REVIEW

Conservation translocations of fauna in Aotearoa New Zealand: a review

Kevin A. Parker[1*], John G. Ewen[2], Emily L. Weiser[3], Aisling Rayne[4], Tammy Steeves[4], Philip J. Seddon[3], John Innes[5], Lynn Adams[6], Natalie Forsdick[5], Matt Maitland[7], Troy Makan[6], Denise Martini[3], Elizabeth Parlato[8], Kate Richardson[9], Zoe Stone[8], Doug P. Armstrong[8]

[1]Parker Conservation Ltd, 549 Rocks Road, Nelson 7011, New Zealand
[2]Institute of Zoology, Zoological Society of London, Regent's Park, London, UK
[3]University of Otago, PO Box 56, Dunedin 9054, New Zealand
[4]University of Canterbury, Private Bag 4800, Christchurch 8140, New Zealand
[5]Manaaki Whenua-Landcare Research, Private Bag 3127, Hamilton 3240, New Zealand
[6]Department of Conservation, PO Box 10420, Wellington 6243, New Zealand
[7]Auckland Council, Private Bag 92300, Victoria Street West, Auckland, New Zealand
[8]Massey University, Private Bag 11222, Palmerston North 4442, New Zealand
[9]Waikato Regional Council, Private Bag 3038, Waikato Mail Centre, Hamilton 3240, New Zealand

*Author for correspondence (Email: k.parker@parkerconservation.co.nz)

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Abstract

There have been extensive declines and extinctions of native fauna in Aotearoa New Zealand since human settlement. Against this background of loss there have been remarkable advances in conservation management, particularly in the large-scale eradication and control of exotic mammalian pests. Pest control creates opportunities to return animals to former habitats via conservation translocations, an important tool for conservation management. Here, we review conservation translocations in Aotearoa. Our review draws together knowledge from Aotearoa's rich history of fauna translocations, outlines a decision-making framework to better support translocations, and highlights emerging tools and key knowledge gaps. A successful translocation always results in the establishment of a population, but establishment can be measured in many ways. We recommend measuring translocation success by defining a clear set of a priori fundamental objectives. If translocation objectives are clearly defined all subsequent decisions about factors that influence conservation translocation outcomes, including the cultural and social context, habitat quality, especially vegetation associations, pest densities and dispersal opportunities, and genetic management, will be easier. Therefore, we encourage careful thinking in formulating conservation translocation objectives. We discourage a focus on any single element of planning and rather encourage all people involved in translocations, particularly decision makers, to explicitly recognise the multiple values-based objectives associated with translocations.

Keywords: Conservation translocation, reintroduction, restoration

Introduction

There have been extensive declines and extinctions of native fauna in Aotearoa New Zealand (Aotearoa hereafter) following two waves of human settlement (Caughley 1989; Holdaway 1989). For example c. 50% of all native bird and frog species have become extinct since first human contact (Caughley 1989; Holdaway 1989), and the remaining species show varying levels of vulnerability to exotic pests (Innes et al. 2010). This history of extinction and drastic reduction in population size and range is neatly captured in Māori whakataukī (proverbs) including "*Ko te huna i te moa- destroyed like the moa*", (Wehi et al. 2018) or by Diamond (1984) who stated that "*New Zealand doesn't have an avifauna, just the wreckage of one*".

Against this background of loss there have been remarkable advances in conservation management, particularly in large-scale pest eradication and control (pest, as used here, primarily refers to exotic mammalian predators and competitors but also includes other unwanted harmful vertebrates, invertebrates, plants and pathogens). Multi-species eradications have been completed on several large islands (Towns & Broome 2003). Many fenced mainland sanctuaries offer island-like conditions on the mainland in that they are often isolated from other indigenous habitats and most significant pests are absent most of the time (Innes et al. 2019). The number of unfenced mainland sites under varying forms of protection is also increasing every year (Innes et al. 2019). There was considerable excitement - and scepticism - around the New Zealand Government's 2016 announcement of Predator Free 2050. Regardless of whether this is an achievable goal it is likely to lead to an increase in control of some pests (especially rats (*Rattus* spp.), stoats (*Mustela erminea*) and possums (*Trichosurus vulpecula*)) and a pest landscape ranging from areas with complete eradication/zero density through to areas with lower density pest levels than are currently present. Surprisingly, there has been little detail about what a predator-free Aotearoa might look like, but implicit is the goal of exchanging pest biomass for native and endemic biomass. Conservation translocations, the intentional movement of animals from one place to another for a conservation benefit (referred to as "translocations" hereafter), are an important tool for achieving this goal.

We are very good at doing translocations to islands. However, we are also making gains, at least for some forest birds, close to many urban areas, where growing community conservation initiatives have established mainland ecological restoration projects involving varying levels of pest control, planting, and translocations. Many such projects have been successful in achieving high-density populations of native wildlife, again with an emphasis on forest birds. A critical limitation is that most of these restored sites are small (c.100-1000ha), and mice (*Mus musculus*) have rarely been eradicated, or even sufficiently controlled, with important implications for the recovery of endemic lizards, amphibians, invertebrates, bats, and threatened plants. In contrast, the bulk of our biodiversity is contained within vast areas (1000s of hectares) of back country conservation estate which are much harder to protect and harder for the public to engage with. The Department of Conservation (DOC) "Tiakina Ngā Manu/Battle for our Birds" programme is achieving impressive pest control over huge areas of Aotearoa forests (c. 500 000 ha in 2022), operating in parallel with species-focussed mainland recovery programmes (e.g. kakī/black stilt (*Himantopus novaezelandiae*) and kākāriki karaka/ orange-fronted parakeet (*Cyanoramphus malherbi*)). Nevertheless, vast tracts of land, especially non-forested habitats, remain unprotected, and biodiversity continues to decline. This is reflected in the NZ threat classification for birds (Robertson et al. 2017, 2021) that has seen some species previously ranked "non-threatened" move to "at risk, declining", including North Island (NI) and South Island (SI) toutouwai/robins (*Petroica longipes* and *P. australis*), and NI and SI mātātā/fernbirds (*Bowdleria punctata vealeae* and *B.p. punctata*).

The current situation on mainland Aotearoa is neatly captured by Caughley's (1994) small population and declining population paradigms. Our small protected populations, which by definition includes all translocated populations, are subject to the many risks of being small, for example pest incursions, dispersal, extreme weather events, novel pathogens, and loss of genetic diversity. In contrast, many of our large mainland populations are declining because of the pervasive impacts of pests. The ongoing tension in Aotearoa conservation management is in deciding how to allocate resources to maintain small populations, because this seems generally easier and currently achievable, while also securing the large mainland areas that contain the bulk of our biodiversity, a much harder challenge largely reliant on the continued use of aerially applied toxins. Both approaches are necessary.

Small intensively protected populations provide insurance against further declines, and can serve as source populations for colonisation of, or translocation to, pest free habitats when these become available. The sites such populations occupy also provide a glimpse of what a predator-free Aotearoa might look like, and thus are critical tools for engaging the general public in conservation management (Parker 2008). In contrast, ongoing pest control in large mainland areas is essential for protecting biodiversity not able to be protected on islands, or in small intensively protected areas. When these large mainland areas are released from the pervasive effects of pests (primarily a question of social license and technical advance) they will further buffer threatened species against the challenges of being constrained in small populations.

In this paper we focus on small population management in Aotearoa, specifically translocated populations that have been established following local extinction. Conservation translocations are not easy and many fail (Miskelly & Powlesland 2013) urging the Parliamentary Commissioner for the Environment (PCE) to state that there is "*An urgent need for translocation policy based on clear principles*" (Parliamentary Commissioner for the Environment 2017). This is an odd statement because our collective experience across many translocations is that they are guided by very clear principles. Furthermore, the DOC translocation proposal document captures many of the principles of sound translocation practice, including those described in the IUCN "*Guidelines for reintroductions and other conservation translocations*" (IUCN 2013). However, the PCE is correct in that these principles are not currently captured in DOC policy, which sometimes compromises the ability of DOC to assess and approve translocation proposals. This is important, especially as we move beyond translocations to typical sites (islands and relatively small protected mainland areas), towards release sites with much more uncertainty, e.g. very large areas (1000s of hectares) of contiguous habitat, and urban (van Heezik & Seddon 2018) and rural landscapes.

Here, we review conservation translocations of fauna in Aotearoa. We are especially interested in "successful" translocations which we define as those that meet a clear set of measurable a priori fundamental objectives (see Box 1 and Ewen et al. 2014). For the authors, our fundamental objectives typically include the creation of large populations (100s-1000s of individuals) with a high probability of persisting in the long term (100s of years). The distinction between reaching a long-term state of persistence versus any single point in time at which success is measured is important: see Seddon (1999) and Armstrong & Seddon (2008). Achieving this objective requires critical, careful, and measurable evaluation of all factors that might contribute to translocation success, and an understanding of the species-specific time scales over which such factors might act, rather than focussing on single factors and arbitrary timeframes. We also note the increasing demand for translocations and that some might proceed with quite different objectives to those posited above, especially where there is a high level of uncertainty about translocation of a particular species and/or a particular release site. However, a translocation cannot be considered successful if a population fails to establish, even though uncertainty means that this sometimes happens, and that failures are informative for future efforts to establish populations.

This review draws together knowledge that has been gained from Aotearoa's rich history of fauna translocations and outlines a framework for translocation decision-making. First, we discuss the need to set clearly defined objectives for each translocation, to measure outcomes against those objectives, and to test our predictions that our management actions will achieve these objectives (Box 1 and Figure 1). Objectives are always value based so the critical question is what problem are we trying to resolve through translocation and what are the underlying cultural, social, political and management values? We then address 1) the extirpation and management history of the translocation candidate species (e.g. what has been the outcome of previous translocations of the species to the chosen release site and/or to similar release sites?), and 2) the biological and physical aspects of the release site, i.e. habitat, and its ability to support the translocated species, including pests and dispersal opportunities. This is followed by a discussion about 3) suitable source populations and how they can be matched to release sites, including issues around health screening, founder size, population growth, and whether ongoing post-release management, including genetic management, is required or even feasible. Finally, 4) we briefly discuss the future of translocations in Aotearoa. The framework we describe can be applied to most fauna but the examples we use are mainly drawn from translocations of birds, simply because they are numerically dominant in fauna translocations in Aotearoa (Miskelly & Powlesland 2013). However, even for bird translocations significant information gaps exist, although these are smaller than those for bat, lizard, amphibian and invertebrate translocations.

The cultural and social setting of translocations

Translocations are most frequently conducted on public land administered by national or local government and they usually involve the use of at least some public money. Accountability for the appropriate management of translocated species is also vested in government, i.e. DOC, which is in turn bound by a commitment to Te Tiriti o Waitangi/The Treaty of Waitangi. Therefore, there is a legal requirement to consult with Treaty Partners about the translocation, including ongoing management of the source population, the translocated population, and the release site. However, this obligation is not purely economic and legal because Treaty Partners, and often other stakeholders, have deeper connections to, and interests in, the source population, the translocated species, and the release site (Bioethics Panel 2019). Therefore, a translocation is usually more than just an opportunity to establish a new population as it includes broader cultural and societal desires, aspirations and objectives (Parker 2008).

The objectives of any particular translocation often seem obvious to the project instigators, managers and decision makers but they might overlook key fundamental objectives of Treaty Partners and other stakeholders. For example, a manager trained in modern science might see a translocation as an opportunity to restore a component of an ecosystem. In contrast, a Treaty Partner might see it as an expression of kaitiakitanga (guardianship) and the restoration of mauri (not easily defined but often translated as life essence), whereas a community conservation group or private landowner might simply want a particular species living in their area. These objectives might seem similar but this should not be assumed, nor will they necessarily be measured in the same way. Furthermore, a review by Ewen et al (2014) showed that the setting, reporting and, critically, the measurement of objectives is highly variable among reintroduction programmes, most of which are rooted in modern science. Fundamental objectives are often mixed with means objectives, not measured in an appropriate way, nor even explicitly stated (Ewen et al. 2014). For example, what does predator-free NZ really mean? Is this all that we want? Predator Free NZ (www.predatorfreenz.org) think not but rather see it as a means to something much more ambitious, i.e. a landscape dominated by native biodiversity.

However, in many cases native species will not just reappear if we remove pests from the Aotearoa NZ landscape so translocation will be necessary

Ideally, all stakeholders should be directly involved in setting fundamental and means objectives for every translocation, and then deciding between management alternatives as to how we might achieve them. For example, translocation planning for pekapeka or short tailed bats (*Mystacina tuberculata*) was initiated at Te Kiri marae (meeting house) alongside Ngāti Manuhiri who led the kōrero (discussion) on a mātauranga (knowledge, wisdom) Māori fundamental objective for assessing translocation options (McMurdo Hamilton et al 2021). Similarly, iwi to iwi consultation is often preferable at first request to harvest a population for translocation. Therefore, Ngāti Kuta and Ngāti Patukeha led kōrero with Ngāti Rereahu when requesting pitoitoi/NI toutouwai for translocation from Pureora to Ipipiri/Bay of Islands. Kaimahi (workers) from both iwi were also involved in the capture of translocated animals, thereby gaining new skills.

Ultimately, meaningful engagement, consultation and decision sharing with Treaty Partners, and other stakeholders, provides a means to deepen support, interest, and engagement in conservation. This is particularly important where translocated species might disperse from the release site into the surrounding area (e.g. NI kākā (*Nestor meridionalis*) in Wellington are damaging fruit trees and ornamental plantings), or if site management can impact local communities (e.g. cat control). However, resourcing for genuine consultation is challenging because it takes time and energy for hui (meetings) and site visits. Where translocations are initiated by DOC they might cover this cost. But translocations initiated outside of DOC often result in poorly resourced community conservation groups asking poorly resourced Treaty Partners for time and energy. It is difficult to know how to resolve this, other than increasing funding bids to cover all translocation costs, although it could equally be argued that these groups are contributing to Predator Free 2050 aspirations and might therefore qualify for government assistance.

Setting objectives

Ewen et al (2014) characterised a conservation translocation as a sequence of decisions, and argued that poor planning, implementation, and monitoring is a consequence of not approaching the decision-making process in a deliberate and rational manner. They, along with several other authors, advocate a more structured approach to decision making (Maguire 1986; McCarthy et al. 2012; Converse et al. 2014; Ewen et al. 2014). Structured decision making is an iterative process whereby uncertainty is addressed by 1) defining clear objectives and how they will be measured; 2) identifying a range of possible management alternatives; 3) predicting the outcomes of the chosen management alternatives relative to the stated objectives; 4) evaluating trade-offs and uncertainty; 5) implementing the optimal management alternative and monitoring its results (Figure 1) (Gregory et al. 2012; Ewen et al. 2014). This approach to decision making has been characterised as "*a formalisation of common sense for decision problems which are too complex for informal use of common sense*" (Keeny 1982).

An obvious starting point for setting objectives and informative performance measures is by understanding the extirpation history and the outcomes of previous translocations of the candidate species. As an example, NI toutouwai have persisted on the mainland at sites with no predator management whereas NI tīeke have been extinct on the mainland for >120 years. These two species clearly have very different levels of vulnerability to pests and will require different performance measures for pest control (a means objective) even though the fundamental objective (establishment and persistence of a translocated population) remains the same.

However, we note that it can be extremely difficult to determine why a translocation failed. One way is to model vital rates from another species to model the focal species vulnerability to pests. For example Parlato and Armstrong (2018) used NI toutouwai data to predict rat tracking indices that might correlate with NI tīeke translocation success. Alternatively, factors other than pests might lead to translocation failure. For instance, of nine korimako/bellbird (*Anthornis melanura*) translocations (Miskelly & Powlesland 2013) only one (to Mana Island) appears to have been successful. While several factors might have contributed to these failures it is unequivocal that dispersal from the release site has been a critical factor, even at sites where some breeding occurs (for example, Zealandia). Given such low success it is questionable whether any further translocations of korimako are justified, especially given their ability to naturally recolonise protected sites (Brunton et al. 2008), unless there is a significant change in methods or understanding. Clearly, if a species has rarely or never been translocated then the outcomes of previous translocations are not useful indicators of future outcomes. In these cases, the translocation of other species, along with the ecology and conservation history of the candidate species, will have to be assessed against extirpation history, vulnerability to pests, dispersal abilities and other habitat requirements. However, there will naturally be a higher degree of uncertainty regarding establishment and persistence of the translocated population.

The release site

Conservation translocations are typically, but not always, carried out within the former range of a species, i.e. reintroductions (IUCN 2013), following local extirpation and where natural recolonisation is unlikely on a time scale acceptable to site managers. Clearly, the conditions that we predict animals need to persist must be present in the release area, although these might also be provided through supportive management, for example supplementary feeding of translocated hihi (*Notiomystis cincta*) (Ewen et al. 2013).

Unfortunately, the concept of habitat is often poorly used and poorly defined in translocation planning (Stadtmann & Seddon 2018). Here, we use the definition of Hall et al. (1997), in describing habitat "*...as the resources and conditions in an area that produce occupancy – including survival and reproduction – by a given organism.*" This includes all physical (e.g. climate, aspect) and biological (e.g. predators, vegetation associations, landscape connectivity) aspects of an area where a species lives. Habitat quality refers to "*...the ability of the environment to provide conditions appropriate for individual and population persistence*" (Hall et al. 1997), specifically survival, reproduction and population growth. Habitat quality is a continuous variable ranging from low quality to high quality habitats, and can be very difficult to define explicitly, although there are useful proxies (Hall et al. 1997). Lambda (annual population growth rate) is the most useful proxy for measuring translocation success as it needs to be >1 for population growth to occur, until density dependence, or other limiting effects, regulate population growth. High quality habitat is typically perceived as places where animals formerly occurred. However, habitat conditions need not replicate past states so long as they provide the critical habitat characteristics that a translocated species requires.

Pest control

Pests are virtually always considered in translocation planning but are rarely explicitly defined as a habitat variable in Aotearoa, where discussions of habitat quality have focussed on vegetation associations that animals are either known or assumed to rely on for survival, while noting that remnant populations don't necessarily survive in high quality habitat (Griffith et al. 1989). However, any discussion on habitat quality in Aotearoa must define the presence and density of pests because they have such a critical impact on the survival of so many native and endemic species (Innes et al. 2010; Richardson et al. 2014). While other biological and physical habitat variables, especially vegetation associations, are clearly essential for translocation success pests are so pervasive that suitable control is almost always a prerequisite for translocated populations to establish and persist. The target pests and the level of control required will vary depending on the translocated species (Table 1). The removal or control of pests also allows the influence of other habitat variables on translocation outcomes to be assessed. In Aotearoa, current (2022) management of mammalian pests includes three major regimes of control: 1) total eradication on offshore islands, 2) maintenance of pests at "zero density" within fenced mainland sites, and 3) suppression of pest densities in unfenced mainland areas (Byrom et a. 2016). These are not mutually exclusive and there is often overlap between them. For example, peninsula fences, such as at Tāwharanui Open Sanctuary, are leaky but have extensive areas of pest control outside the fences. This hopefully reduces incursions while also providing some protection for animals that disperse outside the fence.

Pest densities at the release site must be within the tolerance of the translocated species (Table 1). For example, NI toutouwai can persist with moderate levels of ship rats (*Rattus rattus*) but will have highest survival and reproduction rates if rats are reduced to low levels (≤5% tracking tunnel indices) before each breeding season, with mustelid control also likely to be beneficial. NI toutouwai persist at some sites with ship rat tracking indices of > 25%, but female survival, reproductive output and ultimately population growth will be reduced (Parlato & Armstrong 2012, 2013). As well as reducing the likelihood of population persistence, slow population growth and loss of founders will increase the loss of genetic diversity. In stark contrast, the mainland extinction history, and current distribution, strongly suggests that species such as tīeke, hihi, and red-crowned kākāriki (*Cyanoramphus novaezelandiae*) are much more vulnerable to pests as they currently persist only in sites where pests have either been eradicated or reduced to zero density.

A further challenge when making translocation decisions is that the impact of varying densities of pests is well understood for a few bird species, poorly predicted for many others and virtually unknown for most invertebrates, lizards, amphibians and bats (Table 1). For example, on the mainland pest thresholds and population growth in response to pest control have only been demonstrated for Otago (*Oligosoma otagense*) and grand (*Oligosoma grande*) skinks (Reardon et al. 2012), just two of 106 endemic lizard species.

Other biological and physical habitat variables

In addition to vegetation associations and pests, other habitat variables might be equally important. The physical size of the release site, often defined by the extent of pest control, is a critical consideration simply because large well-protected sites can support large populations. In contrast, small populations at small sites are more vulnerable to extinction. This can be managed through ongoing expansion of protected sites, the creation of natural corridors to other protected sites and supplemental translocations (Weiser et al. 2013; Frankham et al. 2017). However, these options require ongoing commitment and resources which must be planned for (Box 1).

Further habitat variables, including climate, altitude, aspect, and soil type will be associated with vegetation but might shift habitat quality from high to low, i.e. decrease the probability of establishment and persistence, depending on the needs of the translocated species and their ability to adapt to variable conditions. This might be especially difficult at sites that experience climatic extremes relative to those with more benign conditions. Predicted climate change might also mean high quality habitat will become low quality in the future. Furthermore, the impact of these variables is not consistent across species. For example, some species, such as NI toutouwai and NI mātātā, appear to be flexible in their habitat requirements and have been translocated successfully to very contrasting habitats, although productivity and population growth has varied between sites suggesting that some are better than others (Parlato & Armstrong 2012, 2013; KAP *unpublished data*). In stark contrast, species such as hihi need protection from mammalian pests but also seem to have other unknown habitat needs (Ewen et al. 2013), i.e. pest control alone is not currently enough for hihi to establish without additional intensive management via supplemental feeding.

Habitat connectivity and dispersal

Habitat connectivity, and the ability for species to disperse between habitat patches, is typically seen as a highly positive landscape feature and a desirable management objective. However, dispersal from managed release sites into adjacent unmanaged areas appear to be an important cause of failure of many translocations (Richardson et al. 2014). Dispersal generally affects population growth at two levels. First, post-release dispersal following the initial release can cause the loss of individuals from the founding population, thereby reducing the probability of establishment and persistence. For example, in an analysis of 14 reintroduced NI toutouwai populations Parlato and Armstrong (2013) showed that habitat connectivity was a key factor in determining individual establishment following translocation, with individuals released at highly connected sites having a lower establishment probability than those at less connected sites, such as an island or isolated mainland reserve. Second, natal dispersal, i.e. the loss of juveniles raised at the release site, can also reduce establishment and persistence if juveniles move from managed to unmanaged sites (Richardson et al. 2014). Critically, the interaction of post-release dispersal and natal dispersal can limit population growth, erode genetic diversity, and reduce the likelihood of the long-term persistence of a translocated population.

The dispersal of translocated species from release sites is highly variable and sometimes difficult to predict (Table 1) (Richardson et al. 2014). For instance, some birds are very strong dispersers regardless of habitat connectivity. This includes korimako, miromiro/tomtit (*Petroica macrocephala*), and red-crowned kākāriki (Parker et al. 2004; Brunton et al. 2008; Ortiz-Catedral 2010) whereas others, such as NI toutouwai and NI tīeke, are less likely to disperse from sites with low connectivity (Newman 1980; Richard & Armstrong 2010). The dispersal abilities of a translocated species interact with the degree to which the release site is connected to surrounding unprotected habitats, although the shape of this relationship is unknown for all species, and connectivity is difficult to measure (Figure 2). Many species, including some with relatively strong dispersal abilities, rarely leave isolated sites such as islands or forest patches surrounded by pasture. In contrast, species with poor dispersal abilities can move out of protected areas if connected to habitat that the species will willingly move through (Richard & Armstrong 2010), although this is likely to be a greater problem for birds and bats than reptiles, amphibians and invertebrates.

The best way to manage dispersal in contiguous landscapes is to manage as large an area as possible, including potential dispersal routes, through an integrated landscape management approach (Richardson et al. 2014). However, it is not currently known how big a site needs to be to accommodate post-release and natal dispersal in most species, and it will often be difficult, too expensive, or simply not feasible to protect very large sites. This currently limits our ability to translocate some species to large sites. A variety of alternative approaches have been used to try to reduce dispersal, albeit with variable results. Holding animals in captivity at the release site (delayed release) has been tried with many taxa, and many sites, but the results have been extremely variable, i.e. generally ineffective for wild to wild releases, but sometimes useful when releasing captive-reared animals (Parker et al. 2012b; Richardson et al. 2015; Smuts-Kennedy & Parker 2013; Richardson et al. 2014; Parker et al. 2015). Supplementary feeding has also been used with success for some species at some release sites (e.g. kākā, pāteke/brown teal (*Anas chlorotis*) Rickett et al. 2013), but has been less useful for others (e.g. hihi, Richardson et al. 2014). Acoustic anchoring (playback of pre-recorded calls) was attempted with NI kōkako, NI toutouwai, and popokatea in Aotearoa, but was not effective (Leuschner 2007; Molles et al. 2008; Bradley et al. 2011).

Another option for mitigating the impact of dispersal in the establishment phase is the release of large numbers of individuals, either in one big release or in a series of smaller releases over several years. This is intuitively appealing but is rarely effective because if initial post release dispersal is a problem then dispersal will likely remain a problem via natal dispersal (Richardson et al. 2014). In addition, there are many examples where relatively large numbers of animals have been released but the translocations have failed (Miskelly & Powlesland 2013). For instance, single popokatea translocations of 40-100 birds to sites up to 3300ha have typically been successful. However, translocation of 653 birds over 12 years into a 2450 ha protected block within the Waitakere Ranges (c.17 000 ha) appears to have been unsuccessful (KAP *unpublished data*). The relationship between release group size and establishment is also unclear. This is because high quality sites where translocations are successful following the release of large numbers of animals could have been equally successful if fewer animals were released. In contrast, managers typically release fewer animals when they have less confidence in a site, creating a reporting bias towards success with larger releases (Armstrong & Seddon 2008; Armstrong & Wittmer 2011). There are also significant welfare, ethical and relationship risks around translocating large numbers of animals with the expectation that many will die following translocation, especially where translocation is not essential for species management. This uncertainty needs to be carefully and openly discussed at the policy level, so that decision makers can make good defendable decisions at a national level, and with all Treaty Partners and stakeholders involved in any given translocation project.

Ultimately, the best way to reduce dispersal is to release animals at isolated or relatively isolated sites. However, the great challenge with managing dispersal is that we want translocated species to establish populations within large contiguous sites, and we want individuals to be able to freely disperse between sites. This will protect against the problems of populations being small and will largely remove the need for supplemental translocations for genetic management, i.e. natural dispersal via safe dispersal corridors will essentially act as passive meta-population management. It will also provide new opportunities for populations in smaller sites. In the current environment safe corridors generally means protection from pests but as pest control improves other habitat variables will become more important. For example, what size, shape, and structure do corridors need to be to cater for as wide a range of native species as possible? Perhaps the best way to measure the ability of animals to safely disperse from intensively managed areas will be as a performance measure for Predator Free 2050 aspirations. Furthermore, dispersal pathways should be incorporated into decisions about which landscapes to protect first.

Matching source populations to the release site

The choice of source population raises several important considerations. The first is simply whether the source population can sustain a harvest (There are exceptions to this, especially mitigation translocations where the source population habitat is destroyed). Most source populations are “black boxes” in that we know little about their population dynamics and vital rates. However, data from closely monitored populations (Armstrong & Ewen 2013), along with translocation records (Lovegrove 1996; Miskelly & Powlesland 2013; Parker 2013), demonstrate that some populations can be harvested at surprisingly high rates.

How similar are the source and release sites?

Does the source site share similar habitat characteristics especially the presence or absence of pests, vegetation associations and pathogens? This is not necessarily critical because, as noted above, some species seem to be quite tolerant of contrasting habitats. However, translocation between similar habitats is likely an easier transition than translocation between contrasting habitats. For instance Parlato and Armstrong (2012, 2013) showed that translocation of NI toutouwai between habitats with similar pest assemblages and vegetation associations had a small advantage over those between contrasting habitats. The similarity of the source and release site, the objectives of the translocation, and the risk profile or level of uncertainty associated with the translocation will also influence decisions about health screening. For example, translocation between two mainland sites and/or inshore islands that are relatively close together likely represents a low pathogen risk because their pathogen communities are likely to be similar. In contrast, translocation between distant sites with different habitats might prompt a more considered approach, especially if the recipient site has resident populations of highly valued species that could be put at risk through the introduction of novel pathogens. Ideally, there is also an understanding of potential pathogen impacts on the translocated species, on conspecifics and heterospecifics at the release site, and/or a documented history of health screening to inform decisions about health management (Parker et al. 2006; Ewen et al. 2007; Ortiz-Catedral et al. 2011; Ewen et al. 2012; Massaro et al. 2012). Unfortunately, this information is usually lacking or of poor quality.

Managing genetic diversity

Genetic diversity is critical for maintaining evolutionary potential by providing populations with long-term capacity to adapt to changing conditions (Frankham et al. 2012; Frankham et al. 2017). All populations lose genetic diversity over time because of chance events through genetic drift. However, small populations are especially because mutations to replace lost alleles accumulate slowly vulnerable (Frankham et al. 2012; Frankham et al. 2017). Inbreeding (mating between relatives) is also problematic in small populations because it can reduce survival and reproductive success (i.e. inbreeding depression) which in turn threatens population persistence (Frankham et al. 2012; Frankham et al. 2017). Translocations often impose a genetic bottleneck on new populations because of the number of founders released. This is often compounded because the number of founders that recruit and contribute to the new population is usually smaller than the number released. In addition, translocated populations at small sites will always be small. Translocated populations are thus particularly susceptible to genetic drift and inbreeding depression.

Therefore, careful thinking is required in setting genetic objectives to minimise the loss of genetic diversity, to select a source population or populations, to define ongoing genetic management , and to predict the genetic diversity of the translocated population (Weeks et al. 2015). It is also essential to clarify whether genetic objectives are fundamental or means based. For example, we are rarely interested in maintaining genetic diversity for its own sake, i.e. as a fundamental objective (although some, including several of the authors, consider the maintenance of evolutionary potential as a fundamental objective). Rather our interest in genetic diversity is usually as a means objective that contributes to the long-term persistence of the translocated population by maintaining evolutionary potential. If this is the case, then a means objective might be releasing enough animals to maximise genetic diversity in the founders and therefore the long-term adaptive potential of the new population.

Alternatively, there are many reasons why small (≤100 individuals) translocated populations are created, including because only small numbers of animals exist, ease of management, advocacy, or simply that only small sites are available for release. In these cases, genetic means objectives might include informed supplemental translocations to maintain genetic diversity across a metapopulation. All management involves trade-offs. For example, the best source populations are typically large and have no history of tight (<40-100 individuals) and/or long-term bottlenecks (the effects of bottlenecks are sometimes acceptable if the bottleneck is of short duration, e.g. Boessenkool et al. 2007). However, an inshore island might be an easier and cheaper option as a source population, but have lower genetic diversity, than a more expensive and logistically challenging offshore island population with higher genetic diversity. A creative option is to combine populations that have low, but different genetic diversity. This approach was used by Heber et al. (2013) who mixed SI toutouwai from two low diversity translocated populations, to increase diversity in mixed offspring. Similarly, all translocated populations of NI tīeke descend to Taranga/Hen Island via Whatupuke, Whakau/Red Mercury or Repanga/Cuvier Island (Parker et al. 2012a). However, the Repanga lineage is overrepresented with 15 descendent populations followed by Whatupuke (7 descendent populations) and Red Mercury (2 populations). Therefore, recent translocations have used multiple source populations including, where possible, underrepresented lineages, to maximise diversity in new populations and the metapopulation (KAP, unpublished data). Alternatively, there might be uncertainty as to whether animals will establish and persist in the short-term meaning that lower value animals (e.g. males or juveniles) might be released to test a new site. If they survive, further animals might be released to maximise genetic diversity in the medium to long-term. This approach is used for hihi translocations where the primary founders for new sites are juveniles from Tiritiri Matangi while the remaining wild population on Hauturu o Toi, which is viewed as higher value by some managers, is reserved for supplemental translocations to established sites. Another option would be increasing the size of the release area through improved pest control thereby enabling a larger population to establish and removing or reducing the need for supplemental translocations. Alternatively, the cost of ongoing maintenance of a large release site, and translocation of a large diverse founder population, might be greater than managing a much smaller site with ongoing supplemental translocations, at least in the short to medium term.

Useful additional considerations in aligning genetic management with translocation objectives include what is the genetic profile and history of the source population or populations and will it provide genetically diverse individuals for the translocation? How many individuals are needed to capture that diversity? These questions are not easy to resolve, as they rely on high resolution genetic data for source populations and species. These data are usually lacking, especially for taxa that show significant geographic variation in genetic structuring, such as lizards and invertebrates. However, in the absence of data, a combination of knowledge of individual population history and theory allows reasonable assumptions to be made (Weiser et al. 2013; Frankham et al. 2017). Following release, how many animals can the site eventually support? If supplemental translocations are recommended how easy will they be to achieve? The feasibility of follow-up translocations is often presented in a simplistic manner with little recognition of the cost and difficulties in getting additional animals to recruit into an established population. Often, very large numbers of individuals must be added to ensure that at least a few will be able to recruit and breed in the established population (Weiser et al. 2013), as density dependence (Armstrong et al. 2005) or behavioural barriers (Parker et al. 2010a;

Parker et al. 2012a) are likely to reduce recruitment of immigrants. As noted above, releasing large numbers of animals in the expectation that few survive also has welfare, ethical and relationship implications.

Regardless of the management alternative selected for maintaining genetic diversity, it is important to remember that not every translocated population needs to represent maximal or ideal genetic diversity. Overall genetic diversity can also be represented and conserved within a metapopulation connected either via natural dispersal or management. This likely represents a more “natural” scenario (e.g. genetic diversity will not be equal across all natural populations, especially when moving from the core of a species range to the edges), whilst also increasing options for establishing and maintaining translocated populations that cater to a wide range of values and objectives.

The future of conservation translocations in Aotearoa New Zealand

Translocations will continue to play an important role in conservation in Aotearoa. Experience and research will increase our understanding of the values driving translocations including, but not limited to, societal desires, cost, animal welfare, genetic and pathogen management, translocation techniques and dispersal. We also need to fill the significant knowledge gaps that exist for many species, especially invertebrates, lizards, amphibians and bats (Table 1). In Aotearoa the biggest opportunities will come about through improved control of pests over large, unfenced areas of the mainland, including forests, wetlands, dryland and braided river systems, and alpine zones. This will provide a means to translocate species that are currently in higher threat categories, along with providing further options for management and translocation of all species, especially habitat specialists such as whio/blue duck (*Hymenolaimus malacorhynchos*), kāki, and pīwauwau/rock wren (*Xenicus gilviventris*), and neglected fauna, such as lizards, amphibians, bats and invertebrates. While opinion varies on the feasibility of effective pest control over vast swathes of Aotearoa (Urlich 2015) it will clearly be a game changer if it can be achieved. However, in the short term (c. 20 years) large (≥3000 ha) fenced sanctuaries will likely protect the greatest diversity of mainland biodiversity, especially if mice can be effectively controlled within them. We also expect to see an increasing shift away from translocations for single-species recovery toward those where the fundamental objective is ecosystem restoration (Parker 2013). Pathogens and predators, such as weka (*Gallirallus australis*), small rails (*Rallus* spp. and *Porzana* spp.) and NZ karearea/falcons (*Falco novaeseelandiae*) are obvious components of NZ ecosystems that are currently either actively avoided in restoration plans or relegated to some point in the distant future once their potential prey or host species are well established (Carpenter et al. 2021). It seems logical to stage restoration sequences such that prey species are established before predators, although it is important to distinguish between a pest, against which native species have few defences, and a native predator that they have co-evolved with over 1000s of years. For example, translocated Middle Island tusked wētā (*Motuweta isolata*) and wētāpunga (*Deinacrida heteracantha*) have established in the presence of very high densities of a natural predator, the NI tiēke, whereas pests caused the extinction of many large wētā populations elsewhere. Therefore, translocations of predators will require acceptance that there will be ongoing predation, possibly a reduction in population size, and changes in the behaviour of prey species. This will be difficult for some people to accept and could become problematic for very small prey populations, but it is a logical objective for true ecosystem restoration. It might also require flexible thinking in the management of predator species, and pathogens, especially where there is a management need or perception that natural predators and pathogens must be controlled.

There has also been considerable debate about the ongoing impacts of global climate change and how translocations can be used as a tool for species whose habitat will deteriorate under current climate change predictions (Hoegh-Guldberg et al. 2008; Seddon et al. 2009; Seddon 2010). In Aotearoa this would likely mean moving animals across latitudinal gradients, e.g., between the North and South Islands. For instance, climate modelling suggests that the northern South Island, where hihi have never existed, might provide more suitable habitat in the future than the North Island, to which they are currently restricted (Chauvenet et al. 2013). Any decision to undertake a translocation beyond a species natural range will also clearly raise challenges in setting appropriate objectives, especially if it would bring closely related species into contact, although we note that we have already done this for some species (see below).

Another interesting proposition is the suitability of translocating close relatives of extinct species as ecological replacements in ecosystem restoration (Atkinson 1988). For example, the tutukiwi/Snares Island snipe (*Coenocorypha huegeli*) was translocated to replace the extinct tutukiwi/SI snipe (*Coenocorypha iredalei*) and the NI kōkako was translocated as a replacement for the presumed extinct SI kōkako (*Callaeas cinerea*). SI takahē (*Porphyrio hochstetteri*) are also frequently translocated to the North Island (Jamieson & Ryan 2001; Parker et al. 2010b; Miskelly, Charteris & Fraser 2012), although takahē translocations are motivated by species recovery goals rather than as a replacement for the extinct mōho/NI takahē (*Porphyrio mantelli*). It has also been suggested that the Australian brown quail (*Synoicus ypsilophorus*) is a suitable ecological replacement for the extinct New Zealand quail (*Coturnix novaezelandiae*) (Parker et al. 2010b). These species, and others, might be useful for restoring ecosystem services, known or otherwise. In addition, genetic techniques are advancing to the point where de-extinction, the resurrection of functional proxies of extinct species, might become feasible (Seddon et al. 2014; Seddon 2017). This is a contentious issue and the objectives of any such proposal will have to be very carefully considered, including the opportunity cost of diverting funds from extant species to de-extinction proposals (Bennett et al. 2017).

Emerging genomic tools will further enhance translocation decisions (Luikart 2018; Santure & Garant 2018; Funk et al. 2019). Advanced high-throughput sequencing technologies, combined with rapidly decreasing costs, increased capability and capacity in the conservation genetics community, can provide ready access to10s-10 000s of markers from across the entire genome, even for non-model species (Harrisson et al. 2014; Galla et al. 2019). These genome-wide markers can increase resolution for translocation questions previously answered using just a handful of neutral genetic markers. For example, genomic markers can provide more robust estimates of relatedness for pairing decisions in conservation breeding programmes that include translocations (e.g., Galla et al. 2020). Similarly, genomic markers are increasingly used to identify suitable source populations for translocations to enhance adaptive potential (e.g., McLennan et al. 2020; Rayne et al. In Review). Indeed, the promise of characterising adaptive variation has also reignited debate over how we should source, or mix, populations to enhance adaptive potential (Robinson et al. 2018; Ralls et al. 2018; DeWoody et al. 2021; García-Dorado & Caballero 2021; Kardos & Shafer 2018; Kardos et al. 2021; Kyriazis et al. 2021; Teixeira & Huber 2021a; Teixeira & Huber 2021b; Hansson et al. 2021). However, translating theory into practise remains difficult (Flanagan et al. 2017) despite a surge of theoretical and simulation based papers focussed on characterising adaptive variation (Funk et al. 2019; Hoelzel et al. 2019). Indeed, for many threatened species it may prove challenging to characterise adaptive variation at all (Box 2).

Recent years have seen the rise of a new era of conservation genomics that reintegrates the packaging and function of DNA and considers how these mediate the transfer of genomic information between parent and offspring (Deakin et al. 2019; Liberles et al. 2020). For example, emerging chromosomic approaches combine genomic data with cytogenetics (chromosome architecture), epigenomics (histone modifications) and cell biology to reveal the mechanisms underpinning behavioural and phenotypic traits under selection (Mérot et al. 2020). Although these approaches certainly come with their own caveats (Potter & Deakin 2018; Deakin et al. 2019), genomic and chromosomic approaches are a valuable addition to the translocation toolbox, particularly in the face of novel challenges such as climate change (Hoffmann et al. 2021; Wold et al. 2021).

Conclusions

There often seems to be a perception that translocations are relatively easy and success is assured, something not demonstrated by data on success rates either in Aotearoa (Miskelly & Powlesland 2013), or internationally (Griffith et al. 1989; Wolf et al. 1996; Fischer & Lindenmayer 2000). The frequency of translocations is also increasing (Cromarty & Alderson 2013), including calls for urban translocations (van Heezik & Seddon 2018). Furthermore, the quality of translocation proposals presented to DOC is highly variable, with some poorly written, poorly thought out, or just a bad idea for the candidate species. The DOC approval process itself also produces variable outcomes. We want to see more successful translocations in Aotearoa. Here, we discuss factors that we think are essential for translocation planning, including the cultural and social setting, habitat quality (specifically pest control, vegetation associations and dispersal opportunities) and genetic management. We also highlight emerging issues and opportunities for translocations in Aotearoa such as climate change, predator translocations and filling extinct niches with closely related species, or even de-extinct species.

Ultimately, our goal is to encourage careful thinking in the formulation of translocation objectives that capture these factors (Box 1), along with the derivation of appropriate performance measures for determining success. We discourage a focus on any single factor and rather encourage all people involved in translocations, particularly decision makers, to explicitly recognise the multiple values-based objectives associated with translocations (Box 1).

Haphazard conservation translocations can cause problems at the release site, for future translocations, and in maintaining equitable relationships with Treaty Partners, other stakeholders, relevant agencies, and the public. We disagree with the suggestion that conservation translocations in Aotearoa have not been guided by clear principles (Parlimentary Commisioner for the Environment 2017). However, we do agree that the principles of good translocation practice are not currently captured in policy. Furthermore, the fundamental objectives of many translocations have rarely been stated explicitly or are dominated by singular means objectives. Therefore, a clear and widely consulted translocation policy framework would enable DOC decision makers to make better decisions about all translocations. This policy should specifically acknowledge that translocations are values based, should be driven by an understanding of the problem at hand, require informed decisions between management alternatives (including rejecting translocation as a management tool for some species/programmes), and should be measured by explicitly stated objectives with appropriate performance indicators. Ultimately, being clear about what DOC, Treaty Partners and other stakeholders really want will set us on the right path towards the Aotearoa landscape being one that is once again dominated by indigenous biodiversity.

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References

Armstrong DP, Seddon PJ 2008. Directions in reintroduction biology. Trends in Ecology & Evolution 23: 20-25.

Armstrong DP, Wittmer HU 2011. Incorporating Allee effects into reintroduction strategies. Ecological Research 26: 687-695.

Armstrong DP, Ewen J 2013. Consistency, continuity and creativity: long-term studies of population dynamics on Tiritiri Matangi Island. New Zealand Journal of Ecology 37: 288-297.

Armstrong DP, Davidson RS, Perrott JK, Roygard J, Buchanan L 2005. Density-dependent population growth in a reintroduced population of North Island saddlebacks. Journal of Animal Ecology 741: 160-170.

Atkinson IAE 1988. Presidential address: opportunities for ecological restoration. New Zealand Journal of Ecology 11: 1-12.

Attard CRM, Brauer CJ, Sandoval-Castillo J, Faulks LK, Unmack PJ, Gilligan DM, Beheregaray LB 2017. Ecological disturbance influences adaptive divergence despite high gene flow in golden perch (*Macquaria ambigua*): Implications for management and resilience to climate change Molecular Ecology 271: 196-215.

Barrett RDH, Laurent S, Mallarino R, Pfeifer SP, Xu CCY, Foll M, Wakamatsu K, Duke-Cohan JS, Jensen JD, Hoekstra HE 2019. Linking a mutation to survival in wild mice. Science 363: 499–504.

Bennett JR, Maloney RF, Steeves TE, Brazill-Boast J, Possingham HP, Seddon PJ 2017. Spending limited resources on de-extinction could lead to net biodiversity loss. Nature Ecology and Evolution 1: 1-4.

Bioethics Panel 2019. Predator Free New Zealand: social, cultural, and ethical challenges. Bioheritage Challenge, 26 p.

Boessenkool S, Taylor SS, Tepolt CK 2007. Large mainland populations of South Island robins retain greater genetic diversity than offshore island refuges. Conservation Genetics 8: 705–714.

Bradley DW, Ninnes CE, Valderrama SV, Waas JR 2011. Does 'acoustic anchoring' reduce post-translocation dispersal of North Island robins? Wildlife Research 38: 69-76.

Brunton DH, Evans BA, Ji W 2008. Assessing natural dispersal of New Zealand bellbirds using song type and song playbacks. New Zealand Journal of Ecology 322: 147-154.

Byrom AE, Innes J, Binny RN 2016. A review of biodiversity outcomes from possum-focused pest control in New Zealand. Wildlife Research 43: 228-253.

Carpenter JK, Innes JG, Wood JR, Lyver POB 2021. Good predators: the roles of weka (*Gallirallus australis*) in New Zealand's past and present ecosystems. New Zealand Journal of Ecology 45: 3425.

Caughley G 1989. New Zealand and plant-herbivore systems: past and present. New Zealand Journal of Ecology 12: 3-10.

Caughley G 1994. Directions in conservation biology. Journal of Animal Ecology 63: 214-244.

Chauvenet ALM, Ewen JG, Armstrong D, Pettorelli N 2013. Saving the hihi under climate change: a case for assisted colonization. Journal of Applied Ecology 50: 1330-1340.

Converse S, Moore C, Folk M, Runge M 2014. Optimal release strategies for cost-effective reintroductions. Journal of Wildlife Management 77: 1145-1156.

Cromarty PL, Alderson SL 2013. Translocation statistics (2002-2010), and the revised Department of Conservation translocation process. Notornis 60: 55-62.

Deakin JE, Potter S, O'Neill R, Ruiz-Herrera A, Cioffi MB, Eldridge MDB, Fukui K, Graves JAM, Griffin D, Grutzner F, Kratochvil L, Miura I, Rovatsos M, Srikulnath K, Wapstra E, Ezaz T 2019. Chromosomics: bridging the gap between genomes and chromosomes. Genes 108: 627.

DeWoody JA, Harder AM, Mathur S, Willoughby JR (2021.) The long-standing significance of genetic diversity in conservation. Molecular Ecology doi:10.1111/mec.16051.

Diamond JM 1984. Distributions of New Zealand birds on real and virtual islands. New Zealand Journal of Ecology 7: 37-55.

Ewen JE, Soorae PS, Canessa S 2014. Reintroduction objectives, decisions and outcomes: global perspectives from the herpetofauna. Animal Conservation 17: 74-81.

Ewen JG, Thorogood R, Nicol C, Armstrong DP, Alley M 2007. *Salmonella typhimurium* in hihi, New Zealand. Emerging Infectious Diseases 13: 788-790.

Ewen JG, Renwick R, Adams L, Armstrong DP, Parker KA 2013. 1980-2012: 32 years of re-introduction efforts of the hihi (stitchbird) in New Zealand. In: Soorae PS ed. Global re-introduction perspectives: 2013. Abu Dhabi, IUCN/SSC Re-introduction Specialist Group & Environment Agency-ABU DHABI. 282 p.

Ewen JG, Armstrong DP, Empson R, Jack S, Makan T, McInnes K, Parker KA, Richardson K, Alley M 2012. Parasite management in translocations: lessons from an endangered New Zealand bird. Oryx 46: 446-456.

Fischer J, Lindenmayer DB 2000. An assessment of the published results of animal relocations. Biological Conservation 96: 1-11.

Flanagan SP, Forester BR, Latch EK, Aitken SN, Hoban S 2017. Guidelines for planning genomic assessment and monitoring of locally adaptive variation to inform species conservation. Evolutionary Applications 117: 1027-1193.

Frankham R, Ballou JD, Briscoe DA 2012. Introduction to conservation genetics. USA, Cambridge University Press. 618 p.

Frankham R, Ballou JD, Ralls K, Eldridge MDB, Dudash MR, Fenster CB, Lacy RC, Sunnucks P 2017. Genetic management of fragmented animal and plant populations. United Kingdom, Oxford University Press. 401 p.

Funk WC, Forester BR, Converse S, Darst C, Morey S 2019. Improving conservation policy with genomics: a guide to integrating adaptive potential into U.S. Endangered Species Act decisions for conservation practitioners and geneticists. Conservation Genetics 20: 115-134.

Galla SJ, Forsdick NJ, Brown L, Hoeppner MP, Knapp M, Maloney RF, Moraga R, Santure AW, Steeves TE 2019. Reference genomes from distantly related species can be used for discovery of single nucleotide polymorphisms to inform conservation management. Genes 10: 1-19.

Galla SJ, Moraga R, Brown L, Cleland S, Hoeppner MP, Maloney RF, Richardson A, Slater L, Santure AW, Steeves TE 2020. A comparison of pedigree, genetic and genomic estimates of relatedness for informing pairing decisions in two critically endangered birds: implications for conservation breeding programmes worldwide. Evolutionary Applications 13: 991-1008.

García-Dorado A, Caballero A 2021. Neutral genetic diversity as a useful tool for conservation biology. Conservation Genetics 22: 541–545.

Gregory R, Failing L, Harstone M, Long G, McDaniels T, Ohlson D 2012. Structured decision making: a practical guide to environmental management choices. UK, Wiley-Blackwell. 299 p.
Griffith B, Scott JM, Carpenter JW, Reed C 1989. Translocation as a species conservation tool: status and strategy. Science 245: 477-480.
Hall LS, Krausman PR, Morrison ML 1997. The habitat concept and a plea for standard terminology. Wildlife Society Bulletin 25: 173-182.
Hansson B, Morales HE, Oosterhout C van 2021. Comment on "Individual heterozygosity predicts translocation success in threatened desert tortoises". Science 372: 6546.
Harrisson KA, Pavlova A, Telonis-Scott M, Sunnucks P 2014. Using genomics to characterize evolutionary potential for conservation of wild populations. Evolutionary Applications 7: 1008-1025.
Harrisson KA, Amish SJ, Pavlova A, Narum SR, Telonis-Scott M, Rourke ML, Lyon J, Tonkin Z, Gilligan DM, Ingram BA, Lintermans M, Gan HM, Austin CM, Luikart G, Sunnucks P 2017. Signatures of polygenic adaptation associated with climate across the range of a threatened fish species with high genetic connectivity. Molecular Ecology 2622: 6253-6269.
Heber S, Varsani A, Kuhn S, Girg A, Kempenaers B, Briskie J 2013. The genetic rescue of two bottlenecked South Island robin populations using translocations of inbred donors. Proceedings of the Royal Society B 280: 1-8.
Hoegh-Guldberg O, Huhes L, McIntyre S, Lindenmayer DB, Parmesan C, Possingham HP, Thomas CD 2008. Assisted colonization and rapid climate change. Science 321: 345-346.
Hoelzel AR, Bruford MW, Fleischer RC 2019. Conservation of adaptive potential and functional diversity. Conservation Genetics 20: 1-5.
Hoffmann AA, Weeks AR, Sgrò CM 2021. Opportunities and challenges in assessing climate change vulnerability through genomics. Cell 184(6): 1420–1425.
Holdaway RN 1989. New Zealand's pre-human avifauna and its vulnerability. New Zealand Journal of Ecology 12: 11-25.
Innes J, Kelly D, Overton J. McC., Gillies C 2010. Predation and other factors currently limiting New Zealand forest birds. New Zealand Journal of Ecology 34: 86-114.
Innes J, Fitzgerald N, Binny R, Byrom A, Pech R, Watts C, Gillies C, Maitland M, Campbell-Hunt C, Burns B 2019. New Zealand ecosanctuaries: types, attributes and outcomes. Journal of the Royal Society of New Zealand 49: 370-393
IUCN 2013. Guidelines for reintroductions and other conservation translocations. Version 1.0. Gland, Switzerland, IUCN Species Survival Commission. 57 p.
Jamieson IG, Ryan CJ 2001. Island takahe: closure of the debate over the merits of introducing Fiordland takahe to predator-free islands. In: Lee WG, Jamieson IG ed. The takahe: Fifty years of conservation management and research. Dunedin, University of Otago Press. Pp. 96-113.
Kardos M, Armstrong EE, Fitzpatrick SW, Hauser S, Hedrick PW, Miller JM, Tallmon DA, Funk WC 2021. The crucial role of genome-wide genetic variation in conservation. Proceedings of the National Academy of Sciences 118: e2104642118.
Kardos M, Shafer ABA 2018. The peril of gene-targeted conservation. Trends in Ecology & Evolution 33: 827–839.
Keeny R 1982. Decision analysis: an overview. Operations Research 30: 803-838
Keller LF, Biebach I, Ewing SR, Hoeck PEA 2012. The genetics of reintroductions: inbreeding and genetic drift. In: Ewen JG, Armstrong DP, Parker KA, Seddon PJ eds. Reintroduction biology: integrating science and management. West Sussex, U.K., Wiley-Blackwell Ltd. Pp. 360-394.

Kyriazis CC, Wayne RK, Lohmueller KE 2021. Strongly deleterious mutations are a primary determinant of extinction risk due to inbreeding depression. Evolution Letters 5: 33–47.

Leuschner N 2007. Ecology and behaviour of the whitehead (*Mohoua albicilla*) in its translocated ranges in New Zealand. Unpublished thesis, University of Auckland, Auckland. 109 p.

Liberles DA, Chang B, Geiler-Samerotte K, Goldman A, Hey J, Kaçar B, Meyer M, Murphy W, Posada D, Storfer A 2020. Emerging Frontiers in the Study of Molecular Evolution. Journal of Molecular Evolution 88: 211-226.

Lovegrove TG 1996. Island releases of saddlebacks *Philesturnus carunculatus* in New Zealand. Biological Conservation 77: 151-157.

Luikart GKM, Hand BK, Rajora OP, Aitken SN, Hohenlohe PA 2018. Population genomics: advancing understanding of nature. In: Rajora OP ed. Population Genomics: concepts, approaches, applications. New York, Springer. Pp. 3-79.

Maguire L 1986. Using decision analysis to manage endangered species populations. Journal of Environmental Management 22: 345-360.

Massaro M, Ortiz-Catedral L, Julian L, Galbraith JA, Kurenback B, Kearvell J, Kemp J, van Hal J, Elkington S, Taylor G, Greene T, van de Wetering J, van de Wetering M, Pryde M, Dilks P, Heber S, Steeves T, Walters M, Shaw S, Potter J, Farrant M, Brunton DH, Hauber M, Jackson B, Bell P, Moorhouse R, McInnes K, Varsani A. 2012. Molecular characterisation of beak and feather disease virus (BFDV) in New Zealand and its implications for managing an infectious disease. Archives of Virology 157: 1651-1663.

McCarthy MA, Armstrong DP, Runge MC 2012. Adaptive management of reintroduction. In: Ewen JG, Armstrong DP, Parker KA, Seddon PJ ed. Reintroduction biology: integrating science and management. West Sussex, U.K., Wiley-Blackwell. Pp. 256-289.

Mérot C, Oomen RA, Tigano A, Wellenreuther M 2020. A roadmap for understanding the evolutionary significance of structural genomic variation. Trends in Ecology & Evolution 35: 561–572.

Miskelly CM, Powlesland RG 2013. Conservation translocations of New Zealand birds, 1863-2012 Notornis 60: 3-28.

Miskelly CM, Charteris MR, Fraser JR 2012. Successful translocation of Snares Island snipe (*Coenocorypha huegeli*) to replace the extinct South Island snipe (*C. iredalei*). Notornis 59: 32-38.

McLennan EA, Grueber CE, Wise P, Belov K, Hogg CJ 2020. Mixing genetically differentiated populations successfully boosts diversity of an endangered carnivore. Animal Conservation 23: 700-712.

McMurdo Hamilton T, Canessa S, Clark K, Gleeson P, Mackenzie F, Makan T, Moses-Te Kani G, Oliver S, Parker KA, Ewen JG 2021. Applying a values-based decision process to facilitate comanagement of threatened species in Aotearoa New Zealand. Conservation Biology 35: 1162-1173.

Molles LE, Calcott A, Peters D, Delamare G, Hudson JD, Innes J, Flux I, Waas JR 2008. 'Acoustic anchoring' and the successful translocation of North Island kokako (*Callaeas cinerea wilsoni*) to a New Zealand mainland site within continuous forest. Notornis 55: 57-68.

Newman DG 1980. Colonisation of Coppermine Island by the North Island saddleback. Notornis 27: 146-147.

Ortiz-Catedral L 2010. Homing of a red-crowned parakeet (*Cyanoramphus novaezelandiae*) from Motuihe Island to Little Barrier Island, New Zealand. Notornis 57: 48-49.

Ortiz-Catedral L, Prada D, Gleeson D, Brunton DH 2011. Avian malaria in a remnant population of red-fronted parakeets on Little Barrier Island, New Zealand. New Zealand Journal of Zoology 38: 261-268.

Parker KA 2008. Translocations: Providing outcomes for wildlife, resource managers, scientists, and the human community. Restoration Ecology 16: 204-209.
Parker KA 2013. Avian translocations to and from Tiritiri Matangi 1974-2013. New Zealand Journal of Ecology 37: 282-287.
Parker KA, Brunton DH, Jakob-Hoff R 2006. Avian translocations and disease; implications for New Zealand conservation. Pacific Conservation Biology 12: 155-162
Parker KA, Hauber ME, Brunton DH 2010a. Contemporary cultural evolution of a conspecific recognition signal following serial translocations. Evolution 64: 2431-2441.
Parker KA, Seabrook-Davison M, Ewen JG 2010b. Opportunities for non-native ecological replacements in ecosystem restoration. Restoration Ecology 18: 269-273.
Parker KA, Hughes B, Thorogood R, Griffiths R 2004. Homing over 56 km by a North Island tomtit (*Petroica macrocephala toitoi*). Notornis 51: 238-239.
Parker KA, Anderson MJ, Jenkins PF, Brunton DH 2012a. The effects of translocation-induced isolation and fragmentation on the cultural evolution of bird song. Ecology Letters 15: 778-785.
Parker KA, Dickens MJ, Clarke RH, Lovegrove TG 2012b. The theory and practise of catching, holding, moving and releasing animals In: Ewen JG, Armstrong DP, Parker KA, Seddon PJ ed. Reintroduction biology: integrating science and management. West Sussex, U.K., Wiley-Blackwell. Pp. 105-137.
Parker KA, Adams L, Baling M, Kemp L, Kuchling G, Lloyd B, Parsons S, Ruffell J, Stringer I, Watts C, Dickens MJ 2015. Practical guidelines for planning and implementing fauna translocations. In: Armstrong DP, Hayward MW, Moro D, Seddon PJ ed. Advances in reintroduction biology of Australian and New Zealand fauna. Australia, CSIRO Publishing. Pp. 255-272.
Parlato EH, Armstrong DP 2012. An integrated approach for predicting fates of reintroductions with demographic data from multiple populations. Conservation Biology 26: 97-106.
Parlato EH, Armstrong DP 2013. Predicting post-release establishment using data from multiple introductions. Biological Conservation 160: 97-104.
Parlato EH, Armstrong DP 2018. Predicting reintroduction outcomes for highly vulnerable species that do not currently co-exist with their key threats. Conservation Biology 32: 1346-1355.
Parliamentary Commissioner for the Environment 2017. Taonga of an island nation: Saving New Zealand's birds. Wellington, Parliamentary Commissioner for the Environment. 139 p.
Potter S, Deakin JE 2018. Cytogenetics: an important inclusion in the conservation genetics toolbox. Pacific Conservation Biology 24: 280-288.
Ralls K, Ballou JD, Dudash MR, Eldridge MDB, Fenster CB, Lacy RC, Sunnucks P, Frankham R 2018. Call for a paradigm shift in the genetic management of fragmented populations. Conservation Letters 11: e12412.
Rayne A, Blair S, Dale M, Flack B, Hollows J, Moraga R, Parata RN, Rupene M, Tamati-Elliffe P, Wehi PM, Wylie MJ, Steeves TE *In Review*. Weaving place-based knowledge for culturally significant species in the age of genomics: Looking to the past to navigate the future. Evolutionary Applications.
Reardon JT, Whitmore N, Holmes KM, Judd LM, Hutcheon AD, Norbury G, Mackenzie D 2012. Predator control allows critically endangered lizards to recover on mainland New Zealand. New Zealand Journal of Ecology 36: 141-150.
Rellstab C, Gugerli F, Eckert AJ, Hancock AM, Holderegger R 2015. A practical guide to environmental association analysis in landscape genomics. Molecular Ecology 24: 4348-4370.

Richard Y, Armstrong DP 2010. Cost distance modelling of landscape connectivity and gap-crossing ability using radio-tracking data. Journal of Applied Ecology 47: 603-610.

Richardson K, Castro IC, Brunton DH, Armstrong DP 2015. Not so soft? Delayed release reduces long-term survival in a passerine reintroduction. Oryx 49: 535-541.

Richardson K, Doerr V, Ebrahimi M, Parker KA 2014. Considering dispersal in reintroduction and restoration planning. In: Armstrong DP, Hayward MW, Moro D, Seddon PJ ed. Advances in Reintroduction Biology of Australian and New Zealand Fauna. Australia, CSIRO Publishing. Pp. 59-72.

Rickett J, Dey CJ, Stothart J, O'Connor CM, Quinn JS, Ji W 2013. The influence of supplemental feeding on survival, dispersal and competition in translocated brown teal, or pateke (*Anas chlorotis*). Emu 113: 62-68.

Robertson HA, Baird K, Dowding JE, Elliott GP, Hitchmough RA, Miskelly CM, McArthur N, O'Donnell CFJ, Sagar PM, Scofield RP, Taylor G 2017. Conservation status of New Zealand birds, 2016. New Zealand Threat Classification Series 19. Wellington, Department of Conservation. 27 p.

Robertson HA, Baird K, Dowding JE, Elliott GP, Hitchmough RA, McArthur NJ, Makan T, Miskelly CM, O'Donnell CFJ, Sagar PM, Scofield RP, Taylor GA, Michel P 2021. Conservation status of New Zealand birds, 2016. New Zealand Threat Classification Series 36. Wellington, Department of Conservation. 43 p.

Robinson JA, Brown C, Kim BY, Lohmueller KE, Wayne RK 2018. Purging of strongly deleterious mutations explains long-term persistence and absence of inbreeding depression in Island Foxes. Current Biology 28: 3487-3494.

Santure AW, Garant D 2018. Wild GWAS—association mapping in natural populations. Molecular Ecology Resources 18: 729-738.

Seaborn T, Andrews KR, Applestein CV, Breech TM, Garrett MJ, Zaiats A, Caughlin TT 2021. Integrating genomics in population models to forecast translocation success. Restoration Ecology 29: e13395.

Seddon PJ 1999. Persistence without intervention: assessing success in wildlife reintroductions. Trends in Ecology & Evolution 14: 503.

Seddon PJ 2010. From reintroduction to assisted colonization: moving along the conservation translocation spectrum. Restoration Ecology 18: 796-802.

Seddon PJ 2017. The ecology of de-extinction. Functional Ecology 31: 992-995.

Seddon PJ, Moehrenschlager A, Ewen JG 2014. Reintroducing resurrected species: selecting DeExtinction candidates. Trends in Ecology & Evolution 29: 140-147.

Seddon PJ, Armstrong DP, Soorae P, Launay F, Walker S, Ruiz-Miranda CR, Molur S, Koldewey H, Kleiman DG 2009. The risks of assisted colonization. Conservation Biology 23: 788.

Smuts-Kennedy C, Parker KA 2013. Reconstructing avian biodiversity on Maungatautari. Notornis 60: 93-106.

Stadtmann S, Seddon PJ 2018. Release site selection: reintroductions and the habitat concept. Oryx 54: 687-695.

Suding K, Higgs E, Palmer M, Callicott JB, Anderson CB, Baker M, Gutrich JJ, Hondula KL, LaFevor MC, Larson BMH, Randall A, Ruhl JB, Schwartz KZS 2015. Committing to ecological restoration. Science 348: 638-640.

Teixeira JC, Huber CD 2021a. The inflated significance of neutral genetic diversity in conservation genetics. Proceedings of the National Academy of Sciences 118: 10.

Teixeira JC, Huber CD 2021b. Authors' Reply to Letter to the Editor: Neutral genetic diversity as a useful tool for conservation biology. Conservation Genetics 22: 547–549.

Towns DR, Broome K 2003. From small Maria to massive Campbell: Forty years of rat eradications from New Zealand islands. New Zealand Journal of Zoology 30: 377-398.
Urlich SC 2015. What's the end-game for biodiversity: is it time for conservation evolution? New Zealand Journal of Ecology 39: 133-142.
van Heezik Y, Seddon PJ 2018. Animal reintroductions in peopled landscapes: moving towards urban-based species restorations in New Zealand. Pacific Conservation Biology 24: 349-359.
Weeks AR, Moro D, Thavornkanlapachai R, Taylor HR, White NE, Weiser EL, Heinze D 2015. Conserving and enhancing genetic diversity in translocation programs. In: Armstrong DP, Hayward MW, Moro D, Seddon PJ ed. Advances in reintroduction biology of Australian and New Zealand fauna. Australia, CSIRO Publishing. Pp. 127-140.
Wehi PM, Cox MP, Roa T, Whaanga H 2018. Human perceptions of megafaunal extinction events revealed by linguistic analysis of indigenous oral traditions. Human Ecology 46: 461-470.
Weiser EL, Grueber CE, Jamieson IG 2013. Simulating retention of rare alleles in small populations to assess management options for species with different life histories. Conservation Biology 27: 335-344.
Wold J, Galla S, Eccles D, Hogg CJ, Koepfli K-P, Lec ML, Guhlin J, Price K, Roberts J, Steeves T 2021. Expanding the conservation genomics toolbox: incorporating structural variants to enhance functional studies for species of conservation concern. Molecular Ecology 30: 5949-5965.
Wolf CM, Griffith B, Reed C, Temple SA 1996. Avian and mammalian translocations: update and reanalysis of 1987 survey data. Conservation Biology 10: 1142-1154.

Box 1. Some considerations for conservation translocations in Aotearoa New Zealand. Of these, the first is the only critical step because, if done correctly, it will naturally envelop all other considerations, both listed and unlisted.

1. <u>All conservation translocation decisions are values based</u>. Therefore, the cultural and social setting of a translocation is the most critical factor in determining fundamental objectives (what we want) and means objectives (how we get what we want). If this is done correctly all other decisions will be better and easier.
2. What is the extirpation and management history of the translocation candidate and is natural recolonisation likely on an acceptable time scale?
3. Does the release site habitat (e.g. pests, vegetation associations, pathogens) match the proposed source population? If not, why is the release site considered appropriate? Can management ameliorate differences?
4. How connected is the release site and is dispersal a likely impediment to establishment and persistence?
5. How big is the release site and what is the maximum population size it can support?
6. Can the proposed source population/populations sustain harvest and what is its genetic history (e.g. size, bottlenecks)?
7. Will genetic management be required and how realistic is it that the management will actually be implemented (e.g. increase the number of founders, conduct supplemental translocations, increase the management area)?
8. Will future developments (e.g. improved pest control or emerging genomic tools) improve management of the translocation at hand?

Figure 1. Steps in the conservation translocation structured decision-making process (adapted from Gregory et al. 2012). Note the double loop learning whereby monitoring might lead to a revision of management alternatives.

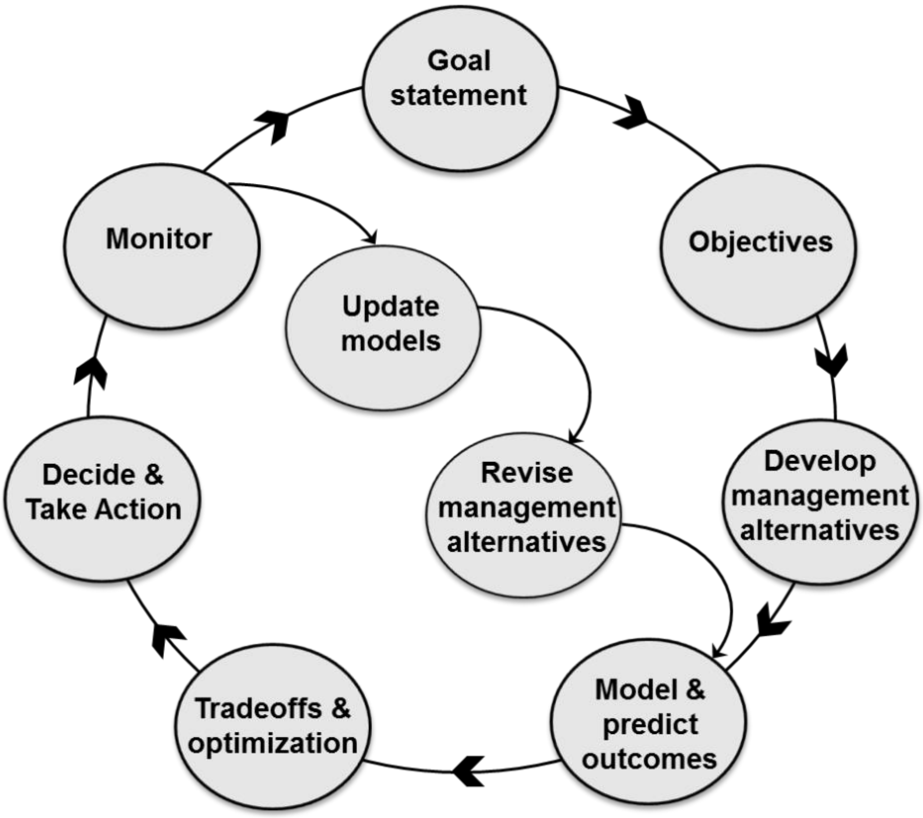

Figure 2. A hypothetical relationship between expected population equilibrium density and habitat connectivity mediated dispersal following translocation. The grey areas with solid black lines are managed habitat. Those surrounded by dashed lines are unmanaged. The light stippled area surrounding the first three managed areas represents habitat with a high resistance to dispersal (e.g. open water or pasture). Resistance to dispersal decreases as connectivity increases. The managed area on the right is within contiguous habitat (grey stipple) that provides no resistance to dispersal. In this case dispersal/emigration is acting as mortality. A similar shaped curve would be seen for other sources of mortality, e.g. increasing predator density. While it is unequivocal that dispersal is problematic and directly related to connectivity the exact shape of the curve is unknown for most species.

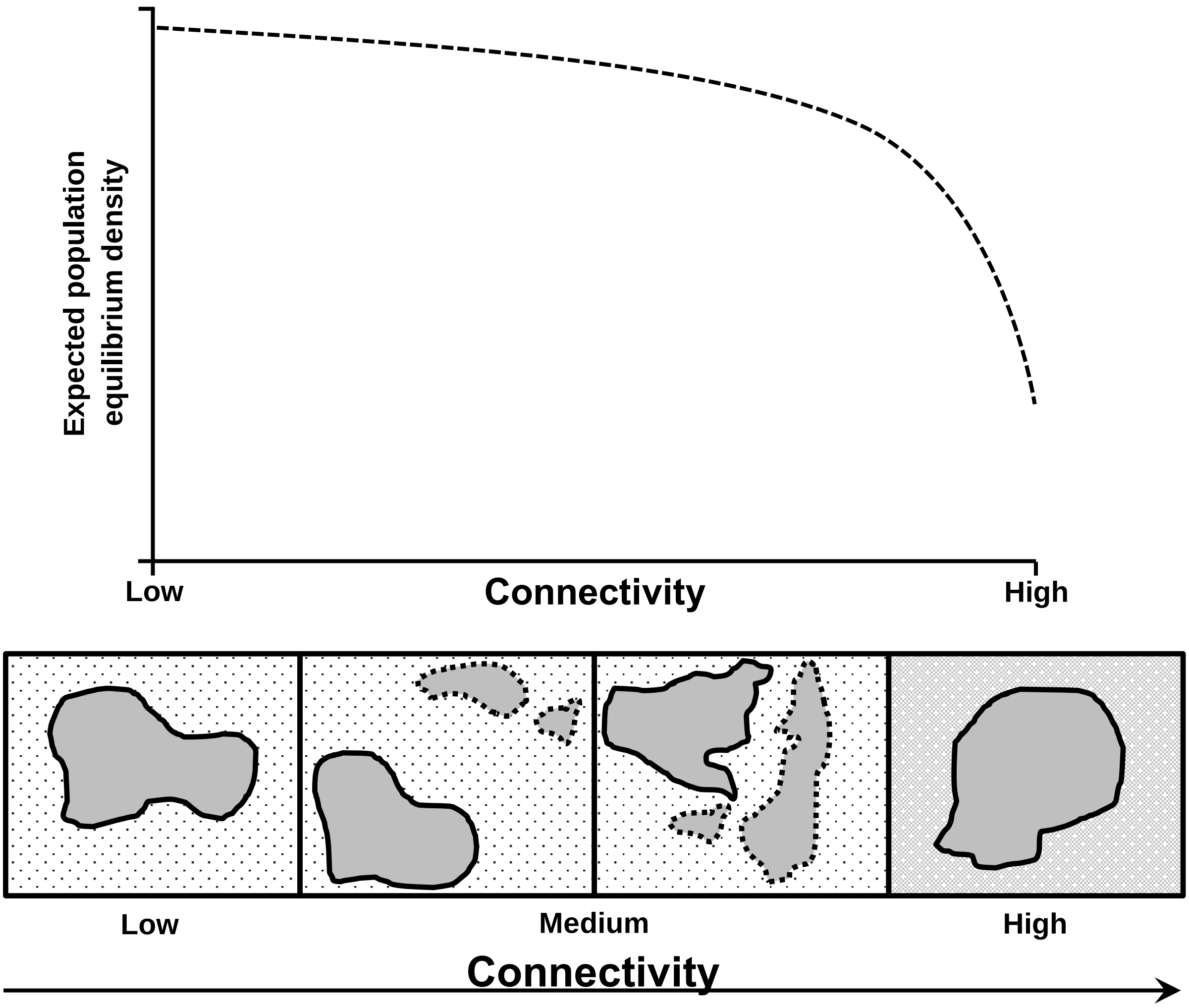

Table 1. Known or probable pest control thresholds, extinction history, and key uncertainties, for some terrestrial species that might be translocated in Aotearoa NZ. Knowledge is patchy, even for many bird species, and there is a lot of uncertainty to resolve, especially for herpetofauna and invertebrates. Other habitat variables, such as ideal vegetation associations, can be difficult to resolve until suitable pest control is in place.

Pest control delivery	**Translocation candidates**	**Extinction history and current distribution**	**Ability to disperse when connectivity is:**			**Key uncertainties**
			High	**Medium**	**Low**	
Key pest species controlled to low density, typically mustelids	Kiwi spp.	Extinct across most of their natural range Declining at unmanaged mainland sites Stable/increasing at managed sites	High	High	?	Availability of birds, i.e. balancing community desires with national recovery objectives
	Weka spp., particularly NI and buff weka	Extinct across most of their natural range Persisting at some unmanaged mainland sites Stable/increasing at managed sites	High	High	Low	Weka are generally neglected and need managed sites, especially NI and buff weka Prone to population fluctuations in response to drought Possible undesirable impacts on reptiles and threatened invertebrates, although likely less of a problem at very large mainland sites Incompatible with burrowing seabirds at small sites and islands Weka often interfere with management devices such as bait stations and traps
	Whio	Extinct across most of their natural range Persisting at some unmanaged mainland sites Stable/increasing at managed sites	High	High	?	Habitat plasticity?

Multi-species pest control to low density, typically including ship rats, mustelids, possums and cats, sometimes including ungulates and pigs. Mice usually present, sometimes at high density Control is sometimes delivered seasonally (e.g. over the bird breeding season)	Robin spp.	Extinct across most of their natural range Persisting at some unmanaged mainland sites Stable/increasing at managed sites	High	?	Low	Density is highly variable at managed sites, likely due to climate and vegetation associations
	Yellow crowned kākāriki	Extinct across most of their natural range Persisting at some unmanaged mainland sites Stable/increasing at managed sites	High	High	?	Suitable source populations (logistically and genetically)
	Whiteheads	Extinct across most of their natural range Persisting at some unmanaged mainland sites Stable/increasing at managed sites	High	Moderate	Low	
	Mohua	Extinct across most of their natural range Present at some unmanaged mainland sites Stable/increasing at some managed sites	High?	?	Low	
	Rifleman	Extinct across most of their natural range Persisting at some unmanaged mainland sites Stable/increasing at managed sites	?	?	Low	
	Kākā	Extinct across most of their natural range Present at some unmanaged mainland sites	High	High	High	Suitable source populations (logistically and genetically) Cost

		Stable/increasing at managed sites				
	North Island kōkako	Extinct across most of their natural range Stable/increasing at managed sites	High	?	Low	Availability of birds, i.e. balancing community desires with national recovery objectives
	Short-tailed bats	Extinct across most of their natural range Stable/increasing at managed sites	High	?	?	Successful translocation techniques have not been developed
	Mainland herpetofauna, e.g. Northern spotted skinks and the infrapunctatum complex, jewelled and forest geckos, Hochstetter's frog	Patchily distributed Persisting at unmanaged mainland sites but true status usually unknown Status at managed sites usually unknown	?	?	?	Successful translocation techniques have been developed for many species but usually overlooked in restoration projects The impacts of mice, especially at high densities, are poorly known but probably significant Often displaced by development thereby potentially providing a source of animals for translocation to appropriate sites Typically less likely to disperse c.f. birds, but much remains unknown.
	Mainland invertebrates	Poorly known	?	?	?	With few exceptions (e.g. some land snails) there is little knowledge about the impacts of pest management and connectivity on most mainland invertebrates
Multi-species pest control to eradication or zero density of all mammalian pests with the probable exception of mice (as is	Saddleback spp.	Extinct on the mainland late 1800s	High	Low	Low	Vulnerable to even very low densities of mustelids (individual animals) and rats (rat threshold currently unknown). NI saddlebacks persisted with kiore, SI saddlebacks did not, suggesting a greater degree of vulnerability

typical of all mainland fenced sanctuaries).	Hihi	Extinct on the mainland late 1800s	High	Moderate?	Low	Likely similar vulnerability and pest thresholds as saddlebacks
	Kākāpō	Last males extinct on the mainland c. 1980s/1990s	High	?	?	Size and suitability of site and alignment with national recovery objectives
Multi-species pest control to eradication or zero density of all mammalian pests, including mice.	Highly threatened herpetofauna, e.g. McGregor's, robust, and Whitaker's skink, Duvaucel's gecko, tuatara	Extinct on the mainland	?	?	?	Vulnerability to mice and dispersal abilities unknown
	NZ snipe	Extinct on the mainland	?	?	?	Vulnerability to mice and dispersal abilities unknown
	Large native and endemic threatened invertebrates, e.g. giant wētā, weevils and beetles	Mostly extinct on the mainland	?	?	?	Vulnerability to mice unknown Dispersal abilities unknown but probably low

Box 2: Can we really characterise adaptive variation in threatened species?

With the emergence of next-generation sequencing in applied conservation has come the promise of characterising adaptive variation (Flanagan et al. 2017). Approaches that incorporate information from the entire genome (e.g., whole-genome resequencing) or target putatively adaptive regions (e.g., SNP arrays) should dramatically increase our ability to identify adaptive genomic variants. There is growing interest in incorporating this additional information into translocation decisions (e.g., Hoffmann et al. 2021; Seaborn et al. 2021), but there are caveats. To date, successful characterisation of adaptive variants has largely been restricted to species, with a high-quality reference genome and comprehensive genomic and non-genomic data, such as informative fitness measures and environmental data (Attard et al. 2017; Flanagan et al. 2017; Harrisson et al. 2017). For these well-studied species, we are better able to explore a range of analytical approaches (e.g., outlier-detection based approaches, genotype-environment association studies and genome-wide association studies) (Rellstab et al. 2015). Further, new studies indicate that our chances of detecting locally-adaptive variants are highest in large, connected populations distributed across heterogenous habitats (e.g., Barrett et al. 2019). Thus—while genomic approaches are more likely to capture regions of the genome under selection compared to genetic approaches—characterising adaptive variation may still prove challenging for many threatened species (Fig. 3). Although characterising adaptive variation remains a promising conservation genomics tool, scientists and practitioners must be realistic about how readily it can be incorporated into translocation decisions.

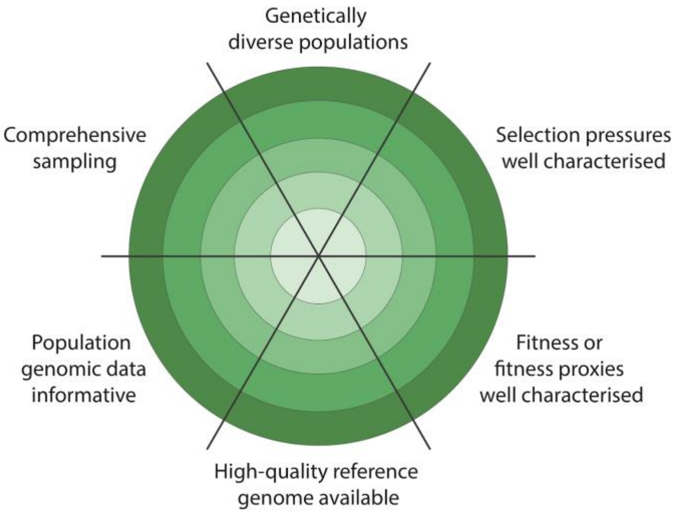

Figure 3. A novel framework for assessing key criteria for characterising adaptive variation in threatened species, including whether (i) populations are sufficiently large and genetically diverse to differentiate between selection and genetic drift; (ii) differential selection pressures are well characterised; (iii) fitness measures—or suitable proxies—are well characterised; (iv) a high-quality reference genome is available; (v) population genomic data adequately captures genome-wide diversity; (vi) comprehensive sampling is representative of relevant locally adapted populations. The further each coloured section extends toward the green circle edge reflects how well that consideration is met. Overall image design after Suding et al. (2015).