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Title

Conservation Genetic Resources for Effective Species Survival (ConGRESS): bridging the divide between conservation research and practice

Running Title

Advancing genetic data in conservation policy

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Abstract

Policy makers and managers are increasingly called upon to assess the state of biodiversity, and make decisions regarding potential interventions. Genetic tools are well-recognized in the research community as a powerful approach to evaluate species and population status, reveal ecological and demographic processes, and inform nature conservation decisions. The wealth of genetic data and power of genetic methods are rapidly growing, but the consideration of genetic information and concerns in policy and management is limited by currently low capacity of decision-makers to access and apply genetic resources. Here we describe a freely-available, user-friendly online resource for decision-makers at local and national levels (http://congressgenetics.eu), which increases access to current knowledge, facilitates implementation of studies and interpretation of available data, and fosters collaboration between researchers and practitioners. This resource was created in partnership with conservation practitioners across the European Union, and includes a spectrum of taxa, ecosystems and conservation issues. Our goals here are to (1) introduce the rationale and context, (2) describe the specific tools (knowledge summaries, publications database, decision making tool, project planning tool, forum, community directory), and the challenges they help solve, and (3) summarize lessons learned. This articles provides an outlook and model for similar efforts to build policy and management capacity.

Keywords

capacity-building; conservation planning; data; decision-making; management; online resource; policy

1. Introduction

The potential applications of genetic data and tools, and the importance of genetic concerns, in conservation policy and practice are numerous and growing (Frankham 2010). Genetic data and powerful computational analyses are now routinely used to reveal demographic processes, identify gene flow and barriers, assist prioritization of population protection, detect hybrids, and more. The increasing maturity of conservation genetics as a research discipline, with hundreds of peer-reviewed articles in the field each year (Vernesi et al. 2008), does beg the question: how do we ensure that the wealth of knowledge produced by researchers is actually applied to practice and policy? This question is familiar in conservation biology generally (Knight *et al.* 2008; Githiru *et al.* 2011), but is particularly thorny for conservation genetics- the available laboratory and computational tools are diverse and rapidly evolving, the gap between recommendations derived from assumption-laden models and on-the-ground constraints is substantial, and the concepts and research results are often ensconced in jargon and academic debates. The impression can be that conservation genetics is locked in an ivory tower rather than being shared and discussed by a community oriented towards action.

Indeed, the relative scarcity of genetics considerations in nature conservation policy at the global and European Union (EU) level (Laikre 2010) despite clear opportunities for such consideration (Santamaria & Mèndez 2012; Hoban *et al.* 2013b), suggests that the scientific knowledge base is largely untapped by conservation practitioners and decision-makers, regardless of recurring reviews of topics and techniques in the academic literature (DeSalle & Amato 2004; Allendorf *et al.* 2010). If the goal of conservation genetics research is to contribute to monitoring and evaluating genetic biodiversity, and developing policy regarding genetic resources (and thus, also conserving the species and ecosystems that depend on sufficient genetic diversity), the generation and publication of genetic data and theories are insufficient. Improved synthesis, clarification, and dissemination of knowledge is necessary (Osmond *et al.*

2010). Simultaneously, the capacity of managers and policy-makers to absorb and use key information must be enhanced through education, training, and practical tools. In addition, academics need to be further empowered to conduct genetic research directed at specific conservation problems (Laurance *et al.* 2012). On December 1st 2012, the ConGRESS project launched a web-portal (http://www.congressgenetics.eu/) to tackle these challenges by collating research results, summarizing foundational knowledge (e.g. for what applied questions can genetics be used, how can relevant genetic information be obtained), explaining best practice, facilitating the planning of genetic studies and interpretation of results, and establishing networking and collaboration opportunities. ConGRESS (Fig 1), which may be a useful model for capacity-building, features six sections (plus news/event announcements). Notably, there are diverse entry points allowing access by users with different background knowledge, goals (e.g. policy, learning, research), and time commitments (e.g. practitioners/managers, decision-makers, technicians, researchers).

2. How do the elements of ConGRESS address specific challenges?

The importance of communicating scientific outcomes to managers and policy makers is widely recognized but generally unsuccessful, partly because conservation researchers rarely utilize accessible, concise language (Laurance *et al.* 2012). Ensuring basic familiarity with central topics can provide a common vocabulary for discussion, and guard against misunderstandings or misinterpretation (Osmond *et al.* 2010). The first output of ConGRESS is a "Knowledge Pack," comprising a series of downloadable information sheets explaining genetic concepts and issues in non-technical language, designed for uptake by policy-makers and managers with little or no genetics background. These short, engaging documents also summarize best practice for genetic-based interventions, including the use of new laboratory and analytical techniques, and types of genetic data. In addition, there is a one-hour annotated slideshow presentation explaining how conservation genetics is relevant to management, with recent case studies (e.g. Vähä et al., 2007; Bourke et al., 2010) to illustrate different applications of genetic data in conservation. This material is available in five main European languages (English, French, German, Italian and Spanish) to help end-users achieve genetics or conservation genetics literacy even without access to or understanding of the primarily English-only academic literature.

Important advances in conservation theory and tools reported in peer-reviewed journals often remain inaccessible and unusable to practitioners, although journals targeted to practitioners (e.g. Conservation in Practice, Conservation Evidence) as well as Open Access publications are helping to unlock the literature. To distill the academic genetics literature into a list of papers of conservation relevance, the "Publications Database" is a collection of >3000 genetics-based articles applicable to conservation, searchable by taxon, genetic marker type, subject (conservation issue), and keyword. Each entry is linked to Google Scholar and the Encyclopedia of Life (http://eol.org). We anticipate that the database will help non-academics identify a broad range of possible genetic applications, as well as the knowledge, resources and methodologies available for their taxa or topic. Equally, genetics specialists can use the database to identify and study policy and management issues.

Interpreting patterns of genetic variation in light of conservation management requires data with statistical power to detect population processes (e.g. migration) relevant to choosing appropriate interventions (e.g. supplemental stocking, protection status). To collect such data requires a sampling scheme tailored to the study goal, in terms of number and type of markers, and number and distribution of individuals sampled (Ryman *et al.* 2006; Schwartz & McKelvey 2008). The "Sample Planning Tool" allows testing the effectiveness of possible sampling schemes, before project implementation, to optimize study design and therefore best apportion limited financial or technical resources (Hoban, *et al.* 2013a). It may be used directly in study design, help calculate funding needed, or be used by an agency to evaluate feasibility of a proposal. It may also be used to determine the power (and reliability) of previously collected datasets. This tool was recently used to investigate whether practitioners can detect realistic population declines, including a case study in a forest tree (Hoban et al. 2013c).

Decision-support tools are important for guiding decision-makers to specific actions, and can also be used to spark discussions and highlight knowledge gaps (Howes et al. 2009). The "Decision-Making Tool" provides a formal path for practitioners to identify how conservation genetics can help them address familiar management issues and questions. Users choose among a series of topic options to refine their question, leading to an Outline/Recommendations page explaining the issue, why and when it is of concern, and which genetic approaches and data are suitable. Applications on the chosen topic are illustrated with case studies exemplifying best practice, and advice is given about practical aspects of establishing a study.

The paucity of communication and collaboration between researchers and practitioners is often an obstacle to effectively applying conservation knowledge (Smith *et al.* 2009; Hoban & Vernesi 2012). To help facilitate contacts between local experts in diverse fields and establish collaborations, we created a "Community" section, a directory of conservation professionals (agency officials, geneticists, enforcement officers), searchable by expertise (species, subject), country or keyword. Registration is free and open to all. This expandable list is foreseen as an effective way to design robust projects, share resources, match management and policy questions to appropriate tools, and analyze and interpret results (Smith *et al.* 2009; Osmond *et al.* 2010).

Last but not least, the "Forum" enables open and ongoing discussion about common issues and questions, as well as sharing tips and data. Frequent enquiries include: what is the proper protocol for a given technique (e.g. DNA storage), what is a starting point to use genetics for a given species, how relevant is a particular topic or tool, where can I find genetic data, and what is the cost to conduct or commission a study? The fluid nature of a forum allows exploration of these queries (which may change over time), and archiving of answers for future reference. Its inclusive, democratic nature reflects the pluridisciplinarity of modern conservation efforts (Jones-Walters & Cil 2011; Torkar & Mcgregor 2012).

Each section is explicitly linked to the others, e.g. links from the Decision-Making Tool to the Community search and to relevant pages of the Sample Planning Tool (Fig 1).

3. Lessons and Prospectus

While the scaffolding of ConGRESS (Fig 1) was determined in advance, the specific topics for the knowledge packs, the end points and issues for the decision and project-planning tools, and the search categories for the database and community were determined in a collaborative, iterative way (*sensu* Githiru *et al.* 2011). At a series of ten workshops distributed spatially across the EU, local and regional conservation professionals were engaged to identify and discuss key practitioner questions, constraints, needs, and opportunities for application of genetics in conservation. The workshops were a crucial aspect of the project, as they helped generate trust among participants, ensured input from a variety of perspectives (Jones-Walters & Cil 2011), and established a core network for the Community. Scientists also shared recent genetic data and potential projects with an audience of policy-makers and managers, who pointed out social or economic considerations. During each workshop, ConGRESS tools were tested and improved for clarity and usability. Key feedback included the need for practical information (e.g. feasibility, cost), simple language, explicit communication of risk and uncertainty by researchers (who sometimes promise too much), and examples of issues and genetic information using clear and iconic case studies. An additional lesson was that knowledge sharing projects such as ConGRESS could greatly benefit from dedicated PR personnel for communication, networking, and “scaling up”. Graphic designers and science communicators are also valuable. Lastly, a firm delineation of the target audience is necessary to tailor comprehensible messages, and a definition of the roles for project participants is essential to ensure that all professional skills are utilized and respected, e.g. policy makers must not replace researchers, nor vice versa.

The long-term goal of ConGRESS is to build coordinated infrastructure on genetic biodiversity at the EU-level, where the complications of transborder issues and national policy divergence make the need for community-wide action particularly urgent. Direct and easy access to relevant material and tools, as well as scientific advice and the experience of fellow practitioners, should contribute towards a community of professionals who are ready and able to use genetic data in policy-relevant conservation decisions. However, the long-term outlook for consideration of genetic diversity in policy and management will require additional steps beyond the resources we describe above. For example, ConGRESS workshops were successful in stimulating dialogue, sharing results and perspectives, and forging collaborative partnerships, but additional outreach, especially at local and regional levels, are needed to strengthen and expand these ties. Increased cooperation for cross-border monitoring, intervention efforts, shared protocols and data, and coordination of national policies between bordering states are also needed (López-Hoffman *et al.* 2010). Lastly, the EU-focus of ConGRESS is both a strength and a weakness: the small nature of the network allows strong ties, but some issues and taxa that are relevant in other regions of the world are not included. The development of similar resources in other continents, or globally, would therefore be valuable. We note that some users of ConGRESS may be reluctant to register; a challenge is to make as much content available as possible to non-registered users but also to provide incentive to registration, helping build the Community.

One limitation of an online resource to build the capacity of decision-makers is that the knowledge and techniques of biodiversity conservation evolve rapidly. Therefore one principal challenge for projects like ConGRESS is that they require very frequent updates. Indeed, the success of such efforts will depend on identification of and active efforts from "champion" end-users, scientists and stakeholders in governmental and non-governmental conservation or natural resource management organizations. Champions are needed to add ongoing research to the database, moderate forum topics, recruit Community members, and summarize and broadcast outcomes (including negative results) of conservation genetic studies and interventions. A useful extension of the database will be to include reports from "grey literature" or user-added results and perspectives, but this also will require extensive quality assurance and management. Lastly several issues were not addressed in the Sampling Planning Tool, such as planning projects using phylogenetics, forensics, and environmental DNA; these are high priorities for members of the conservation genetic software development community. Emerging technologies such as Next Generation Sequencing will also soon need to be added. For such updates, projects like ConGRESS must build in legacy plans and funding on a decade scale (longer than many current governmental and non-governmental funding cycles).

A more formal and complementary venture to ConGRESS would be creation of a conservation genetics interface organization (Osmond *et al.* 2010), or establishment of a working group on conservation genetics policy and practice, similar to the IUCN Conservation Breeding Specialist Group. In addition, the ConGRESS community could provide the array of viewpoints and authority necessary for consensus statements or policy briefs on relevant topics, such as Essential Biodiversity Variables (Pereira et al 2013).

The Community and Forum tools of ConGRESS will help researchers understand the needs and interests of practitioners, a critical dialogue for integrating data in conservation programs (Githiru *et al.* 2011). Researchers must then respond by developing and testing tools and methods with real-world applicability, e.g. multiple interacting species in complex, changing landscapes (Landguth *et al.* 2010), and data on local adaptations (Vasemägi & Primmer 2005). A new wave of statistical and simulation tools could help analyze data for such situations, if they are user-friendly and broadly disseminated (Frankham 2010; Hoban et al. 2012; Bertorelle et al. 2004). The Forum can enable introduction, discussion and critique of such tools, ensuring their proper use and further improvement. Such active participation from the research community is another challenge for ConGRESS, because academic researchers are constrained by the priorities of their funding agencies, high pressure to publish basic research, and few institutional incentives for applied conservation projects or policy involvement.

Lastly, ConGRESS and similar projects could be improved in the future by establishing formal but easy-to-use infrastructure for online storing and sharing large biodiversity datasets. Dryad (http://www.datadryad.org/), which features >6000 freely-accessible population genetic data files, and the Barcode of Life Database (http://www.barcodinglife.com/), which features ~2 million sequences for species identification, show that there is strong interest in sharing genetic biodiversity data. The recent forest genomics resource Cartogratree (http://dendrome.ucdavis.edu/cartogratree/) is a model of how such databases can be augmented with an easy-to-explore map, and accompanying ecological and demographic data. A similar organized and searchable collection of conservation genetic datasets would be a valuable resource.

Genetic data is well-integrated in North American conservation efforts and policy, especially for delimiting units for conservation (Fallon 2007; Howes *et al.* 2009). To truly embed, enhance and broaden consideration of genetic biodiversity in conservation within the EU and globally will require explicit recognition of genetic diversity in official policy at multiple levels. This process would be facilitated by stronger scientific agreement on how genetic diversity should be measured, valued, and monitored (Frankham 2010). This includes more precise definition of how much (and what type of) genetic diversity is crucial, and explicitly what benefits genetic diversity provides to society and the planet (Ten Brink *et al.* 2009). We hope that ConGRESS will galvanize and facilitate coordinated action on such issues, while also serving as a framework for future web-based capacity building exercises.

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Figure 1 Legend

Schematic diagram of ConGRESS web resource, showing potential entry points for simplified user groups (circles). Arrows show potential workflow between sections, but other connections are possible. Within each section is an example query (non-bold type). The issue “connectivity” is used as an example, but is only one of various problems considered in ConGRESS.