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Short communication

The importance of non-academic coauthors in bridging the conservation genetics gap

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ABSTRACT

DNA sequence data from genetic (traditional) and genomic (high-throughput) instruments have been highlighted as important information for biodiversity conservation. Despite a high number of publications, a gap has emerged between fundamental research and real-world application, meaning genetic studies often do not have a substantive link to policy or conservation science. We conducted a meta-analysis on conservation studies using genetic and genomic datasets and found the majority of publications were on species that were data deficient or of low conservation priority (66%); only 38% of studies specifically identified how the data could inform conservation or management through clearly stated recommendations for action or policy. Importantly, our mixed-model found a 2.5-fold increase in the odds of a publication making a specific recommendation when non-academic affiliated authors were included. This suggests the conservation genetics gap has arisen, in part, by academic authors failing to make explicit links to policy and conservation outcomes. Conservation geneticists should refrain from hyperbole and collaborate with agency and non-government scientists to accelerate development and implementation, and ultmately help bridge the conservation genetics gap.

1. Introduction

Conserving biodiversity is a difficult task fraught with competing interests and often limited knowledge of species and biological systems. Governments, academics, and conservation practitioners are faced with the immense challenge of stemming the rapid loss of species and habitat under limited budgets in an increasingly polarized world. Working in an interdisciplinary science, conservation biologists are quick to try new tools, and any promising technological advancements garner much attention in this regard (Pimm et al., 2014). Genetics and genomics, the latter defined as high-throughput sampling of nucleic acids (McMahon et al., 2014), have been highlighted as important tools for conservation (Frankham, 2003; Ouborg, 2010; Ouborg et al., 2010). Genetics has numerous applications of conservation relevance such as mark-recapture, parentage and population assignment, and estimates of effective population size; these data have made clear inroads with well-known examples like Atlantic Salmon management (Nielsen, 1998), seed collection programs (Silva et al., 2008), and the restoration of the Florida Panther (Johnson et al., 2010). The impact of genomic data on conservation is less clear and debated (see Cronin, 2007; Shafer et al., 2015, 2016; Garner et al., 2016); in principle, genomic data should increase the precision and accuracy of demographic estimates and allow for the identification of adaptive loci (McMahon et al., 2014). It has also been suggested that analysis of whole genomes will become routine task in conservation biology (Fuentes-Pardo and Ruzzante, n.d.).

Despite the high number of publications and noteworthy examples, a gap has emerged between basic genetic and genomic research, and real-world applications; this has been dubbed the conservation genetics gap and is reflected by the limited integration of genetic data into conservation management (Hoban et al., 2013b; Shafer et al., 2015; Haig et al., 2015; Taylor et al., 2017). European researchers were among the first to recognize the gap and in 2012 initiated the project known as Conservation Genetic Resources for Effective Species Survival (ConGRESS); ConGRESS had the stated goal of bridging the gap and providing (genetic) resources for biodiversity managers and policy makers (Hoban et al., 2013a). Following a European Science Foundation funded meeting on the role of genomics in conservation, Shafer et al. (2015) argued that the gap would only become exacerbated in the genomics era due to the infancy of the field and uncertainty surrounding datasets and bioinformatics tools. In response, Garner et al. (2016) provided a list of genomic case studies showing real-world

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application, although these examples were restricted to economically important species and the widespread implementation of genomic tools was still a limiting factor (Shafer et al., 2016).

It is clear that some disconnect exists between genetics research and its application to conservation issues. In a survey of 150 New Zealand conservation practitioners, Taylor et al. (2017) found that access to expertise and funding were the main barriers to uptake and implementation. While access to funds and expertise might be limiting factors, it does not explain the absence of genetic targets and tools in conservation priority and implementation plans (Carter et al., 2000; Groves et al., 2002; Groves, 2003; Knight et al., 2006). Similarly, only 1 of the 100 so-called questions of importance to the conservation of global biological diversity mentioned genetics, and this was in relation to genetically modified organisms (Sutherland et al., 2009). Collectively, this suggests that many, perhaps most, conservation problems do not need genetic or genomic solutions and leads to an alternative explanation of the conservation genetics gap that has to do with the perception of molecular tools having limited use in solving most conservation problems.

The idea of a perception problem is not unfounded (Amos and Balmford, 2001). When surveyed, stakeholders ranked access to genetic resources 18th out of a list of 35 priority issues (Nagulendran et al., 2016). Anecdotally, such a low ranking for molecular tools among conservation priorities and planning is not uncommon. Even though the majority of practitioners said they would use genetic data if it were available (Hoban et al., 2013b), the perceived lack of real-world applications suggests more than expertise and access being a barrier. When presented with a problem, practitioners and committees generally consult the scientific literature and there is an increasing value placed on peer-reviewed conservation science (Game et al., 2015). If publications provide nebulous applications and inaccessible tools with respect to a subdiscipline like conservation genetics, this could create a scenario where practitioners might simply not seek out tools like genetic and genomic assays because their real-world applications are not clear (sensu Soulé, 1985). Here, we conducted a meta-analysis of conservation genetic and genomic studies and collected data on author affiliation, the conservation status of studied species, the molecular marker used, and the conservation recommendations made in the study. The aim of this meta-analysis was to shed light on the actors and drivers behind the conservation genetic research-implementation gap, and offer solutions to better link genetic and genomic research to policy and conservation action.

2. Methods

We collected data from four peer-reviewed journals; two of which are conservation-oriented and publish genetic research, while the other two focus on genetics research but include papers of conservation interest. The journals were: Conservation Genetics (CG), Biological Conservation (BC), Evolutionary Applications (EA), and Molecular Ecology (ME). Additional conservation journals were screened but had a small number of genetic and genomic studies and were excluded. Using the keyword search “genetics” within CG, BC, and EA, original empirical research articles from the past ten years (2006–2017) were randomly collected and retained if they focused on a specific species, or multiple named species. The search term “genomics” was also entered within CG, BC, and EA and as many articles as possible were collected based on the aforementioned criteria. Within ME the keyword “conservation” was searched because the journal publishes more than conservation research. We aimed to retain 75 studies from each of the four journals to achieve a representative sample of the literature.

The following information was collected from each article: publication year, number of authors, author affiliations (i.e. government, academic, or non-governmental), focal species and taxonomic grouping (class or kingdom), the species' current global conservation status, the species' regional status if reported in the article (NA if not), the class of molecular marker(s) used (*genetics* being microsatellites, single gene sequencing, low-throughput single nucleotide polymorphism (SNP) assays; *genomics* being tools using high-throughput sequencing or genotyping such as RADseq, SNP chips, whole-genome re-sequencing). In the event that more than one species was included in an article, only one, randomly selected species was included in our analysis. The current global conservation status of each species was obtained from the IUCN RedList or NatureServe. We merged the two ranking systems to create a conservation status scoring system ranging from 0 (i.e. least concern) to 2 (i.e. critically endangered; Table S1). In the event that a species was not listed in one of these collections or article they were given a NA in our database.

We scored the specificity of conservation recommendations provided in each article. We considered recommendations on a binary scale – generic or specific – where a generic recommendation would be broad statements with no explicit direction on how the data can be used to inform conservation and management, or reference to a change in policy or legislation (see also Table S2 for scoring criteria). For example, a generic recommendation would be “we propose maintaining genetic diversity of the species to ensure long-term viability.” This statement reflects a truism in conservation biology. An article was ranked as having a specific conservation recommendation if there was a clear course of action suggested, stated implementation methods, or policy changes that were advocated for. A specific example would be “we propose translocating 10 animals from the mainland to limit genetic erosion and maintain 90% of current genetic variation.” This statement gives direction to a conservation action informed by the genetic or genomic data. If an article proposed an Evolutionary Significant Unit (ESU) or Management Unit (MU) it was scored as specific. All articles were independently scored at least twice.

All summary statistics, statistical models, and data visualizations were conducted in R v. 3.4.1. The repeatability of scoring the conservation recommendation, meaning the same recommendation score was given by both evaluators, was assessed using Krippendorff's α-Reliability, where an α of 1 equals perfect reliability and 0 equates to random chance. As the data were subdivided into two groups (repeated and non-repeated conservation recommendations), we compared the authorship composition (i.e. number of academic, government, non-government authors) using a multivariate analysis of variance (MANOVA). The remaining analysis focused only on the repeated data set. A number of generalized linear mixed models were fitted to the data with the journal in which the study was published as a random effect (i.e., intercepts varying by journal). The four tested predictor variables used were proportion of non-academic authors (to simplify the model we merged government and non-government authors into one variable for non-academic affiliations), global conservation status (categorical values of 0, 1, 2, described in Table S1), marker type and taxonomic group (categories listed in Table 1). Factors that were significant based on an α of 0.05 in a univariate model with a random effect were added to the final model. To aid in interpretation of the logistic model coefficients were converted to odds-ratios, which is the relative odds of the outcome given a condition.

3. Results

In total we reviewed 300 publications from 2006 to 2017 in four scientific journals that focused specifically on, or have a section devoted to, conservation and wildlife management. The mean authorship breakdown and taxonomic affiliation of research organisms, seen in Table 1, shows that academic affiliated authors constituted the majority of coauthors (61–70%), followed by government (18–27%) and non-government (7–18%). We had a scoring repeatability of 77% (231 of 300 studies) which is better than chance (Krippendorff's $\alpha = 0.56$). The authorship breakdown did not differ between repeated and non-repeated studies based on a MANOVA (Pillai's trace = 0.003, $F(1, 298) = 0.323$, $p = 0.808$). The majority of studies were on species of low

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