, Devkota 2000, Dodd *et al.* 2005, Guevara-Escobar *et al.* 2007). As a result, the lower light intensity in the closed exclosures may have an effect on pasture production within these plots.

Despite this negative impact, the results in this study show that the closed exclosures had consistently, significantly higher primary production compared to the open exclosures. Furthermore, no interactions were found. This indicates that, the differences between the main variables are consistent, and therefore the effects the exclosure types have on pasture production are independent of season. Since, at the start of the pasture trials all plots were mowed to an even height, it was not unexpected that no significant differences were found between the exclosures in the first two weeks. The differences between the two exclosures only became apparent in the last two weeks. Moreover, there was an interaction between exclosure types and flock sizes for week four. This was due to a greater primary production between the open and closed exclosures in the flock site compared to the pair site.

It is assumed that the paradise shelducks are the cause of changes in the pasture resulting from these experiments. This was assumed because the paradise shelducks were clearly the most abundant bird species present, mammalian pests, such as rabbits, are controlled in Tawharanui Regional Park and livestock did not have access to the pasture trial plots. Therefore, these results for the present study imply that the paradise shelducks at Tawharanui Regional Park are having a significant negative impact on the primary production of the pastures. In addition, larger groups of paradise shelducks are having a greater impact compared to smaller groups, such as breeding pairs. This last finding is in contrast to a study by Gillespie (1985). Gillespie (1985) found that the severity of mallard and grey duck (*Anas superciliosa*) damage to pasture and crops in Otago, New Zealand, was not related to the number of ducks present.

3.6.2 Pasture species composition

Various theories have been hypothesised to explain the factors that lead to succession in grass species. These include the light-colonisation competition hypothesis, the nutrient-colonisation competition hypothesis, the nutrient:light ratio hypothesis, the maximal growth rate trade-offs and the herbivore trade-offs (Tilman 1990, Mitchell & Wass 1996). These hypotheses explain the dynamics of ecological succession in pastures and thus may explain the changes of plant species and composition observed from one pasture to the next (López 2000). So ultimately, the composition of pastures is determined by three interrelated factors; competition, stress (light intensity, soil nutrients, moisture) and disturbance (defoliation) (Butler 1986).

As stated in the previous section (3.6.1), environmental conditions were taken into consideration and compared between the two enclosure types. No environmental conditions were significantly different between the enclosures, except for light intensity. This suggests that the light-colonisation hypothesis may play a role in the change of species composition found in this study. It is known that certain grass species perform better than others in shade (Devkota 2000) and thus the light-colonisation competition hypothesis may have affected the species composition between the open and closed enclosures. Nevertheless, it is acknowledged that the intensity of defoliation is a major constraint for plant species (Tilman 1990), and thus the herbivore trade-offs hypothesis is still a relevant hypothesis that may be affecting the species composition in this study.

The herbivore trade-offs hypothesis argues that where defoliation is a major limiting factor, there is a trade-off between susceptibility to defoliation and colonisation rate or between susceptibility to defoliation and the ability to compete for the available resources (López 2000). These trade-offs explain the ecological succession of grass species as grazing intensity varies. Grazing animals can affect pasture attributes such as species composition and dry matter production (Milton *et al.* 1994). Grazers can cause changes either directly by selective grazing or indirectly by non-selective grazing. Selective grazing may affect pasture species composition by causing changes such as a decrease in a selected species and an increase of non-selected species, while non-selective grazing may indirectly control the growth of more competitive grass species (Scofield 1970, Briseño de la Hoz & Wilman 1981).

Generally, as shown by Allen *et al.* (1995) and McKenzie *et al.* (2006b) in New Zealand and South-Western Australia, respectively, the overall species composition in pastures shows considerable change from season-to-season, irrespective of grazing. The findings from this study were in agreement with this statement, as significant seasonal differences in ryegrass, kikuyu and white clover were found. This study found that in some circumstances the flock size effect had an influence on the seasonal changes in species composition. More specifically, it was found that species composition in the pair sites had a higher variation. This may be explained by the fact that there is generally higher variation in species composition between un-grazed plots or plots with low grazer abundance. This may be because grazers are keeping the more competitive species under control, and therefore plots with lower grazer density are under more competitive stress (Allen *et al.* 1995).

I found no significant differences in the composition of ryegrass or kikuyu between the open and closed exclosures. In contrast, the proportion of white clover in the two types of exclosures was significantly different. This difference became increasingly significant over time and was greatest in the final week. As no significant interactions occurred, the effect of exclosure types on white clover cover was consistently independent from the flock size across seasons. This supports the argument of selective grazing by paradise shelducks at Tawharanui Regional Park for white clover. This is consistent with Bisset's (1976) findings, who found that generally 80% or more of the paradise shelduck diet is made up of clover species. Paradise shelduck may be selectively grazing white clover as this species has a high nutrient value, is more digestible and has a shorter digestive time in herbivores than most other pasture species (Brock *et al.* 1989). Although alternatively, the higher pasture growth in the closed exclosures may have caused a difference micro-climate between the two exclosure types, and thus effected the pasture species composition.

It has also been shown that pukeko prefer pastoral communities composed of kikuyu, white clover and perennial ryegrass, and that clover represented 21% of their diet in this environment (Jordan 2005). Pukekos are both competing grazers and denuders of grass species, as the whole plant is pulled out and the roots eaten (Jordan 2005, Wedding 2006). Accordingly it may be argued that pukekos are responsible for the change in composition. Despite this, it is assumed that the paradise shelducks are the major cause of the differences in composition found in the results, rather than other competing

species. This is because paradise shelducks were clearly the most abundant bird species present, and mammalian pests, such as rabbits, are controlled in Tawharanui Regional Park and livestock could not have access to the pasture trial plots.

Perennial ryegrass, kikuyu and white clover mixed pastures are not only the preferred diet of paradise shelducks (Bisset 1976) but are also considered the most important perennial pasture used in livestock agriculture (Jagger *et al.* 2006, McKenzie *et al.* 2006a). White clover especially, is regarded as being very important for New Zealand agricultural industries, as they usually reduce the need for synthetic nitrogen fertiliser and improve forage productivity and quality (Leathers & Costello 1986, Elgersma *et al.* 2000, Laberge *et al.* 2005, Rattray 2005). Consequently, the New Zealand pastoral industries are critically dependent on their clover species (Rattray 2005). In Southland, Eerens and Ryans (2000) showed that farmers could produce 25% more dry matter; 40% more carcass weight and 25% more wool with a white clover mixed pasture. The nitrogen fixation by white clover was equivalent to more than NZ\$300 worth of nitrogen per hectare. Additionally, Caradus and Woodfield (1996) estimated that the annual contribution to New Zealand's economy from white clover through agriculture was NZ\$3.095 billion. What is more, a gain of 1% clover production applied nationally is estimated to be worth up to NZ\$48 million annually (Watson & Mercer 2000). Accordingly, any significant reduction in white clover composition caused by paradise shelducks could have a considerable impact on New Zealand's agricultural industry.

3.6.3 Pasture intake rate

The quantity of food consumed by an animal as a function of food availability is a central process in foraging ecology (Durant *et al.* 2003). However, little is known about the intake rates in grazing waterfowl (Jordan 1953, Durant *et al.* 2003). Generally for grazing waterfowl, resources are spatially concentrated and apparent, and thus it is primarily handling that limits the intake rate (Durant *et al.* 2003). So the daily intake is a product of the hours spent foraging per day and the rate of intake per hour. The results from the present study, estimated the intake rate for paradise shelducks at Tawharanui Regional Park to be 104 ± 15 g/day of pasture dry matter during winter

It has been shown that the food intake of captive waterfowl is more or less directly related to body weight (Jordan 1953), the difference between the food intake rates of

wild species is quite remarkable. Gates *et al.* (2001) found that in Mississippi, a Canada geese population feeding on corn crops, consumed 187-190g/day of dry mass. In contrast, a study by Gloutney *et al.* (2001) found lesser snow geese (*Anser caerulescens caerulescens*) and Ross's geese (*Anser rossii*) in Canada to have intake rates of 9.6 and 12.9g/day of dry mass, respectively. Furthermore, White (1986) estimated that Canada geese in New Zealand had an intake rate of 300-400 g/day of dry matter. These examples demonstrate that there is clear danger in extrapolating the food consumption from one species to another merely on the basis of metabolically adjusted size. Intake rates of waterfowl can not only vary between species but also within species. Variables such as age, sex and reproductive status can affect the metabolic needs of individuals within a population and thus affect individual intake rates (Summers & Grieve 1982, White 1986, Gauthier 1993, McNab 2003). Furthermore, environmental variables like quality of food and temperature will also affect the metabolic needs of a species and hence seasonal changes are expected in the intake rates of individuals (Prop & Vulink 1992, Prop *et al.* 2005). Additionally, since intake measurements are subject to considerable errors and different researchers use different methods, many results are not strictly comparable. Accordingly, studies on intake rates for grazing waterfowl should rather be focused on the individual species or even individual populations and its specific food during a particular season.

The feeding management of livestock in New Zealand varies according to livestock age, sex and state of pregnancy and lactation. But a universal rule can be applied to a given stock unit of one 55kg ewe (*Ovis avries*) which rears one lamb per year. One stock unit requires 1kg/day dry matter for approximately seven months, 1.5 kg/day dry matter during the mating and late pregnancy period for approximately 2 months and 3kg/day dry matter during lambing and weaning for 3 months (Wadams 2007). This gives an average estimate of 1.58kg/day of dry matter for one stock unit for the year. When the intake rate of the paradise shelducks is taken into consideration, a comparison can be made between the paradise shelducks and a stock unit; one stock unit is equivalent to 15.19 paradise shelducks. Paradise shelducks are known to gather in large flocks generally between 50 to 1500 individuals (Williams 1979a), an estimate equivalent to 3.29 to 98.75 stock units respectively. This represents a considerable potential foraging impact on New Zealand agricultural land.

3.7 Conclusion

Since its habitat expansion, due to human modification of land for grazing agriculture in New Zealand, paradise shelducks have established a firm foothold in the agricultural environment. Because of their feeding habits, paradise shelducks compete directly with livestock for pasture, and where numbers are high, paradise shelducks may have a significant negative impact on agricultural practices. Despite this, there have been no studies to date that have tried to quantify and evaluate the effects that paradise shelducks may be having on agricultural pastures.

The results from the present study showed that in addition to seasonal changes in pasture production, there was a significant difference between the open and closed exclosures, especially within the flock site. No significant differences were found for ryegrass or kikuyu cover between the two exclosure types. But a significant difference was found between the two exclosures for white clover cover, where the open exclosures had a lower composition of white clover. However, these differences may be due to the difference in light intensity of the two exclosure types. Significant seasonal changes in the composition of ryegrass, kikuyu and white clover were also established and it was found that there was a higher seasonal variation in the flock sites.

Furthermore, it was estimated that the paradise shelducks at Tawharanui Regional Park had an intake rate of 104 ± 15 g/day of pasture dry matter during winter and from this it was estimated that one stock unit is equivalent to 15.19 paradise shelducks. In Tawharanui Regional Park, where paradise shelducks duck numbers range from 45-79, the ducks are displacing an estimated 2.96-5.20 stock units.

During this experiment the paradise shelduck numbers in the flock site were constantly changing, this may have caused inconsistent results during the pasture trials. Additionally, pasture growth is spatially variable, and although this experiment included multiple trials to try overcome this, errors still may have occurred. Furthermore, the different pasture growth rates found between the open and closed exclosures may have caused differences in their micro-climates. Thus differences in pasture composition and subsequent growth rates may be due to differences in micro-climates. As a result the information obtained by the exclusion experiments in this study are not definitive, and additional trials over a longer period are needed to gain a better understanding of the impacts paradise shelducks may have on pasture production and management.

Comparisons between trials are very difficult because of the diverse range of environments, management and measurement techniques. Consequently, the effects that the paradise shelduck are having on the agricultural pasture in Tawharanui Regional Park may not be the same in other agricultural settings where environment conditions, such as pasture composition, are different. Furthermore, the daily intake for paradise shelducks obtained in this study may not be an accurate estimate, as the foraging behaviour and necropsy data were obtained at different times of the year. Thus, the paradise shelducks may have had different metabolic needs at these times and consequently the data for foraging times and dry mass ingested may not be directly related.

In conclusion, this study illustrates that paradise shelducks can have a significant negative impact on pasture production and seem to selectively graze white clover. This as a result can affect pasture management and consequently livestock carrying capacity and production.

3.8 References

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CHAPTER 4: General Conclusion



Plate 4.1. Photo by M. Delaney 2006.

Paradise shelducks (*Tadorna variegata*) are one of the few New Zealand endemic species that have benefited by the major landscape modifications associated with humans. Due to their expansive range, abundance and association with farm land, the main aim for this study was to determine whether farmers should view the paradise shelduck as an agricultural pest and if so to what degree. To assess this aim, the study was divided into two sections; micro-organisms of paradise shelduck faeces and their effects on an agricultural environment (Chapter 2), and the effects of paradise shelducks on pastoral communities (Chapter 3). Although Chapters 2 and 3 in this thesis include an independent discussion of the results, it was considered appropriate to reconsider the relative importance of each component of the study.

The objective to assess the extent to which paradise shelducks are acting as reservoirs for pathogenic micro-organisms and explore the possibility of cross-transmission of pathogenic micro-organisms to humans or livestock was met using faecal sample surveys. No isolates of *Salmonella*, *Campylobacter*, *Yersinia*, *Cryptosporidium* or *Giardia* were found at Tawharanui Regional Park. Relatively low prevalences of non haemolytic and alpha haemolytic *Streptococci*, *Enterococcus*, *Bacillus*, *Clostridium perfringens*, *Proteus mirabilis*, strongyle eggs and *Coccidia* eggs were found. Additionally, *E. coli* was consistently isolated from the faecal samples, with some high prevalences isolated in November and March. Although a similar array of micro-organisms were found in pukeko (*Porphyrio melantus*) and house sparrows (*Passer domesticus*) as well as high contamination levels of faecal indicators in troughs, no conclusive transmission routes for the micro-organisms were found. Furthermore, no significant correlations were found between the number of accumulated faeces sampled and the presence or prevalences of the micro-organisms isolated. It also appears that sampling during the driest times of the year will yield the highest presence of micro-organisms in paradise shelduck faeces.

The results show, that paradise shelducks at Tawharanui Regional Park may be acting as reservoirs for pathogenic micro-organisms isolated in this study. Thus, by contaminating the environment with pathogenic micro-organisms which could lead to possible cross-transmission, paradise shelducks potentially pose a threat to livestock, agricultural practices and human health. Similarly, in a review, Clark (2003) illustrates that geese, such as Canada geese (*Branta canadensis*) and other waterfowl have the potential to act as reservoirs and carriers of agricultural diseases. However, the

serotypes of the micro-organisms isolated the present were not determined, so no conclusions could be drawn in relation to their pathogenicity. Furthermore, apart from *E. coli*, the low prevalences of the micro-organisms isolated suggest that this population would need a continual reinfection from environmental sources to maintain these micro-organisms in their enteric flora. Although, the low prevalence of pathogenic organisms found, could be an underestimate of the true prevalence, as a result of intermittent shedding or latent carriage of pathogens could explain the low rate of isolation of these micro-organisms in this study. However, this seems unlikely considering the consistently low numbers of isolates recovered throughout the sampling period and the prevalence of the micro-organisms in the environment.

It must be noted that the results from this study are not a definitive representation of pathogenic micro-organisms found in paradise shelduck faeces. Bacteria and intestinal parasites found in faeces may not only vary between populations but also within a population over time. This may be a result of changes in climate, habitat, host immunity or pathogen evolution. Accordingly, it can not be assumed that other populations of paradise shelducks are infected with similar micro-organisms to those found in this study. Additional research is needed to provide a comprehensive micro-organism profile for paradise shelducks. Furthermore, the complexity of studying the possible cross-transmission of pathogenic micro-organisms and their transmission routes has been highlighted in this study. This partially explains why questions with regard to some pathogenic micro-organisms have as yet been unanswered despite the wealth of literature already available on the subject. Retrospective and experimental investigations are an important supplement to disease investigation. It is clear from this study that more information on specific potential host species, with regard to susceptibility to the disease, challenge dose required, faecal shedding following infection and the population biology of each species is needed, before a full understanding of the pathogenic micro-organisms in an agricultural environment is possible.

Evaluation of the level of impact paradise shelducks have on pastoral communities, and whether this impact could have negative consequences on agricultural practices in New Zealand was achieved through exclusion experimentation. Two types of enclosure were set up in Tawharanui Regional Park; a 'closed' enclosure to exclude all animals including paradise shelducks, and an 'open' enclosure to exclude livestock, but allow access for paradise shelducks. The results of this aspect of the study show that the

closed enclosures had significantly higher primary production than the open enclosures. Furthermore, no significant interactions were found between the enclosure type and season, indicating that the enclosure effects were independent from the seasonal effects. Similarly, in an exclusion experiment Olofsson *et al.* (2007) found that excluding rabbits (*Oryctolagus cuniculus*) from grasslands decreased primary production in the short term but increased primary production in the long term. Cargill and Jefferies (1984) found by way of an exclusion experiment that lesser snow geese (*Anser caerulescens caerulescens*) consumed approximately 80% of primary production on sub-arctic salt marshes.

Additionally, in the present study, the open enclosures had a lower white clover composition compared to the closed enclosures. Once again no significant interactions occurred, which indicates that the effect of enclosure types on clover cover was independent from the flock size and seasonal variation. Conversely, through the exclusion of sheep (*Ovis aries*) and rabbits from grassland plots in Central Otago, Allen *et al.* (1995) found that grazers caused a decrease in ryegrass frequency. The results from the present study imply that paradise shelducks can have a significant negative impact on pasture production and seem to selectively graze white clover (*Trifolium repens*). This can affect pasture management and consequently livestock production.

However, differences in light intensity found between the two enclosure types may have had an effect on the pasture species composition. Furthermore, the higher pasture growth found in the closed enclosures may have created a different micro-climate within the enclosure compared to the open enclosures. Thus differences in pasture composition and subsequent growth rates may be due to differences in micro-climates. As a result the information obtained by the exclusion experiments in this study are not irrefutable and additional trials over a longer period are needed to gain a better understanding of the impacts paradise shelducks may have on pastoral communities. Additionally, the effects that the paradise shelduck are having on the agricultural pasture in Tawharanui Regional Park may not be the same in other agricultural settings where environmental conditions, such as pasture composition or stocking levels, may be different.

In conclusion, the paradise shelducks at Tawharanui Regional Park do harbour some potentially pathogenic micro-organisms, and through intensive grazing, have a negative impact on pasture growth, especially white clover. Thus, this population can be viewed

as having an impact on an agricultural environment. Although, since the Tawharanui population is relatively small, a significant impact may only become apparent when paradise shelduck densities are high. However, these results may not necessarily be generalisable to other populations. Paradise shelduck numbers will continue to increase primarily because of continued enhancement of the habitat for paradise shelducks, such as land clearance, farmers improving pastures, and wetland restoration. As a result, any negative impact paradise shelducks have on agricultural practices will also increase.

More studies on paradise shelduck populations are needed to increase the understanding of their impact on agricultural practices in New Zealand. A survey of faecal micro-organisms across New Zealand over summer will provide a baseline for pathogenic micro-organisms for paradise shelducks. In addition, serotypes of micro-organisms need to be determined to establish the pathogenicity of micro-organisms associated with paradise shelducks. Furthermore, when out-breaks occur in livestock, micro-organism surveys of paradise shelducks, sympatric species and the environment, will assist to ascertain the most likely transmission routes for pathogenic organisms. Research into the survival rates of micro-organisms in faeces will also help to assess the extent to which paradise shelducks act as reservoirs. Further exclusion trials in different habitats, pastoral communities, and environmental conditions are also needed to investigate the full extent paradise shelducks are having on pastoral communities. This additional research will aid wildlife managers and farmers to better manage paradise shelduck populations and reduce the severity of pasture defoliation and the spread of pathogenic organisms.

4.1 References

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Appendix I:

Antimicrobial susceptibilities for selected bacteria isolated from paradise shelduck faeces

	No. Resistant (%)				
	<i>E. coli</i> (21)*	Non haemolytic <i>Streptococci</i> (7)*	Alpha haemolytic <i>Streptococci</i> (8)*	<i>Proteus</i> <i>mirabilis</i> (10)*	<i>Bacillus</i> spp. (12)*
Ampicillin	—	—	—	—	—
Amox	—	—	—	—	—
Amikacin	4.76	—	100	—	—
Clindamycin	100	95.24	100	100	—
Enrofloxacin	—	—	—	—	—
Trimethoprim/ Sulphamethoxazole	—	—	100	—	—
Tetracycline	—	—	—	100	—

* Number of isolates found in 24 paradise shelduck faecal samples

Search Results Summary by Case and Specimen ID

16/07/2007

Search Criteria: Taxa/Common Name: *Tadorna variegata* (Species)/Paradise Shelduck

Appendix II

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Appendix II:
Huia database paradise shelduck records

Case/Spec. ID	Common Name	Animal Name	Sex	Submitter Name/Organisation	Lab Name	Lab Case ID	Diagnosis
Date Subm.	Taxonomic Name	Animal ID	Age	Presenting Syndrome	Pathologists		
382/ 1	Paradise Shelduck		Male	F Hickford, Veterinary Clinical Sciences, Massey University	Massey University	27533	1 Neuropathy - Degenerative ?trauma
23/12/1996	<i>Tadorna variegata</i>		Adult		Maurice Alley, Caroline Twentyman		
546/ 1	Paradise Shelduck		Male	Wayne Boardman, Auckland Zoo	Massey University	29216	1 Fracture - Femur
28/05/1998	<i>Tadorna variegata</i>		Adult		John Lumsden		2. Emaciation
658/ 1	Paradise Shelduck			Wayne Boardman, Auckland Zoo	Lynfield Animal Health Laboratory	90389480	1. Nephritis - Chronic Granulomatous
	<i>Tadorna variegata</i>				Keith McSparran		2. Cholangio-hepatitis
1374/ 1	Paradise Shelduck		Female	Richard Norman, Pathobiology	Massey University	32699	1. Trauma - Head and Neck
	<i>Tadorna variegata</i>		Adult		Richard Norman		
2288/ 1	Paradise Shelduck		Male		Alpha Scientific Laboratory	AU0300671	1 Unknown Cause of Death
	<i>Tadorna variegata</i>	A20168	Juvenile		Keith Mcsparran		2. Enteritis - Acute, Mild
2289/ 1	Paradise Shelduck		Female	. Auckland Zoo	Alpha Scientific Laboratory	A0208158	1. Aspergillosis - Respiratory
	<i>Tadorna variegata</i>	100335	Adult				2. Hepatic Necrosis -focal
2290/ 1	Paradise Shelduck		Male	. Auckland Zoo			1. Cardiac Arrest Under
	<i>Tadorna variegata</i>	640193					Anaesthetic
2980/ 1	Paradise Shelduck		Male	David Wilson, Department of Conservation	Massey University	36881	2. Fractured Tibiotarsus 1. Toxicity of Unknown Cause
12/02/2005	<i>Tadorna variegata</i>		Adult		Maurice Alley		
3513/ 1	Paradise Shelduck			Kevin Turner, Lynfield Veterinary	Massey University	38326	1. Poxvirus
23/03/2006	<i>Tadorna variegata</i>				Brett Gartrell		2. Aspergillosis
3687/ 1	Paradise Shelduck			Dianne Brunton, Massey University	Massey University	39241	1. Early Embryonic Death
13/09/2006	<i>Tadorna variegata</i>	A (1)	Egg		Maurice Alley		
3687/ 2	Paradise Shelduck			Dianne Brunton, Massey University	Massey University	39241	1. Infertile Egg
13/09/2006	<i>Tadorna variegata</i>	B (2)	Egg		Maurice Alley		
3687/ 3	Paradise Shelduck			Dianne Brunton, Massey University	Massey University	39241	1. Infertile Egg
13/09/2006	<i>Tadorna variegata</i>	C(3)	Egg		Maurice Alley		
3687/ 4	Paradise Shelduck			Dianne Brunton, Massey University	Massey University	39241	1. Infertile Egg
13/09/2006	<i>Tadorna variegata</i>	D(4)	Egg		Maurice Alley		
3687/ 5	Paradise Shelduck			Dianne Brunton, Massey University	Massey University	39241	1. Late Embryonic Death
3/09/2006	<i>Tadorna variegata</i>	E(7)	Egg		Maurice Alley		

Appendix III:

Huia database case 2288 record

Alpha Scientific Laboratory

PATHOLOGY REPORT

Status Pending
Date: 16/06/2003
Type: Mortality

Lab. Case/Spec ID: **AU0300671**
 Submitter's Ref: A20168
 Date Submitted:
 Date Received: 10/06/2003
 Previous Case ID:
 WMD Case/Spec 2288/1

Animal ID: 20168
Animal Name:
Species: *Tadorna variegata*
Common Name: Paradise Shelduck
Sex Class: Male
Age Class: Juvenile
Date Died: 10/06/2003

Number Dead: 1
 Number at Risk:
 Number Sick:
 Number 1

Growth and Development

Parameter	Result Description	Value	Date Measured
Age Group			
Weight		1.622 kg	10/06/2003
Juvenile			

ANIMAL HISTORY

Found semicomatose in pond yesterday afternoon. Treated with Amoxycillin, hospitalised, died

GROSS PATHOLOGY

External - normal
 Body cavity - normal
 Digestive system - no food in proventriculus, otherwise normal
 Respiratory system - normal
 Cardiovascular system - enlarged lymphnodes in chest. Otherwise normal

Gross diagnosis - septicaemia?

HISTOPATHOLOGY

Intestine - focal diffuse, moderately cellular infiltrates of heterophils, lymphocytes and plasma cells in the lamina propria, with small numbers of inflammatory cells in the crypts.
 Liver, heart, lung, kidney, proventriculus - unremarkable.

DIAGNOSIS

1. Unknown Cause of Death 2. Enteritis - Acute, Mild

COMMENTS

The cause of death is not established. The enteritis is unlikely to explain the death.

Pathologist: Keith Mcsporrnan

Appendix IV:

Fish & Game permit to undertake colour banding, blood letting and Radio tracking



Ref:8/1/6

12 October 2005

Mark Delaney
C/- Prof. Dianne Brunton
INR Massey University
Oteharehe
Campus Building 5
Albany
AUCKLAND

Permit to Undertake Colour Banding/Blood Letting and Radio Tracking on Paradise Shelduck

Dear Mark

Further to your email of 11 October 2005 please accept this letter as authority to undertake the above on paradise shelduck at the Te Wharanui Reserve at Warkworth.

When your study is completed we would very much appreciate a copy of such.

Yours faithfully

A handwritten signature in blue ink, appearing to read "D.C. Emmett".

D.C. Emmett
Manager.

Statutory managers of freshwater sports fish, game birds and their habitats

Auckland/Waikato Region

Brymer Rd, RD9, Hamilton, New Zealand. Telephone (07) 849 1666 Facsimile (07) 849 1648

Appendix V:

Auckland Regional Council permit to undertake research on paradise shelducks at Tawharanui Regional Park

Whakatapea te kō, kiā kotahi

We're in it together



27 June 2005

Mark Delaney,
[REDACTED]

Yaldene House, 21 Pitt Street
Private Bag 97 017, Auckland
New Zealand
BX CP 25 005, P.O. Box
Telephone +64 9 504 7000
Facsimile +64 9 506 7188
www.arc.govt.nz

Dear Mark,

Permit to undertake research on paradise shelducks at Tawharanui Regional Park

Thank you for the outline of your research on "Investigating the mating system, genetic and population dynamics of the paradise shelduck" to be supervised by Dianne Brunton of Massey University, Albany. Your application to conduct research activities in the Auckland Regional Council Parks network has been accepted subject to the following conditions:

1. Before visiting Tawharanui, please contact the Northern Parks Administrator, Sue Hill at Wenderholm phone (09) 426 1200, fax (09) 426 3358 or email sue.hill@arc.govt.nz. Please let the Administrator know when you plan to visit Tawharanui to do the work.
2. Please also contact the Duty Ranger via the Administrator prior to arrival and arrange a time on your first day of operation to discuss any operational and/or site-specific health and/or safety issues.
 - a. You must follow the instructions of the Duty Ranger regarding park-specific hazards.
 - b. The Duty Ranger will also instruct you to sign-in and out either on the whiteboard or by phone.
 - c. Attached is the Auckland Regional Council Health & Safety Policy. Please read and discuss with the Duty Ranger.
3. Placement of any equipment on the park must be approved by the Duty Ranger, must be placed well out of view from public walking tracks and recreation areas, will be left at your own risk and must be removed at the end of the project.
4. The research shall not unduly affect the natural character, historic, archaeological, scenic, biological or farming operations on the park and shall not interfere with public access and enjoyment of the park.