



Original research article

Bridging the conservation genetics gap by identifying barriers to implementation for conservation practitioners

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HIGHLIGHTS

- Conservation practitioners want to use genetics, but do not routinely do so.
- This issue is most acute in control of disease and invasive species.
- The main barriers to use of genetics in conservation are funding and expertise.
- Practitioners want to work with geneticists, but are unsure how to reach them.
- Researchers must facilitate better communication with practitioners.

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ABSTRACT

Despite its recognised importance for species' persistence, integrating genetics into conservation management has proved problematic, creating a “conservation genetics gap”, which could widen with the advent of advanced genomic techniques. Bridging this gap requires a clear understanding of the barriers to use of genetics by conservation practitioners, but few (if any) papers on this topic involve direct consultation with practitioners themselves. We surveyed 148 conservation practitioners in New Zealand's Department of Conservation regarding their attitude to, knowledge of, and experiences with genetics for conservation. Although practitioners were largely receptive to using genetics for conservation management, access to expertise and funding remains a barrier to use. Practitioners would like to collaborate with geneticists at universities or other institutes, but do not necessarily know who to talk to or fully understand how genetics might benefit them. We contend these barriers or similar likely exist at an international level, suggest ways they might be overcome, and emphasise the need for clearer communication between geneticists and practitioners.

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1. Introduction

Genetics is a useful tool for conservation, but it is routinely not integrated into conservation management strategy. The potential of genetics to inform conservation was first formally suggested over 40 years ago (Frankel, 1974) and there is now an entire research field devoted to conservation genetics (Allendorf et al., 2013; Frankham et al., 2010). Applications

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of genetics to conservation range from monitoring biodiversity (Thomsen and Willerslev, 2015), to wildlife forensics (Johnson et al., 2014; Ogden, 2011), and from defining conservation units (Palsbøll et al., 2007) to detecting hybrids (McKelvey et al., 2016). The rapid development of genomic techniques, such as the generation of large genetic marker panels and whole genome sequencing for non-model species, has the potential to add even more power to conservation genetic studies (Allendorf et al., 2010; Taylor and Gemmell, 2016). Crucially, after decades of argument (e.g. Caro and Laurenson, 1994; Craig, 1994), it is now clear that genetic diversity and inbreeding can influence a species' likelihood of extinction (Frankham, 2010; O'Grady et al., 2006). Preserving adaptive potential has also been recognised as important to ensuring long-term persistence, especially in the face of climate change (Harrisson et al., 2014; Sgrò et al., 2011). However, the inclusion of genetics in species management plans is usually the exception rather than the rule, especially outside the USA. While genetic data or plans to collect it are currently incorporated into 82% of species recovery plans in the USA, only 52% of Australian and 17% of European plans do the same (Pierson et al., 2016). Only 10% of species recovery plans across these three geographic areas consider key concepts such as effective population size and inbreeding (Pierson et al., 2016). In conservation policy documents, the most commonly mentioned genetic concept is genetic diversity, but it features in only 50% of national and provincial conservation policy documents in Australia, 30% of those in Canada and 18% of those in South Africa (Cook and Sgrò, 2016). Genetic diversity is usually discussed quite generically in policy documents and there is a clear mismatch between the concepts emphasised in conservation genetics research and in conservation policy (Cook and Sgrò, 2016). Similar issues have been noted in Latin America (Rodriguez-Clark et al., 2015) and the countries bordering the Baltic Sea marine protected area (Laikre et al., 2016). This particular research implementation gap has come to be known as the “conservation genetics gap” (Haig et al., 2016; Hoban et al., 2013b; Shafer et al., 2015).

The drivers of the conservation genetics gap have been discussed extensively, but few data have been collected to establish why this gap persists. Various conservation genetics researchers have hypothesised that the reasons for the gap could include: use of jargon by geneticists combined with poor communication between researchers and conservation practitioners (Hoban et al., 2013a); genetic factors being perceived as long-term threats and thus of lower priority than immediate concerns (Cook and Sgrò, 2016; Jamieson et al., 2006); perceived costs of acquiring genetic data (Vernesi and Bruford, 2009); a lack of awareness among conservation practitioners of the benefits of genetics (Pierson et al., 2016); a lack of access to published research (Cook and Sgrò, 2016); the complexity of linking genetics to demographic data (Waples et al., 2008); and a perception that genetics is inappropriate to address specific conservation issues (Haig et al., 2016). There are also few funding or academic incentives for geneticists to bridge the gap with practitioners (Haig et al., 2016; Shafer et al., 2015). To our knowledge, there are no published studies on the drivers of the conservation genetics gap that incorporate feedback from conservation practitioners in addition to the opinions of researchers. Researchers have surveyed practitioners to establish that the gap exists (Hoban et al., 2013b), but not why it is there. The increasing use of genomics has the potential to exacerbate the conservation genetics gap, as complex concepts within this field are couched in jargon that can cause confusion. Now, more than ever, it is important to ascertain the forces behind the conservation genetics gap, before rapidly evolving genomic technologies make it too wide to cross. Here, we identify drivers of the conservation genetics gap by collecting data directly from conservation practitioners, using New Zealand's main government conservation agency as a case study.

A conservation genetics gap was formally identified in New Zealand (NZ) in 2006 (Jamieson et al., 2006). Genetic issues associated with small and isolated populations had historically been ignored by NZ's conservation practitioners because NZ species were considered less vulnerable to threats such as inbreeding (e.g., Craig et al., 2000), and because there were more pressing threats (e.g., introduced predators) to contend with (Jamieson et al., 2006). Genetic factors are now included in recovery plans for several NZ species (e.g., Cresswell, 1996; Holzapfel et al., 2008; Wickes et al., 2009) but are not fully integrated into the threat classification system (Townsend et al., 2008). The extent to which attitudes to conservation genetics have shifted among NZ conservation practitioners since 2006 is unclear. We assessed attitudes and identified barriers to use of genetics in species management through a survey of conservation practitioners working for NZ's Department of Conservation (DOC). Our survey addressed: (i) perceptions of genetics; (ii) implementation of genetics; (iii) barriers to use of genetic tools; and (iv) understanding of genomics. We identify factors that could perpetuate a conservation genetics gap in NZ, and use these factors to devise strategies to close the gap. We acknowledge that our study represents a case study in one country and discuss how our results might translate to other locations.

2. Methods

2.1. Sampling

The DOC is NZ's main government conservation body, employing 1637 staff, with ~400 directly involved in biodiversity management. Survey data were gathered using internal email lists targeting the majority of these 400 staff (hereafter referred to as practitioners). An essential part of any survey effort is ensuring respondents are representative of the wider group being targeted (Groves et al., 2011, pp. 40). To compare our respondents with DOC staff in general, we also obtained data on the age-structure, and length of service for all DOC employees. Data on educational background for all DOC staff were not available. We tested for differences between the age, and length of service distributions in our sample and in DOC overall using a chi-squared test of proportions.

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