



Letter to the Editor

Finding the “Conservation” in Conservation Genetics— Progress in Latin America

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Where is the Conservation in Conservation Genetics?

Genetics has a long and successful history as an applied science, most notably in agriculture and medicine. Conservation emerged as an important application in the 1980s and 1990s, with an increasing appreciation of threats to biodiversity, as well as advances in genetic technologies, nonequilibrium theories, and computing power (Hauffe and Sbordoni 2010). An early narrow focus on genetic variation as a conservation concern in its own right (Frankel and Soulé 1981) gave way to a realization that genetic tools could also help identify and solve conservation problems (Milligan et al. 1994). As the field matured into the 2000s, textbooks appeared (Frankham et al. 2002; Allendorf and Luikart 2007) and then dedicated journals and conferences, showcasing an increasing number of elegant, cutting-edge studies. But as the organizers of one such conference asked, where was the conservation in all this conservation genetics? (Vernesi et al. 2008).

Conservation challenges start with, at minimum, a 2-species interaction: on one side the conservation target, and on another,

Homo sapiens. Genetic theories, approaches and tools may be universal, but the context that creates conservation challenges is less so. Human culture, history, economy, society all vary a great deal spatially, so a regional focus can serve to reduce complexity and to reveal patterns, facilitate comparisons and contrasts with other regions, and point to better, more effective applications.

Latin America is a region where it makes inherent sense to search for the conservation in conservation genetics. It contains a major proportion of the world's biodiversity, wilderness areas, and conservation hotspots (e.g., Mittermeier et al. 1998), and is also undergoing intense economic development. This development puts an inevitable strain on natural resources, but has also strengthened the region's scientific community, increasing technical capacity to support local solutions to local problems (Oliveira-Miranda et al. 2013; Van Noorden 2014).

This special issue of *Journal of Heredity* is the result of a decade of efforts to advance the field of conservation genetics via a focus in Latin America, culminating in a conference in Caracas, Venezuela, in May 2014. Below, we briefly examine the results of those efforts; present a simple framework that has emerged to address the application

challenge; and conclude with ideas on how the application of conservation genetics can be increased in Latin America and across the world into the next decade.

A Decade of *La Red de Genética Para la Conservación* (ReGeneC)

La Red de Genética para la Conservación (ReGeneC, or in English, The Conservation Genetics Network), was born in 2004 (Aguilera Meneses 2014). At ReGeneC's workshop-symposium that year, participants and invited speakers realized we shared a common goal: to advance the science and practice of conservation genetics in a region facing enormous conservation challenges and yet insufficient capacity in any one country to train the local scientists needed to take up these challenges. To address this problem, we built an annual, intensive course, offered 8 times thus far, in either Venezuela, Chile, Brazil or Argentina. Thirty-eight different professors have volunteered their time to teach a total of 163 students from 19 countries across the region. While technologies and analyses have come and gone, ever shifting the content of our lectures and computer labs, our core emphasis has remained unchanged and unique among similar courses worldwide: a central focus on students developing their own research projects, in their own languages, through in-depth one-on-one discussions with those professors with most experience in their project areas.

In one sense, we have clearly been "successful"; in anonymous evaluations of our most recent offering, we earned top scores (Table 1). Furthermore, our 10th anniversary celebration conference last year in Caracas had no trouble attracting 95 eager participants (both ReGeneC graduates and those new to the network) to hear 7 plenary speakers and 55 original contributions, and 50 participants in 3 pre- and post-congress short courses.

But beyond being popular, we wanted to know: have ReGeneC's efforts *worked*? We contacted all 304 course applicants for feedback; students who had applied but in the end did not attend served as controls. We asked them 7 questions about the course, their current activities, and their project results, and we received responses from 38 participants and 10 applicants who did not participate. We found that the course attracted applicants who already had a strong vocation, as both groups were highly and equally likely to still be working or studying in both genetics (86% of participants, 80% of controls) as well as conservation (76% vs. 80%). Both groups were also equally likely to have published the research they proposed as their course project (61% vs. 50%), and both agreed that the training offered in ReGeneC courses was simply unavailable in their home countries (95% vs. 100%). However, there were important differences between the 2 groups. Participants had a greater tendency to be involved in training others in conservation genetics (55% vs. 30%). Most encouragingly, more participants reported that their research had been applied in some concrete way to solve a conservation problem (33% vs. 10%).

Clearly, we have not entirely solved the application problem in conservation genetics: differences between the 2 groups were not significant. Though course participants more than tripled the rate at which their project results were applied to conservation relative to controls, two-thirds of course projects have not contributed in any concrete way. Following cohorts over longer time frames may reveal more significant differences, as the initial projects that participants

Table 1. Mean score of the most recent ReGeneC course, offered in 2013 in Misiones, Argentina, in course logistics, content and teaching quality ($n = 19$ anonymous evaluations, on a scale of 0 for worst to 5 for best)

Element	Score
Logistics	
Web site	4.58
Transportation	5.00
Meals	4.67
Communication	4.67
Housing	4.75
Snacks	4.50
Overall organization	5.00
Course content	
Diversity of topics	5.00
Clarity of teaching aims	4.83
Achievement of aims	4.83
Logical topic progression	5.00
Depth of each topic	4.67
Supporting materials	4.83
Pacing	4.67
Teaching quality	
Exams and homework	4.83
Lectures	5.00
Practicals/labs	4.83
Project discussions	5.00
Professor expertise	5.00
Responsive to questions	5.00
Summary	
Course relevant to student's goals	5.00
Would recommend course to friend	5.00
Global mean	4.84
Minimum	4.50
Maximum	5.00

Global mean is indicated in bold.

brought to the course may have been inappropriate for practical application.

A Framework for Integrating Genetic Tools into the Conservation Process

The question of how ReGeneC course graduates will choose and execute new conservation genetic research projects in the future is closely related to course contents. A 2-week intensive course is almost too short to cover evolutionary models for phylogenetic reconstruction, Bayesian clustering algorithms, or relatedness calculations (to name a few topics covered)—much less an overview of all of conservation biology. However, we have found that a simple framework can help students see that conservation genetics is much more than just the genetic study of species that happen to be threatened, and shows how the body of research presented here helps find the conservation in conservation genetics.

The framework we highlight is based on a standard conservation (or indeed any management) project cycle (Groom et al. 2006; Conservation Measures Partnership 2013). It starts with conceptualizing its problems. It then continues with prioritizing, executing, and evaluating conservation actions, before the cycle is repeated and refined until goals are reached. Addressing the major steps in this cycle has also been recognized as key in other areas of applied genetics (Houry et al. 2007). The 15 articles offered in this special issue cover not only a wide range of countries and species (from Cuba to

Chile, and trees to toads to tamarins); they come from all stages of this conservation cycle, and in many cases explicitly indicate how they expect their results will be used—or have been used—in later stages or future cycles.

Genetic tools find their greatest application in the initial stages of the conservation cycle, where defining conservation units and understanding problems dominate. The present collection reflects this, with two-thirds of contributions focused on these early stages. In the first step, the unit or target of concern must be defined: what is it we wish to conserve? The first article in this collection leads the way in the classic setting of fisheries management, which as Escobar et al. (this issue) point out, is essential work that has barely begun in the enormous freshwater fisheries of the Amazon and Orinoco. Their research reveals that the commercially important pirapitinga (*Piaractus brachyomus*) is not a panmictic species, but is subdivided by river basin into 2 evolutionarily significant units. González-Weaver et al. (this issue) also find surprisingly strong subdivision in the puye (*Galaxias maculatus*), with implications for restocking this coastal fish, whose artisanal exploitation has collapsed in some regions. On the other hand, Quintanilla et al. (this issue) identify important demographic rather than evolutionary segments in need of protection: nursery areas for scalloped hammerhead sharks (*Sphyrna lewini*). González et al. (this issue), Caballero et al. (this issue) and Castellanos-Morales et al. (this issue) then take the search for phylogeographic divisions from exploited fish species to persecuted terrestrial mammals, focusing on how to retain genetic diversity across natural divisions they uncover in the maned wolf (*Chrysocyon brachyurus*), the giant river otter (*Pteronura brasiliensis*), and 2 species of black-tailed prairie dog with contrasting range sizes (*Cynomys ludovicianus* and *C. mexicanus*).

With conservation units identified, the problem(s) these units face must then be understood. Perhaps the widest range of genetic techniques is employed at this stage, with contributed articles honing in on 2 fundamental issues in Latin American conservation: over-exploitation and habitat loss. Presti et al. (this issue) present detective work using data from wild and confiscated hyacinth macaws (*Andoflynychus hyacinthinus*) to push phylogeographic and demographic analyses beyond the identification of units, by showing how poachers catch birds from across the range of this species, and traffic them across the Pantanal to São Paulo and other major markets. A further set of articles focused on habitat loss show how expanding agricultural and urban frontiers can create anthropogenic genetic structuring that must be actively countered, in contrast to the historical structuring described in the first set of articles above, which must be retained and protected. Valdez et al. (this issue) find less genetic structuring in jaguars (*Panthera onca*) from the continuous Pantanal than in the recently and highly fragmented Atlantic Forest, suggesting recovery targets for restoring natural connectivity. Farias et al. (this issue) reveal an even more extreme version of the problem of habitat fragmentation in pied tamarins (*Saguinus bicolor*). For this species, the former single continuous population around Manaus has been divided by urban expansion into subpopulations confined to small forest patches; they suggest populations will need active management, including translocations, to prevent further rapid differentiation and genetic loss due to bottlenecks. However, Napolitano et al. (this issue) highlight the need for a nuanced understanding, by showing that the effects of habitat fragmentation cannot always be assumed to follow the classic predictions borne out in Farias et al.'s work. Some species, such as the small felid *Leopardus guigna*, can have plastic behavioral responses. In *L. guigna*, a surprising increased dispersal in response to fragmentation on Chiloe Island,

Chile, creates an unanticipated conservation problem (lowered population density, rather than increased inbreeding) and so indicates that a different set of management actions will be most useful (e.g., habitat restoration rather than translocations).

Although fewer contributions tackle the later stages in the conservation process—setting priorities, taking action, and evaluating results to guide future cycles—their work represents the vanguard of what genetics has to offer conservation. Souto et al. (this issue) lead off this set of articles, using chloroplast and isozyme data from hundreds of populations in 9 widespread tree species to develop a novel method to identify “genetic hotspots” to set spatial priorities for conservation in Argentina. Victoriano et al. (this issue) set priorities on a more detailed level, within the marbled water frog (*Telmatobius marmoratus*) species complex; they similarly push phylogeographic analyses beyond unit identification, to show how including different populations in the Chilean protected-area system could most efficiently increase the protection of phylogenetic diversity in this taxon. Next, Goncalves et al. (this issue) move us into the realm of direct action, where their application of forensic genetics in confiscated parrot eggs to build a stronger legal case is a classic example of one of the very few genetic applications useful for direct action. Similarly, Cunha et al. (this issue) use forensic techniques to reveal the scope of the problem surrounding suspect “douradinho” fisheries, including the use of threatened dolphins as bait, and go one step further, contributing to concrete conservation actions via a fishing moratorium.

Finally, conservation actions must be evaluated: Did they work? How can we do better next time? Although the scope for the application of genetic tools at this stage may be at least as large as initial stages, examples are surprisingly few. This scarcity of evaluations is not unique to genetic applications within conservation (Sutherland et al. 2004), and the present collection does not escape this pattern. Milian-García et al. (this issue) provide the only study evaluating past conservation actions, in their case the initiation and maintenance of multiple captive populations of the Cuban parrot (*Amazona leucocephala*) as insurance against loss of natural diversity. They find that these populations have not succeeded in preserving natural phylogeographic divisions, although they are able to provide practical recommendations for reducing and eventually eliminating admixture in the future.

We have found that highlighting the ways in which studies fit within the conservation process outlined above is useful in 3 ways. First, it helps new practitioners overcome initial disappointment at finding themselves greatly removed from where the “action” is, by showing how effective conservation processes consist of much more than a particular, splashy intervention. Second, it helps them find the route to more effective application, by forcing them to ask what the next step is in the process, who will take it, and how end users will understand and apply the results produced. And finally, it helps students see patterns in application, to realize that they are not endless, and need not be invented anew with each conservation problem.

Closing the Knowing-Doing Gap in Conservation Genetics, and Latin America

So, what is needed for the research presented here to move from the published page into a manager's to-do list, a politician's talking points, or a local community's harvesting practices? Building conservation genetics as a field with outputs that actually improve the status of the world's biodiversity is a challenge, but we see several paths forward.

The first involves learning from other applied fields. The challenge of application is far from unique to conservation genetics

or to Latin America. Other fields of applied genetics, and indeed applied pursuits in general face this “knowing-doing” gap (Pfeffer and Sutton 1999; Knight et al. 2008) and thus have much to teach us, in spite of differences in scale. Within agriculture and medicine, translation of genetic research is a major mandate for government agencies (e.g., <https://www.embrapa.br/en/recursos-geneticos-e-biotecnologia>; <http://inta.gov.ar/biotecnologia>), as well as public-private or fully private initiatives (<http://isa.ciat.cgiar.org/urg/>; <http://www.catie.ac.cr/>). Such initiatives create chains of relationships connecting researchers to users, establishing links to the larger political/economic/social context, and enhancing communication, to find out what end users need, to focus work on priority problems, and to reduce barriers to action (Sutherland and Freckleton 2012; Ronald 2014). Similar efforts to promote interactions between researchers and end users will likely be helpful in conservation genetics in Latin America.

To promote these interactions in conservation genetics, of course, they must be recognized as a funding priority. In Latin America, initiatives such as the United Nations University Biotechnology Programme for Latin America and the Caribbean, which gave ReGeneC its start, are not nearly as common as needed, but important opportunities do exist (UNU-BioLAC 2015). For example, both Chile and Brazil fund programs to promote training courses in biotechnology (e.g., <http://www.iniciativamilenio.cl/centros/activIntro.php>; <http://www.fapesp.br/>; <http://www.cnpq.br/>). However, increased student–researcher interactions alone are not enough. Funders need to support researcher–end user interactions as well.

While additional funding remains a challenge, technology can also help researchers reach end users in a cost-effective manner. Online tools can link practical management problems to the genetic tools for solving them (e.g., Allendorf et al. 2011; ConGRESS 2012). Such platforms can be extended to include interaction and networking opportunities, additional languages, and feedback from their user community, taking a page from scientific social networking sites (e.g., www.researchgate.net, www.academia.edu) and existing regional portals for genetic information (e.g., <http://bioinformatica.cecalc.ula.ve/>).

Technological solutions also highlight steps institutions can take to promote application in conservation genetics. Universities and other institutions can broaden the base of scientists’ performance reviews to include books, webpages, and extension activities for a broader audience, in addition to original peer-reviewed research, which may be less accessible to end users. Government agencies and industry can also reward managers for basing actions on scientific evidence. At the same time, journals can offer alternative categories for publishing conservation genetic studies, which emphasize applicability to specific goals in education, policy, or management over scientific novelty. For example, the journal *Conservation Biology* recently introduced a *Conservation Practice and Policy* section for precisely this purpose.

In the meantime, individual researchers must recognize what many authors in the present issue already have: to find the conservation in conservation genetics, it is up to them to start building relationships with end users. In a Latin American context, as is evident in this issue, this means seeking out those involved in fisheries, forestry, agriculture, urban planning, and wildlife management, use, and trade. It means publishing in international journals but providing translations in local languages. (Most of the articles in this special issue include a translation in Spanish or Portuguese as supplementary material.) And it means choosing research questions carefully,

preferring those that can only be answered with genetic tools, those whose answers are needed by stakeholders, and those with the greatest potential to change conservation outcomes.

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