Biological Conservation 159 (2013) 313–320

Contents lists available at SciVerse ScienceDirect

Biological Conservation

journal homepage: www.elsevier.com/locate/biocon

Molecular data contradicts historical records and cautions translocation of the Lord Howe Island masked owl

Fiona E. Hogan [a,*], Catriona Campbell [b], Katherine A. Harrison [c], David Milledge [d], Raylene Cooke [b]

[a] School of Applied Sciences and Engineering and Australian Centre for Biodiversity, Monash University, Gippsland Campus, Victoria 3842, Australia
[b] School of Life and Environmental Sciences, Deakin University, 221 Burwood Hwy., Burwood, Victoria 3125, Australia
[c] School of Biological Sciences and Australian Centre for Biodiversity, Monash University, Melbourne, Clayton Campus, Victoria 3800, Australia
[d] Landmark Ecological Services, PO Box 100, Suffolk Park, New South Wales 2481, Australia

ARTICLE INFO

Article history:
Received 24 April 2012
Received in revised form 3 October 2012
Accepted 4 December 2012

Keywords:
Masked owl
Microsatellite
Mitochondria
Phylogenetic
Translocation
Island
Pest species

ABSTRACT

Masked owls, reputedly all of the Tasmanian race (*Tyto novaehollandiae castanops*) were introduced onto Lord Howe Island (LHI) in the 1920s in an attempt to control the black rat (*Rattus rattus*). This attempt, however, has been unsuccessful and a co-eradication of the rats and masked owls has been planned to reduce the threat to endemic species and breeding seabirds on the island. As the Tasmanian masked owl is considered endangered, translocation of LHI masked owls to Tasmania has been suggested. Before translocation is considered the ancestry of the LHI masked owl needs to be confirmed, as LHI masked owls are typically smaller and paler than individuals occurring in Tasmania. Here we sequenced three sections of mitochondrial gene regions: cytochrome *b*, ATP6 and ND3 to assess the provenance of the LHI masked owl and screened a suite of microsatellite loci isolated from the barn owl (*Tyto alba*) to assess contemporary divergence. Phylogenetic analysis revealed two clades, one exhibited by individuals from LHI and south-eastern mainland Australia and the second by those from Tasmania. Cross species amplification of microsatellite loci was successful, with 18 loci polymorphic. Genotypic data revealed significant sub-structuring between LHI, south-eastern mainland Australia and Tasmania. Data presented here indicate that the south-eastern mainland masked owl was introduced to LHI and subsequently reproduced. The genetic integrity of the LHI masked owl population is therefore questionable and as such LHI individuals may not be suitable for translocation to Tasmania.

Crown Copyright © 2012 Published by Elsevier Ltd. All rights reserved.

1. Introduction

Introduced species are one of the most destructive threatening processes within ecosystems worldwide (Courchamp et al., 2003). These species have been both unintentionally and deliberately introduced to many ecosystems, where they have established populations and facilitated the extinction of numerous native and endemic species (Donlan et al., 2003). One global ecosystem that has been severely affected by such species is islands. Island ecosystems are highly susceptible to introduced species due to the high level of endemism resulting from their isolation (Fordham and Brook, 2010). Management of introduced species on islands, however, can be complex due to interactions that have developed between both introduced and native species and between introduced species themselves. Consequently total removal of introduced species on islands must be approached with caution, but can be highly successful if achieved, due to the remoteness of the area involved (Courchamp et al., 2003). All issues associated with removal require consideration, for example, what happens when the introduced species' ancestral population is listed as threatened? In this situation eradication of the introduced species can be controversial and other management options should be considered to ensure the best outcome for the affected ecosystem and the species in question. An alternative option to eradication could be translocation, where individuals are removed from an island and relocated amongst their ancestral population or used for *ex situ* conservation from which the ancestral population could be re-stocked in the future. An example of where such a strategy has been successful is in the case of the New Zealand brush-tailed rock-wallaby (*Petrogale penicillata*) which was introduced from Australia to New Zealand in the early 1870s (Eldridge et al., 2001). The brush-tailed rock wallaby became well established in New Zealand, which had a significant impact on indigenous flora and fauna. Eradication of the wallaby is being undertaken, and as part of the eradication process wallabies have been translocated back to Australia to aid conservation of dwindling ancestral populations.

* Corresponding author. Address: School of Applied Sciences and Engineering, Monash University, Gippsland Campus, Northways Rd., Churchill, Victoria 3842, Australia. Tel.: +61 3 5122 6466; fax: +61 3 5122 6738.
E-mail address: fiona.hogan@monash.edu (F.E. Hogan).

0006-3207/$ - see front matter Crown Copyright © 2012 Published by Elsevier Ltd. All rights reserved.
http://dx.doi.org/10.1016/j.biocon.2012.12.006

Successful translocation depends on many factors, including the number of individuals released, pre and post translocation environments, demography, logistics of the program (Griffith et al., 1989; Sigg, 2006), whether the original threat has been removed (Fischer and Lindenmayer, 2000) and the genetic makeup of the population involved (Moritz, 1999). Obtaining genotypic information from individuals to be translocated is crucial to the success of the translocation (Larson et al., 2002). This is especially true when translocated individuals are to be integrated with an existing population as the introduction of new alleles can break up co-adapted gene complexes and break down local adaptation resulting in a reduction in the fitness of the recipient population.

The Lord Howe Island (LHI) masked owl (*Tyto novaehollandiae castanops*) represents an example of a native species introduced to an island that is currently considered a pest. The reputed ancestral population of the LHI masked owl, the Tasmanian masked owl (*T. n. castanops*) (Hindwood, 1940; Hutton, 1991), however, is listed as endangered under the Tasmanian Threatened Species Protection Act 1995. LHI was listed as a World Heritage Property in 1982 for its natural values as an example of outstanding natural beauty, containing habitats of considerable importance for *in situ* conservation of its biodiversity (Department of Environment and Climate Change, 2007). The island supports a diverse biota with a high level of endemic species, including the threatened Lord Howe woodhen (*Gallirallus sylvestris*), Lord Howe Island gecko (*Christinus guentheri*) and Lord Howe Island skink (*Cyclodina lichenigera*). There are important breeding colonies of threatened seabirds including most of the world's population of the providence petrel (*Pteradroma solandri*) (Department of Environment and Climate Change, 2007).

Masked owls, reputedly of the Tasmanian race (*T. n. castanops*) were introduced to LHI between 1922 and 1930, along with a number of other Australian and North American owl species to help control the introduced black rat (*Rattus rattus*). The masked owl was the only species to become established and is suggested to have contributed to the extinction of the LHI race of the southern boobook (*Ninox novaeseelandiae albaria*) in the 1950s through competition for resources (Hutton, 1991). The current density of masked owls on LHI is uncertain, although Milledge et al. (2010) estimated the population at between 20 and 30 pairs, and later (2011) at 20 pairs with a small number of non-breeding individuals. These estimates are unusually high for large forest owls which are territorial and generally require large home-ranges (Cooke et al., 2006). By comparison, in Tasmania, an area the size of LHI (1455 ha) would be unlikely to support more than three pairs of masked owls (Milledge et al., 2010). Despite this high density, the masked owl population on LHI has not significantly reduced the black rat population and a large scale poisoning programme to completely remove all rodents (rat and house mouse (*Mus musculus*)) from LHI is planned (Lord Howe Island Board, 2009). The removal of rodents from LHI should greatly benefit biodiversity conservation; however, their removal without the coincident removal of owls could actually have a negative effect, as the owls would be forced to find alternative prey to fill their main dietary requirement. Species likely to suffer from such a prey base shift include endemic species such as the Lord Howe Woodhen and the Lord Howe Currawong (*Strepera graculina crissalis*), as well as breeding seabirds. A co-eradication program which simultaneously removes the masked owl and rodents from the island will therefore deliver the greatest biodiversity benefits.

The most appropriate eradication method for the removal of masked owls from LHI has yet to be determined. One of the major issues in the decision is that its assumed ancestral population, the Tasmanian masked owl, is listed as endangered due to small population size (approximately 615 pairs) and habitat loss (Garnett et al., 2011). LHI masked owls are also suggested to have differentiated from the ancestral population over their 90 years of isolation, as LHI individuals measured are smaller than their Tasmanian counterparts (Milledge, 2011). The observed size difference could be due to the smaller size of the main prey item (black rats) on LHI compared to the range of prey in Tasmania e.g. bandicoots, possums and the European rabbit (*Oryctolagus cuniculus*) (Mooney, 1993). Smaller size could assist manoeuvrability in the densely vegetated forest and shrubland habitats of LHI, enabling more efficient capture of the agile, scansorial black rat. An alternative or concomitant explanation could be related to Bergmann's Rule which predicts that individuals of the same species are smaller in the lower latitudes of their range (Milledge et al., 2010). Milledge (2011) found that the mean morphometric data for a small sample of LHI masked owls measured (both males and females) fell in between the means for Tasmanian and mainland birds, which could suggest either interbreeding between the two or divergence of the Tasmanian birds. The paler colour, however, of many LHI owls is more consistent with the south-eastern mainland masked owl population than the Tasmanian (although the pale morph occurs in Tasmania); and therefore further questions the origin of the LHI population.

The mechanism for removing the masked owl from LHI needs careful consideration. Options include shooting, capture and euthanasia, or capture and translocation. The first two options may not be appropriate if the LHI population can serve as an "insurance population" for the endangered ancestral population. Before management decisions regarding the eradication of the masked owl from LHI are made, there is a clear need to establish the genetic affinities (as the introduction of deleterious genes could be a concern) and potential importance of its population which would include resolving the taxonomic classification of the masked owl in Australia.

Due to advancements in molecular and information technology, DNA can now be readily used to address ecological and taxonomic questions. A combination of mitochondrial and microsatellite markers can be used to assess sub-specific taxonomy, and the levels and nature of genetic variation (Roberts et al., 2011). Mitochondrial DNA is relatively conservative and can provide information for taxonomy, for example, Norman et al. (1998) used mitochondrial sequencing to confirm the taxonomic affinity of the endangered Norfolk Island boobook owl (*Ninox novaeseelandiae undulata*) in an attempt to conserve the genetic integrity of the species. Microsatellites are short tandem repeat sequences (located in the nuclear genome) which are hyper-variable and can provide information on contemporary divergence, population size, mating systems, inbreeding and can be used to equivocally identify an individual.

Here we first investigated whether the LHI masked owl originated from the island of Tasmania and/or from the south-eastern Australian mainland by sequencing partial sections of cytochrome *b*, ATP-6 and ND3 in the mitochondrial genome. Secondarily we screened a suite of barn owl (*Tyto alba*) microsatellite markers for their application in the masked owl and then used the genotypic data to assess contemporary divergence.

2. Methods

2.1. Sample collection

Previously collected individual masked owl samples were obtained from LHI ($n = 6$). Samples included tissue and/or plucked feathers from frozen deceased birds. For comparison, tissue was obtained from three races of masked owl, south-eastern mainland *T. n. novaehollandiae* (Victoria $n = 6$ and New South Wales $n = 4$), Tasmania *T. n. castanops* ($n = 19$) and Melville Island *T. n. melvillensis* ($n = 1$) (Fig. 1). A sample from a single barn owl (*Tyto abla*) was

Download English Version:

https://daneshyari.com/en/article/6300958

Download Persian Version:

https://daneshyari.com/article/6300958

Daneshyari.com