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REVIEW ARTICLE

The coming of age of conservation genetics in Latin America: what has been achieved and what needs to be done

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Abstract Genetic research is a well-recognized component of understanding biodiversity and is an invaluable approach for documenting and mitigating increasingly high rates of loss. Here we present a quantitative synthesis of conservation genetics science in Latin America and its progress, focusing on evolving trends on different taxonomic groups, environments and markers. We reviewed 528 conservation genetics research papers published in 57 journals from 1992 to 2013. Brazil and Mexico were the most represented countries in the literature and there was a marked disparity between terrestrial (~64%) and aquatic-marine research (~36%). More than a third or the articles focused on plants (~35%) while the other (65%) were animal studies with a clear emphasis on mammals (35%) and bony fishes (24%). Most research (42%) addressed patterns of population structure, while 17% focused on genetic diversity issues and 14% focused on the description of novel genetic markers. Finally, although genetics has become an integral part of conservation biology, genetic analyses have often not been completely integrated into the development of conservation and management strategies and formal policies. We discuss the levels to which these types of studies can effectively contribute to biodiversity conservation in this region, and offer suggestions on how conservation genetic approaches may be used more broadly, enhancing the connectivity between scientists and policy makers.

Keywords Biodiversity conservation · Conservation goals · Conservation genomics · Conservation policy makers · Genetic biodiversity

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Introduction

Our planet's biodiversity is rapidly declining as a result of anthropogenic activities (Barnosky et al. 2011; Dirzo et al. 2014). This decline is now referred to as the sixth mass extinction due to the high rate of extinction (Barnosky et al. 2011). Many efforts have been applied to mitigate this rapid loss of species and, in some cases these efforts have involved direct changes in human behavior in attempt to increase remaining wild populations (e.g. humpback whale populations have increased after whaling was banned; Barlow et al. 2011). Unfortunately, rapid declines in population size and species diversity have often occurred faster than humans can detect and respond to them (Costello et al. 2013; Mora et al. 2013). This rapid

decline could lead to insufficient time between the reliable collection of scientific data and effective decision-making. Thus, conservation authorities and managers frequently have to make quick decisions with limited information and resources (Frankham 2010). In this context, genetic and/ or molecular information which often can be more rapidly obtained than other types of data and will provide unique insights on species or population status becomes an important tool for conservation and decision makers.

Since the first attempts to conserve genetic diversity (i.e. germplasm; Frankel and Bennett 1970) and the establishment of conservation genetics as a discipline (Frankel and Soulé 1981), almost half-century has passed. During this time, several technologies for assessing the genetic characteristics of individuals and populations have been developed and applied in a biological conservation context—ranging from cytogenetic techniques to the new approaches involving massive DNA sequencing and genome-wide information (Benirschke and Kumamoto 1991; Steiner et al. 2013). With the advance of these technologies, the volume and variety of genetic data [e.g. karyotypes; allozymes, DNA sequences, short tandem repeats, single nucleotide polymorphisms (SNPs)] and analytical approaches employed to address biological conservation questions have grown dramatically in the last five decades.

Although genetics has become an integral part of conservation biology (Frankham 2010) and the contribution of genetic diversity to the maintenance of biodiversity and ecosystem processes has been widely recognized (Hughes et al. 2008; Struebig et al. 2011), genetic data have often not been totally integrated with conservation policies. This disconnect between theory (e.g. genetics) and conservation practice has thus hampered the resolution of urgent conservation issues, including: (1) identification and reconnection of previously continuous populations, as well as the identification of discrete populations previously thought to be connected, (2) small populations/inbreeding or population decline issues, (3) tracking and mitigation of invasive species, (4) planning and monitoring reintroduction efforts, (5) assessment and mitigation of disease outbreaks, (6) definition and delimitation of threatened taxa and (7) design and prioritization of protected areas (e.g. Fischer and Lindenmayer 2000; Templeton et al. 2001; Lee 2002; Jamieson et al. 2006; Fisher et al. 2009). Therefore, species often descend into the extinction vortex without sufficient knowledge about their original genetic features or without using known information to help inform conservation policies (e.g. Baiji dolphin extinct before its genome was sequenced; Zhou et al. 2013). Despite its importance, only recently (2010) did the Convention on Biological Diversity consider genetic diversity to be a component of the Aichi Biodiversity Targets (http://www.cbd.int/sp/).

Many of the countries with the most biodiversity are located in the Neotropical region. This ecozone, politically known as Latin America, includes the Austral and Neotropical Americas (ANA) from Mexico southward (Ceballos et al. 2009), harbors approximately 17% of the global biodiversity of plants and vertebrates and encompasses seven biodiversity hotspots (Ceballos and Brown 1995; Myers et al. 2000). Habitat degradation and wild population declines within and outside protected areas are a major concern for this region (Leisher et al. 2013; Heino et al. 2015) and the high rate of environmental degradation and biodiversity loss is mainly due to resource exploitation (Ceballos et al. 2009). Moreover, the significant economic importance of biodiversity in this region and human dependence on the natural resources and services continue to be a major contributing factor for biodiversity declines (MEA 2005). This dependency on natural resources, in conjunction with the economic situation of the countries of the region (most are low, lower-middle and high-middle income economies [http://www.data.worldbank.org 2015]), likely will continue to degrade the regions biodiversity. In addition to the socioeconomically issues, some countries in Latin America are or have been immersed in armed conflicts during the last 50 years (e.g. Colombia; El Salvador) which ultimately has had a largely detrimental effect on wildlife habitat and populations (Gaynor et al. 2016).

The high biodiversity of the region suggests that a great number of taxa could face extinction in the near future (Dirzo et al. 2014). Therefore, there is a critical need for comprehensive assessments of their status, trends and threats, incorporating genetic aspects. To date, there have been no systematic studies documenting the state of the art of conservation genetics in Latin America, or identifying the areas that need to be addressed in order to extend conservation genetic/omics science into conservation policy. Here we present a statistical synthesis of published literature on conservation genetics in Latin American, including as assessment of the biological groups studied and their IUCN conservation categories, the distribution of studies by country, the genetic markers used and whether these genetic studies are likely to contribute to the biological conservation of the species studied. With these data we aimed to test whether geopolitical, socioeconomics and biodiversity variables explain the number of conservation genetics papers in the region. Finally, we propose ways that genetics can be integrated into the conservation efforts initiatives carried-out by governmental agencies in the region.

Materials and methods

Reviewed database

We used Web of Science® (WOS) (all databases) to search for either the individual words or complete phrases of

"conservation genetics" or "conservation of genetic diversity" in the title, abstract and keyword fields of all articles published from 1981 to 2013. We then used the "Refine Results" tool to sort the results by Country/Territory. We did not use other words related to genetics such as inbreeding, relatedness, small populations or bottleneck, because all or some of these words could be linked only to population genetic studies, which do not necessarily mean the research has a conservation focus or includes research presented within a conservation genetics context, which was the goal of our survey. Publications conducted in more than one country were classified as "various". A second search was conducted using both search phrases AND the name of each country (in a second search field). This second approach was used because the first search strategy sometimes did not recover studies by non-Latin-American research institutions (institutions and/or researchers located outside Latin America) in Latin American countries. For our search we intentionally did not include Guadeloupe, Martinique, French Guiana, Saint Martin and Saint Barthélemy because these are considered departments and regions of France. Publications were selected independently of author nationality.

Specific statistics

We collected data by searching the text of each manuscript. This strategy is more accurate than relying on the "Analyze results" tool of WOS because the term "conservation genetics" sometimes appears in publications referring to DNA sequence conservation or in taxonomic review papers. Conference abstracts were not included in the analyses.

Information from each article was stored for subsequent analysis, including: *affiliation of authors* (institutional address) (i.e. whether the publication had a Latin American affiliation for the first author, corresponding author, a co-author, or none), *year of publication, category of paper* (research or review), *species studied* (including kingdom, phylum, subphylum/class and species name), and *type of environment* (marine, freshwater, terrestrial). We grouped papers by the type of genetic approaches and/or genetic markers used in the analyses into seven categories: (1) cytogenetics, (2) allozymes, (3) organelle markers (chloroplast, mitochondria), (4) traditional nuclear (nDNA) markers (e.g. RAPDs, AFLPs, nuclear sequences, ISSR), (5) microsatellites, (6) genomic-scale approaches (e.g. transcriptomics, genome sequencing, mitogenomics), and (7) other kinds of markers or analyses (e.g. quantitative genetics). Although microsatellites are also nDNA markers, we distinguished them in a separate category because of their widespread use in conservation genetics. Finally, we classified each paper based on its analytical approaches and area of emphasis into one of the following categories: population structure, genetic diversity, markers, phylogeography, systematics

and taxonomy, landscape genetics, parentage and kinship, cytogenetics, breeding and germplasm, methods, and others. We are aware that some publications could fall on one or more category, but the papers were classified to only one category based on its main goal.

Research productivity analyses

Population size (POP), GDP, government expenditure on tertiary education (GDPEdu), total country area (TA), forest area (% of land area with any tree bigger than 5 m excluding agricultural production; FA), terrestrial and marine protected areas (% of total territorial area; PA), number of scientific papers published by country (SCiP), and endemic species data were obtained from the World Bank (http://www.worldbank.org), UNESCO (http://www.unesco.org) and IUCN (http://www.iucnredlist.org) websites in order to understand the differences among countries. For these analyses, we used data covering the period from 1992 (the year of the first conservation genetics paper in Latin America) to 2013, to the extent it was possible. Single linear regression analyses were performed among the different variables and the response variable (number of papers) for each country to look for any tendency of productivity per country along the years. Multiple regression analyses were conducted in order to understand which of the variables were related to the scientific productivity. Because of scientific productivity often changes year to year for each country, along with other variables (e.g. GDP, PA), we calculated the arithmetic mean for the 22 year period for each of the variables. To minimize multicollinearity for the data, we conducted pairwise correlation analyses (Pearson's correlation) among all variables in R 3.2.3 (R Development Core Team 2016) and removed variables with $|r| \geq 0.8$. After the variables were removed, a "backward stepwise regression" analysis was done and the best model was selected using the Akaike Criterion (AIC). We used two proxies: (1) the mean number of papers in which Latin American institutions were involved and (2) the mean number of papers in which no Latin American institutions participated. For this second approach we only used biodiversity and geopolitical variables in an attempt to assess if the research conducted by non-Latin American institutions depended of any of the biodiversity variables.

Lastly, we explored if there was any relationship between the number of threatened species of each country (IUCN threatened species list) and the number of conservation genetics papers. Relationship between the IUCN studied species and the total IUCN species, as well as between the total number of IUCN species and non IUCN species for each country was tested using linear regression analyses. Although it is possible that a few species not included in IUCN list of threatened species might be protected locally, we chose to use a common criterium to address this question.

Assessment of conservation impact

To evaluate the extent genetic studies have focused on species of conservation concern, we recorded the conservation status of each target species as categorized in the 2015 red list (IUCN 2015). The IUCN category was included in the search to know if species were more or less likely to be counted in the papers retrieved by our search. Papers reporting more than four species were recorded as 'Other' in our database; however, for the total count every species was considered. From each publication, we recorded whether the authors proposed any conservation management action based on their own results (e.g. different management units, different subspecies, no translocation etc.) and whether the article included results beyond genetic analyses. Proposed management actions were classified into any of 13 categories (Table 1). Other management actions, including methodological approaches were classified as 'Others'. Additional information about the proposed conservation actions for each species was reviewed through existing national management plans (if available) and/or the conservation actions for the species as set in the IUCN red list of Threatened Species (IUCN). A species was considered to be under some degree of protection if any of the following four criteria was achieved: (1) the species is under direct protection, (2) it inhabits a protected area, (3) its breeding area is under protection, and (4) other kinds of protection have been implemented (i.e. ex-situ conservation). Because many species occur in more than one country, we analyzed these data by publication and not by species. However, for country-based statistics, each species was considered. After accounting for the year of publication, the proposed conservation actions mentioned in each publication, and each national management plan/IUCN conservation actions, we evaluated if any conservation actions (i.e. any kind of legal protection directly applied to any habitat area of the species or to provide direct protection to the species) were enacted following publication (temporally and not as causality of the publication). These actions were classified as (1) *before* and (2) *after* the publication of the conservation genetics study. Because this information (national management plans) is scarce or difficult to obtain through the Internet, we cannot be certain if ours is an exhaustive list of research papers that have contributed to conservation goals, we will discuss our results based on (1) available 'national management plans' and (2) a internet search of all government documents published online in which the research was cited, following the same criteria used by Bowman et al. (2016), but adding the terms .gov, .gob, .gub and .gc that are the terms used by Latin America governments. We should note, however, that this does not mean that the scientific publication necessarily has any relationship with the promulgation of conservation policies, especially since many conservation laws may take several years to implement after the scientific information is available (when there is any scientific information behind the conservation policies).

Results

Latin America and conservation genetics in numbers

We identified 528 conservation genetics papers, from 57 journals, published with data retrieved within Latin

Table 1 Main conservation genetic objectives linked to conservation management and policy

I. Resolve taxonomic uncertainties

II. Define evolutionarily significant units (ESUs) and/or any other management unit, including protected areas for breeding, nursing or feeding [e.g. management units (MU), protected areas (PA), conservation units (CU)]

III. Minimize inbreeding and loss of genetic diversity in populations (e.g. species conservation, landscape genetics to establish biological corridors, possible translocation effects, etc.)

IV. Manage captive populations to reduce inbreeding and the consequent loss of genetic diversity to ultimately increase reintroduction success (e.g. germplasm, breeding)

V. Manage wild harvest populations (e.g. fisheries, whaling, hunting, forestry)

VI. Manage invasive species and their possible negative effects on native and threatened species

VII. Estimate population parameters estimates (e.g. sex ratio, population size, demographic history)

VIII. Identification of wildlife products (e.g. fisheries, poaching)

IX. Contribute to the inclusion of national or international threatened species list or management plans

X. Predict extinction risks and compare alternative options in species recovery programs

XI. Predict responses to environmental changes based on adaptive genetic variation

XII. Conduct environmental impact assessments and design environmental policies based on DNA evidence (e.g. environmental DNA studies)

XIII. Long-term populations monitoring to understand how populations can face environmental changes

American countries from 1992 to 2013. Of the 528 articles, 498 were research papers, 29 were reviews and one was a commentary. The number of conservation genetics articles has increased considerably since the first paper in 1992, reaching a total of 70 in 2013 (Fig. 1a).

Sixty-seven percent (N = 334) of the research papers had as first or corresponding author a researcher from a Latin American institution. Of the 164 research papers led by non-Latin-American institutions, 91 (55.4%) had a co-author from a Latin American institution. Brazilian researchers/institutions were involved in the largest number of conservation genetics publications (223 or 44.8%). In sharp contrast, there were no conservation genetics publications from several countries, including Haiti, Honduras, and Paraguay (Table 2).

Environments and studied taxa

Among the 498 research papers, 318 focused on terrestrial species, 91 on freshwater species, and 88 emphasized marine species and one was categorized as "undefined" (research paper not focus on any species but instead on methodologies). Regarding the taxonomic groups, Animalia was the focus of the majority of the publications (64.9%). Of these, most focused on vertebrates (88%) and only 12% corresponded to invertebrates (Table 1). Among 'Vertebrates', Mammalia was the most studied class (99 papers), followed by papers on bony fishes (Osteichthyes; 70 papers) (Table 3). Among the invertebrates the most common study class was the arthropods (20 papers) followed by Mollusca and Cnidaria (14 and 6 respectively). Among the non-Animalia species, the most studied groups focused on angiosperms (146 papers), followed by gymnosperms (25 papers) algae (1 paper) and Pteridophyta (1 paper) (Table 3).

Molecular markers and study types

The most widely-used marker for conservation genetics studies in Latin America has been microsatellites (N = 170 or 34.1% of the published papers), followed by mitochondrial or chloroplast markers (N = 110 or 22% of the papers) (Fig. 1b). Although the number of articles using more than one tool has increased since 1992, most have used only one type of marker (N = 430) (e.g. mitochondrial/chloroplast or microsatellites markers) (Fig. 1b). Most studies focused on population structure (N = 208 or 41.8%), followed by those that described the genetic diversity of a single taxon (N = 85 or 17%) or were simply primer notes (14%) (Table 4).
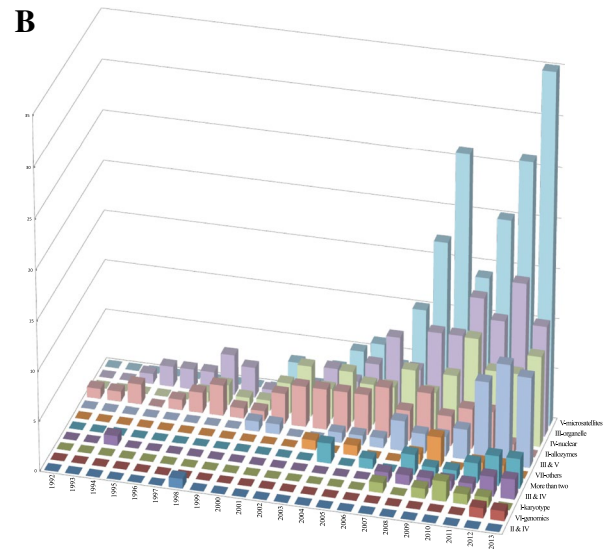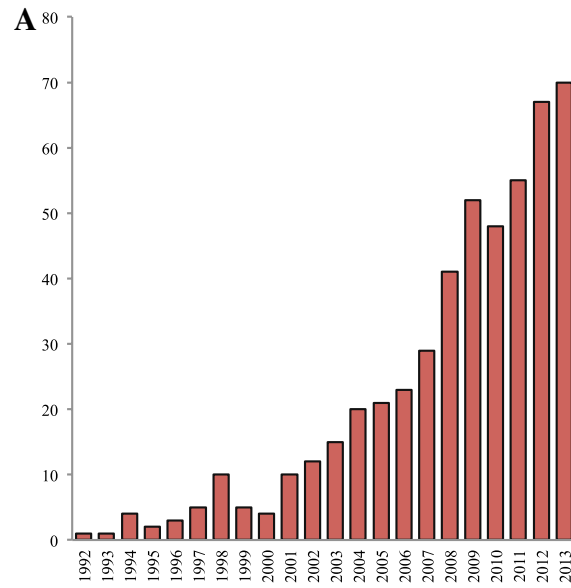
Fig. 1 a Number of conservation genetics articles published each year in Latin America, **b** number of articles published per year sorted by molecular markers or combination of them

Factors contributing to the number of conservation genetics studies per country

Economic and geopolitical variables generally did not correlate with the number of papers published by the different countries, except for Brazil, which had high and significant values ($r^2 = 0.77$–0.93; $p < 0.001$) for the variables GDP, GDPEdu, POP and SciP. Other countries, including Mexico, Colombia and Chile, showed a moderate relationship between the conservation genetics productivity and economic variables ($r^2 = 0.51$–0.67; $p < 0.001$).

Table 2 Number of
conservation genetics papers,
number of species studied in
each country, IUCN red list
species studied for each country
and the total IUCN red listed
species for each country. The
megadiverse countries are
indicated in bold

Country	Research papers	Studied species	IUCN studied species	IUCN listed species	Proportion of IUCN studied spp. vs. IUCN listed spp.
Argentina	20	25	13	243	0.053
Bolivia	2	2	1	216	0.004
Brazil	225	257	92	966	0.095
Chile	34	83	35	182	0.192
Colombia	12	25	24	751	0.032
Costa Rica	10	12	5	323	0.015
Cuba	2	2	1	337	0.003
Dominican Republic[a]	3	1	1	153	0.006
Ecuador	18	39	35	2308	0.015
El Salvador	1	1	0	83	0
Guatemala	2	3	2	282	0.007
Haiti[a]	0	0	0	169	0
Honduras	0	0	0	294	0
Mexico	83	88	57	1109	0.051
Nicaragua	1	1	1	141	0.007
Panama	6	5	3	373	0.008
Paraguay	0	0	0	58	0
Peru	4	7	7	643	0.011
Puerto Rico	9	8	4	127	0.031
Uruguay	7	9	4	103	0.039
Venezuela	4	4	2	312	0.006
Various	59	97	68	–	

[a]Each country is counted separately and not as Hispaniola because some IUCN species could be the same in both countries

After running a multiple regression analysis with the "backward stepwise model", the best estimated model that explained the number of papers done by Latin American institutions included only the variable SciP (Scientific papers in all the disciplines) ($r^2 = 0.99$; $p < 0.01$), however this variable was also strongly correlated with population (Pop; $r^2 = 0.85$; $p < 0.001$) and investment in education (GDPEdu; $r^2 = 0.92$; $p < 0.001$) and slightly correlated with number of endemic species ($r^2 = 0.68$; $p < 0.05$). Papers without Latin American institutions involved were not correlated with any of the biodiversity variables explored.

Using genetics for threatened species and proposed conservation actions

Among the research papers, 287 (58%) focused on species under an IUCN conservation category, whereas 211 publications (42%) focused on species classified as "Not Evaluated". In total, 630 species were studied in the 498 articles. Of these, only 326 (52%) were classified in a IUCN conservation category (Fig. 2). The countries with the most species studied were Brazil (258), followed by Mexico (87) and Chile (83).

There was a significant but weak relationship between the number of conservation genetic papers and the number species listed at the IUCN for each country ($r^2 = 0.21$; $p < 0.05$), with Chile having the most number of studied IUCN species relative to the total number of IUCN species listed for the country (Table 2). Similarly, when we evaluated whether the IUCN studied species in each country was a response to the IUCN total species for the same country, we found a weak but significant relationship ($r^2 = 0.3$; $p < 0.05$). Finally, when we tested for a relationship between the total number of studied species for each country and the IUCN species for the same country, we found a strong correlation ($r = 0.95$; $p < 0.001$), as several countries having a high percentage of the species that were studied also being on the IUCN species list (e.g. Colombia, Dominican Republic, Ecuador, Peru; Fig. 3).

Almost half (48.6%) of the articles included specific suggestions for conservation and management actions, including the protection of specific areas to maintain genetic diversity (e.g. Inza et al. 2012), conducting or avoiding translocations (e.g. Vianna et al. 2006; Woolaver et al. 2013), proposed fisheries management practice designed to reduce bycatch (e.g. Pimper et al. 2010) and the monitoring of harvested populations (e.g. Marín et al. 2009). The most frequent

Table 3 Relative research focused on different model species

|	Number of papers	Percentage
Animalia	323	64.9
Vertebrata	285	
Mammalia	99	
Osteichthyes	70	
Reptilia	52	
Birds	36	
Amphibia	15	
Chondrichthyes	11	
Others	2	
Arthropoda	20	
Insectia	14	
Crustacea	6	
Cnidaria	4	
Anthozoa	4	
Mollusca	14	
Bivalvia	7	
Gastropoda	5	
Cephalopoda	2	
Others	2	
Plantae	174	34.9
Angiosperms	146	
Gymnosperms	25	
Algae	1	
Pteridophyta	1	
Others	1	
None	1	0.2

management proposals (n = 106) were involved suggestions for specific management units and/or evolutionarily significant units (Category II, Table 1). There were no examples, however, suggesting the possibility of using conservation genetics techniques to conduct environmental impact assessments (XII) (Fig. 4).

Out of the 244 articles that proposed conservation and/or management actions, 136 (56%) were centered on species that are currently protected, either by (1) direct species protection, (2) protection of the area they inhabit, (3) protection of their breeding area, or (4) another method. Searches for examples of specific protection or management plans that were taken by the national governments by scanning national management plans or through internet searches for government documents revealed different patterns. Using the first approach we found 136 articles that proposed specific management actions and 16 cases of increased species protection occurring after the publication of the article. However, this does not necessarily prove that there was a causal link between the management actions or decisions and the articles publication. Of these 16 papers, two focused on developing conservation tools for conservation that are now are being employed to identify illegal fishery products (Mariguela et al. 2009; De-Franco et al. 2010). Seven publications conducted population genetics studies addressing the geographic boundaries of different populations (Morafka et al. 1994; Tagliaro et al. 1997; Yahnke et al. 1996; Young and Allard 1997; Pope 1998; Haig et al. 2001; González-Astorga et al. 2005). Six studies distinguished species range areas and/or migratory corridors and suggested protection of the species, specific areas and/or the recovery of specific natural environments/habitats (Bowen et al. 1995; Ramey 1995; Cardoso et al. 1998; González et al. 1998; Sgorbati

Table 4 Relative proportion of the different categories of research conducted in Latin America

Analysis	Description	Number of papers	Percentage
Population structure	Publications that aimed to primarily assess information on genetic population structure	208	41.8
Genetic diversity	Publications that aimed to only describe genetic diversity of one or more populations	85	17.1
Markers	Publications that aimed to describe markers for one or more species, such as the description of microsatellites	69	13.9
Phylogeography	Publications with a primary goal of assessing phylogeography of populations	38	7.6
Systematics and taxonomy	Publications that primarily aimed to resolve phylogenetic relationships among populations or to resolve some species taxonomy	43	8.6
Landscapes genetics	Publications that used primarily a landscape genetics approach to study populations	13	2.6
Parentage and kinship	Publications that aimed to answer questions about parentage and kinship	8	1.6
Cytogenetics	Publications that aimed to answer questions regarding chromosome knowledge by different techniques	6	1.2
Breeding and germplasm	Publications about living genetic resources breeding programs	7	1.4
Methods	Publications that described a new analytical method or that tested the efficiency of a specific method	7	1.4
Others	e.g. Population viability analyses, symbiosis studies, diseases	14	2.8

Fig. 2 Number of Latin America species featured in molecular genetic research publications by their IUCN categories
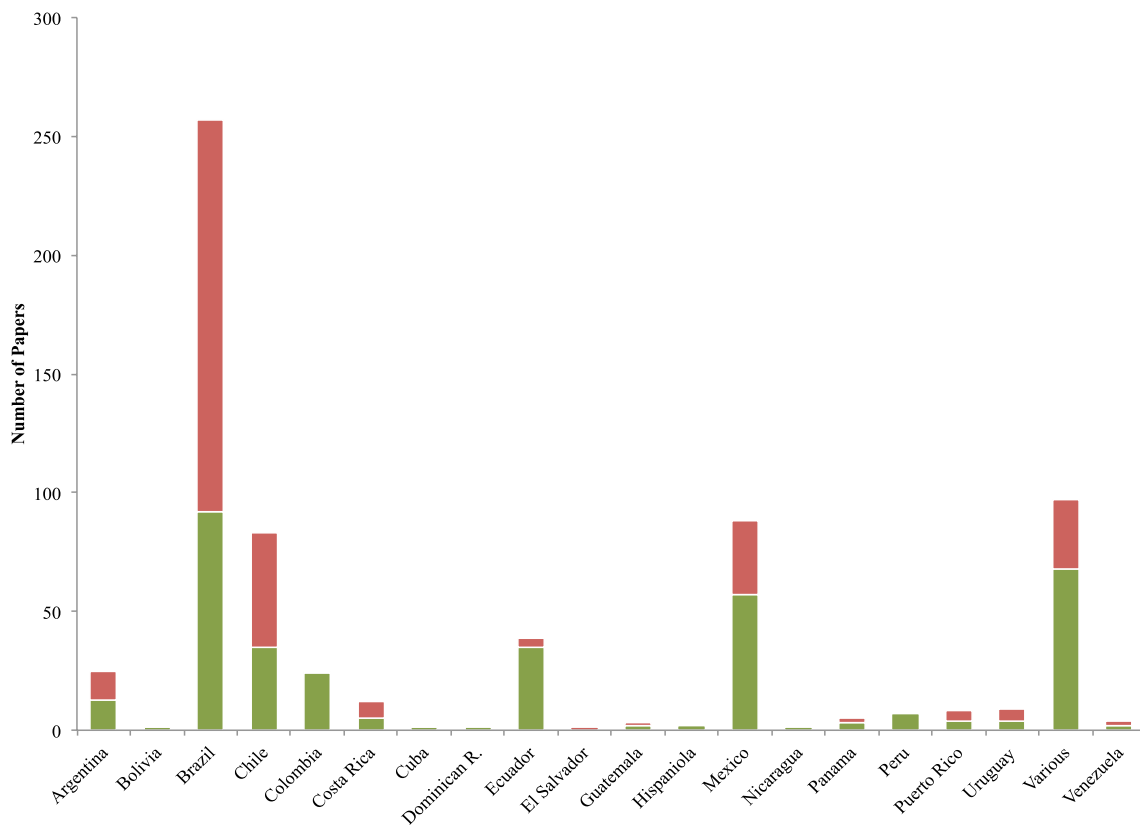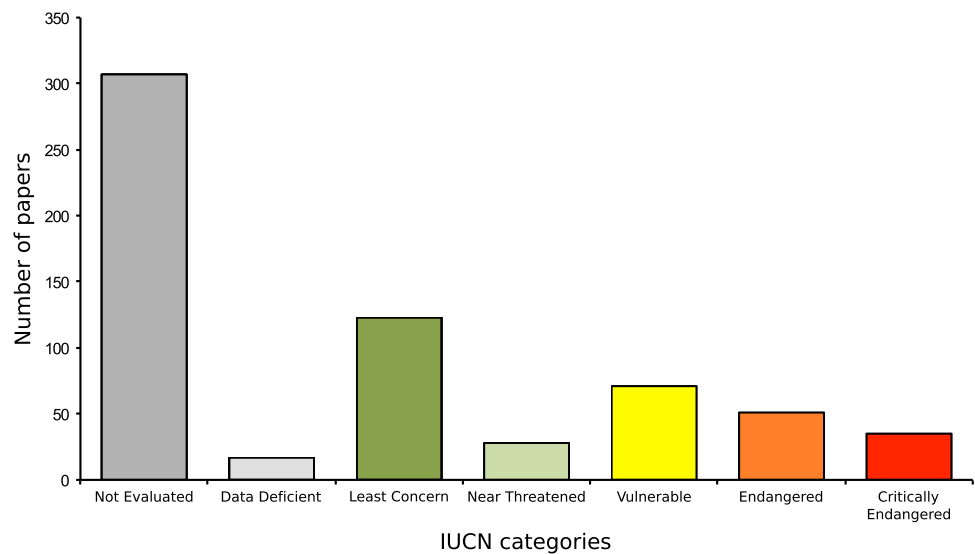

Fig. 3 Total number of species studied in each country. *Green* (*dark gray* print version) corresponds to IUCN listed species. *Red* (*light gray* print version) corresponds to no IUCN listed species. (Color figure online)

et al. 2004; Lara-Ruiz et al. 2008). One study suggested the establishment of captive breeding for the purpose of supporting future reintroductions (Márquez et al. 2006).

Using the second approach we identified 71 papers that had been mentioned in a government publication. Many of these (19) were found in USA, Canada, Australia and

Falkland/Malvinas government publications. Of these 71 papers, 34 were mentioned in government reports, 10 in management plans, 10 in environmental assess presented to the different governments, 7 in species protection, and 3 in environmental assess reports and others. There were only two examples when the scientific publication resulted
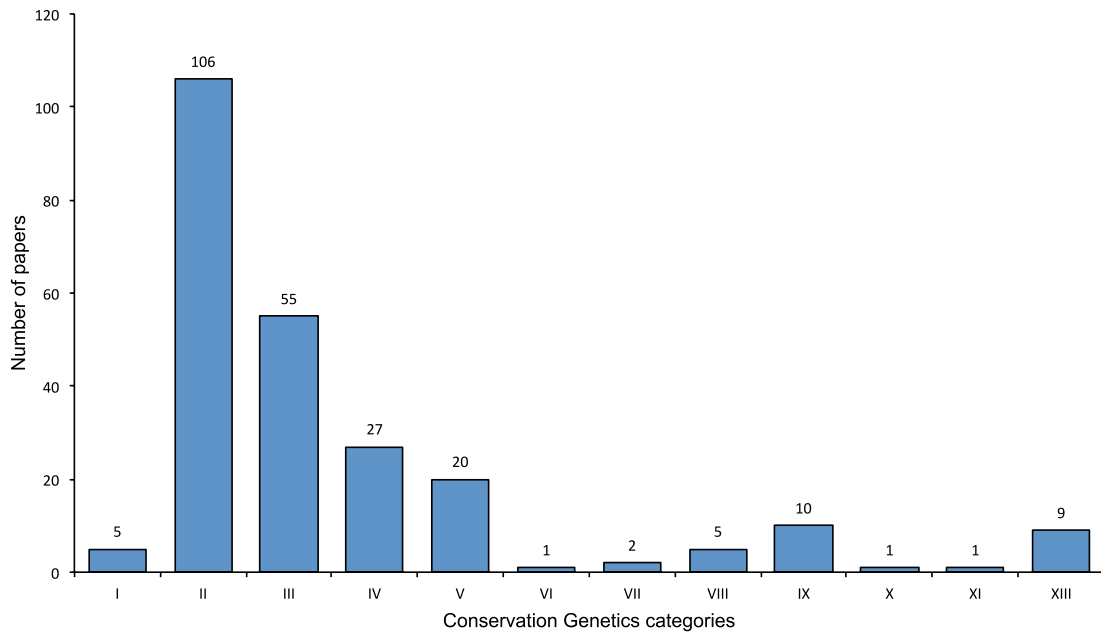
I. Resolve taxonomic uncertainties
II. Define evolutionarily significant units (ESUs) and/or any other management unit, including protected areas for breeding, nursing or feeding (*e.g.* management units - MU, protected areas - PA, conservation units - CU)
III. Minimize inbreeding and loss of genetic diversity in populations (*e.g.* species conservation, landscape genetics to establish biological corridors, possible translocation effects, etc.)
IV. Manage of captive populations to minimize inbreeding and loss of genetic diversity with the ultimately aim of maximize reintroduction success (*e.g.* germplasm, breeding)
V. Manage wild harvest populations (*e.g.* fisheries, whaling, hunting, forestry)
VI. Manage invasive species and their impacts on threatened species
VII. Estimate population parameter estimates (*e.g.* sex ratio, population size, demographic history)
VIII. Identification of wildlife products (*e.g.* fisheries, poaching)
IX. Contribute to the inclusion of national or international threatened species list or management plans
X. Predict extinction risks and compare alternative options in species recovery programs
XI. Predict responses to environmental changes based on adaptive genetic variation
XII. Conduct environamentl impact assessments and design environmental policies based on DNA evidence
XIII. Long-term populations monitoring to understand how populations can face environmental changes

Fig. 4 General topics for the use of genetics in the conservation of biodiversity. Number of articles published proposing any of 13 recommendations to improve conservation based on molecular tools in Latin America

in active monitoring of a species: *Crocodylus moreletii* and *C. acutus* (Mexico) and *Dion* sp. (Mexico) (Ray et al. 2004; González-Astorga et al. 2008). It is noteworthy that 44 of the 71 articles cited in government documents proposed specific management action while the other 27 did not include any specific management actions.

Discussion

Here we provided an assessment of the trends and recent history of conservation genetics publications in Latin America. Our goals were to provide a synthesis of the conservation genetics literature in this region, summarizing the biological groups that have been most-studied and their respective conservation status, the genetic markers used, ecosystems investigated and the kind of studies conducted,

to evaluate whether this published scientific knowledge is contributing to effective conservation. It is worth noting that our results do not necessarily include all the literature and research using conservation genetic tools in Latin America. For example, a search of a regional database such as SciELO recovered and additional six papers that were not analyzed here. Similarly, other information outlets, including "gray literature", are certainly produced in Latin America. However, because this kind of information is not easy to access, they were not included here in our review (although they certainly be taken into account by policy-makers and conservation managers). Ultimately, the difficulty we had in gathering this information highlights the importance of publishing the results of conservation genetic studies in journals of high impact and easy access by policy makers and wildlife managers.

Although conservation genetics is an established and integrative discipline that has experienced a great expansion worldwide, it generally is a tool (and approach) that is not well integrated into conservation efforts (Shafer et al. 2015; Haig et al. 2016). Better integration of the insights available from genetic (and genomic) approaches would certainly be invaluable in high-priority regions with high concentrations of endemic species and where the threats to biodiversity are high, such as Latin America region (Myers et al. 2000). Indeed, the disparities in research emphasis relative to other parts of the world are even more critical in Latin America due to these acute threats to biodiversity (Rodriguez et al. 2005). Our results here are a summary and analysis of information from 528 scientific publications on conservation genetics from 1992 to 2013 that focused on Latin America species. Pérez-Espona and ConGRESS Consortium (2017) published a similar analysis compiled from 4311 publications that appeared from 1992 to 2014 on conservation genetics in European countries. The wide disparity in number of publications over roughly the same period shows that there is a noticeable difference in use of genetic tools in conservation research in Latin America relative to European countries.

Although conservation genetics emerged as a discipline around the end of the 1970s, the first paper published in Latin America appeared only in 1992, representing a gap of nearly two decades compared to other continents. However, once papers with a Latin American focus began to appear, a great number was published in ISI impact factor journals. However, the geographic distribution of these publications was very uneven, with over 44% coming from Brazil, 16% from Mexico, and 6% from Chile. Brazil and Mexico are the most populated countries in America Latina, but Chile is only in the 7th position in the list of Latin countries by population, which highlights the emergence of Chile as a leading country in scientific production in Latin America, despite its small size (Van Noorden 2014). The high productivity of these three countries can only be explained statistically for Brazil using the index we used. In Brazil the discipline has grown along the years based mainly on the increase of the GDP and money allocated for education. This investment in education caused an increase on the overall number of publications in all scientific areas, which is strongly correlated with the number of conservation genetic papers in Brazil. This can also be seen in the number of conservation-oriented academic programs that exist in different countries as mentioned by Mendez et al. (2007). Investment in education seems to be the main factor in the region in relation with the conservation genetics productivity, but other factors such as the biodiversity of the country has also to be taken into account. Thus, roughly, more biodiverse countries produce more conservation genetics research. Of note is the high number of papers (N = 73) generated by non-Latin-American

institutions. This is likely the result of better access to funding in countries such as USA, France and Germany among others. However, in a high number of cases (N = 91) where the research was not conducted by Latin American institutions, foreign institutions work hand-by-hand with local institutions, generating at the end not just peer-review publications but also training of local researchers.

Of the total number of research papers (498), there is a bias towards research on terrestrial species, which could be mainly due to the large number of studies focusing on plant species, since there are few aquatic lineages among them (N = 174). Regarding the taxonomic groups and taking into account the total number of studies, the most studied taxonomic group was vascular plants (29.7%), followed by mammals (19.9%) and bony fishes (14%). Pérez-Espona and ConGRESS Consortium (2017) also found a bias in European publications, and notably, mammals (25%) and vascular plants (24%) were also the most studied taxonomic groups in Europe.

Taxonomic bias was also apparent among the animals studied (323 research papers), with a notable bias towards vertebrates (88%). Among vertebrates, mammals and fishes accounted for 63% of the papers, probably because of their economic and/or recreational importance (Martín-López et al. 2009). Mammalian species are also disproportionally studied, largely because they are generally more "charismatic" and higher profile for the public (e.g. Male and Bean 2005; Wilson et al. 2007). Amphibians, in the other hand, are very underrepresented in our results. They were the focus of only 3% of the total number of conservation genetic studies in Latin America, even though amphibians are considered good biological indicators of ecosystem stress because they are sensitive to perturbations in both terrestrial and aquatic environments (Welsh and Ollivier 1998). Moreover, amphibians are known to be in great risk, facing rapid declines in a very rapid changing world, as the recently reported mass extinction associated with pathogenic chytrid fungus outbreak (Stuart et al. 2004; Pounds et al. 2006). Similarly, although insects also are known to be susceptible to environmental changes and to be good environmental indicators (Lenhard and Witter 1977) they are underrepresented in conservation genetics papers (only 3% of the total) even they represent the bulk of biodiversity in Latin America. Future studies should focus on good biological indicators of environmental stress and health conditions, such as amphibians and insects, especially in the current context of climate change and fast habitat destruction.

The genetic approaches used in conservation genetics in Latin America have been evolving from allozymes (Eguiarte et al. 1992) to the sequencing of complete mitogenomes (Shamblin et al. 2012) as shown in Fig. 1b. Allozymes, one of the most common types of marker on the 1990s, have become less used in the last 5 years, with

a strong shift towards the use of more neutral markers. Microsatellites were the most used genetic marker by Latin American publication (34.1%), followed by mitochondrial or chloroplast markers (22%). Microsatellites were also the predominant genetic marker used in the European publications (49% of the studies; Pérez-Espona and ConGRESS Consortium (2017), revealing that the useful microsatellites are still the favorite marker for conservation studies. However, in Latin America, the increasing presence of microsatellite papers was largely driven by a proliferation of primer notes (N = 69) describing microsatellites without any further elaboration or conservation objective. The appeal of these papers as research in a conservational context seems to be an artifact to call the attention or to get it published easier.

It is noteworthy that conservation research projects have been slow in incorporating broader genomic approaches, as has been seen in other parts of the world (Shafer et al. 2015). The analyzing SNPs through genomic sequencing approaches, despite their promise to deliver improved results, were identified on only 2 studies out of 498. This small number can be partly explained by the relatively high costs of genome genotyping when compared to other markers, and by the difficult in analyzing big databases. However, considering the higher abundance of quality genetic information given by the use of SNPs genotyping, we predict that their use will increase in the next decade, just as the combined use of more than one marker has increased in recent years. Although genomic approaches may not necessarily improve conservation by itself, their great power should be harnessed to promote advances in the field. For example, a good deal of research has focused on quantifying genomic differences between closely related or cryptic species. In some cases, sections of the genome support the morphological definitions, but these sections are small and would not be detected by standard microsatellites or mitochondrial analysis (Poelstra et al. 2014). We therefore strongly encourage research groups and funding agencies to promote the use of large-scale, genome-wide technologies, with the goal of going beyond neutral markers and to address broader conservation issues such as inbreeding depression, local adaptation (including climate change and other anthropogenic effects), demographic history, natural and human-induced hybridization, captive breeding and assisted migration (Allendorf et al. 2010; Gompert 2012). Patterns of genetic variation assessed across the whole genome should enable broader and more efficient conservation measures by greatly enhancing our knowledge of past events and improving methods to design and monitor future management efforts (Bourlat et al. 2013). However, the data provided by these new tools should be interpreted carefully, especially because we are still very limited by our knowledge of the genome to give clear management recommendations which finally could lead to widen the gap between conservation and genetics (Shafer et al. 2015).

Although the focus of research is slowly changing, with a slow increase in the number of broad and multidisciplinary papers, there is still an emphasis on papers focused primarily on describing patterns of population structure (41.8%) using microsatellite markers in combination with either chloroplast or mitochondrial DNA sequence variation. This occurred mainly because many studies are focused on a single-species short-term studies, mostly conducted during graduate student programs, without any integration with other disciplines.

When we evaluated whether there was any apparent bias to focus on IUCN-listed species, we found that a large number of studies have been done on non-listed species (N = 314; 47%) versus IUCN-listed species (N = 357; 53%). This large number of species without a specific evaluation of the level of conservation threat is perhaps unexpected, given the large number of declining species such as mammals and birds in Neotropical regions (Dirzo et al. 2014). However, it may also reflect the relative ease in working with more abundant and less protected species.

We found a strong relationship between the total studied species for each country and the IUCN species for the same country (Fig. 3), maybe because could be easier to obtain funding to study IUCN species. However, contrary to what was expected, a weak relationship existed between the number of conservation genetic papers and the number of IUCN species of each country. Also, there was no correlation between the number of studied IUCN species and the total number of IUCN species listed for any country, although it should be noted that some countries published more papers related to IUCN-listed species (e.g. Chile) than others (e.g. Honduras) (Table 2). These trends probably reflect the difficulties on obtaining sufficient samples from threatened species, as well as the added complication of obtaining appropriate research permits, especially for studies that require invasive sampling. Other contributing factors probably also be that: (1) IUCN listings are limited to 5% of total biodiversity (IUCN 2016), thus, considering national lists of species of conservation concern may be more appropriate; (2) lack of funding for long-term monitoring and research studies using non-model species; (3) lack of political support for the development of policies encouraging conservation of "flagship" and "umbrella" species as model species for conservation; (4) insufficient collaborative efforts among researchers of the same discipline working in different geographic areas, as well as with those of other disciplines, including between theoretical and management-oriented researchers; in particular this should be improved considering highly migratory species (e.g. Torres-Florez et al. 2014); (5) commercial interest species seem to be more attractive to study (e.g. plants) (Oliveira-Miranda et al.

2013) and (6) a great number of species in threatened ecosystems are being studied, in order to anticipate the effect of their extinction debt (i.e. delayed extinction), even though these species are not considered as threatened by national or global red lists. Pérez-Espona and ConGRESS Consortium (2017) found that 61% of the European publications on conservation genetics included listed species in IUCN Red Lists, but that 78% of those studies were on species classified as Least Concern. These results, together with ours on Latin America, indicate that there is a need to focus on strategies that help prioritize research on species that are threatened or data deficient.

Based on the number of peer-reviewed publications in conservation genetics field in Latin America, the search for publications used in government management policies retrieved few results. Moreover, a large number (N = 19) were only cited in non Latin American government documents (e.g. USA, Canada). Also many (N = 34) were just published in government reports, without leading to conservation measures, and others (N = 10) was just cited in environmental assessment or environmental impact studies and presented by private parties to government agencies. With that, we do not intend to say that other conservation and ecology fields have been doing better, but we just want to call the attention to the importance of our discipline to conservation of biodiversity. This gap between theory and practice highlights the necessity that practitioners understand the relevance of genetics research, that scientists make their results more accessible to the conservation practitioners and all parties perceive the importance of increasing their communication to facilitate the knowledge transfer.

Although there are a great number of conservation genetics papers that did not focus on threatened species, some of these: (1) used model species or non-threatened species to develop theoretical models or to propose the protection and management of certain environments (e.g. *Vellozia gigantea*; Lousada et al. 2011), (2) aimed to solve broader species complex (e.g. Amazonian fishes; Piggott et al. 2011), (3) were part of phylogenetic studies (e.g. *Pocillopora*; Pinzon and LaJeunesse 2011), (4) represented previously unrecognized species (e.g. *Leopardus guttulus*; Trigo et al. 2013), (5) focused on species that the authors' suggested be included in the IUCN red list (e.g. *Dion angustifollium;* González-Astorga et al. 2005) or (6) used genetics for disease ecology studies (e.g. *Plasmodium* in birds; Levin et al. 2013). These approaches and conclusions are emblematic of a discipline that is maturing and that is increasingly focusing on new theoretical paradigms and approaches to analyze conservation problems. Moreover, these kinds of studies broaden the scope of conservation genetics by demonstrating the links among model, non-model and threatened species.

Despite the substantial advances in the field of genetics, impediments to application for conservation efforts have been arising around the globe, including Latin America. Thus, it is very important to better connect theory with practical applications, as has been previously discussed (e.g. Laikre 2010; Funk et al. 2012; Hoban et al. 2013a; Gordon et al. 2014; Shafer et al. 2015; Haig et al. 2016; Hogg et al. 2017). In Latin America, as in other regions, more emphasis needs to be placed on the practical application of genetic principles to the management of threatened species, and on the development and enactment of conservation plans. One possible explanation for this disconnect is that the knowledge obtained from scientific research is often not effectively communicated to those with the power to make and enact policy (Hoban et al. 2013a; Haig et al. 2016). Mechanisms and incentives are needed to frame research so that it is relevant and accessible and can be effectively applied in conservation efforts. Another way to attain conservation goals using genetics will be to increase not only the number of formal academic programs in conservation biology in the region (Rodriguez et al. 2005; Mendez et al. 2007), but also workshops and seminars (e.g. ReGeneC in Latin America, ConGRESS in Europe, and USFWS advanced conservation genetics training webinars (https://nctc.fws.gov/topic/online-training/webinars/advanced-conservation-genetics.html), Rodríguez-Clark et al. 2015; Hoban et al. 2013b). It is also important to create governmental laboratories that apply molecular tools to solve, translate and disseminate information about conservation problems (Haig et al. 2016), as is the case of some government agencies in other places of the world (e.g. US National Marine Fisheries Service NOAA or the Canadian Forest Gene Conservation Association). In the same way, the government authorities should support the establishment of genetic reserves (e.g. genetic resources reserves), as well as transnational agencies or conservation programs promoting biodiversity initiatives that cross political borders (e.g. Latin American Forest Genetic Resources Network; LAFORGEN). Moreover, it is essential to increase the financial support for conservation genetic studies and to renew efforts to train more scientists in the use, interpretation, and integration of genetic/genomics research in the development of conservation strategies (Fig. 4).

Conclusions

Here, we reviewed trends and described patterns of published scientific research on conservation genetics in Latin America. Although progress is being made in the application of some of these research tools, there is a great need and opportunity to better integrate genetic research and management actions to improve environmental impact assessments (Sagarin et al. 2009) and for genetic information to be used in the development of management plans. Although there often will be a time lag between the publication of a

research paper and the resulting management action, genetic tools provide a great opportunity to shorten this process, and thereby better conserve our planet's biodiversity, while making decisions and monitoring the effects of management actions using the most informative tools possible. Our results confirm that there is a relative bias in the species that receive the most scientific attention, demonstrated the need to support broader studies and carefully review the research efforts and funding targets. Furthermore, our results highlight the need of linking theory and practice. Bridging the gap is most urgent in countries with high biodiversity and high pressure to extract natural resources. The concrete, measurable data provided by genetic approaches are often very effective tools to help establish and enforce adequate legislation to slow the loss of biodiversity. It is very important that scientists and decision makers interact more to effectively achieve the biodiversity conservation that is needed in this region.

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