Opinion

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Genomics and the challenging translation into conservation practice

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The global loss of biodiversity continues at an alarming rate. Genomic approaches have been suggested as a promising tool for conservation practice as scaling up to genome-wide data can improve traditional conservation genetic inferences and provide qualitatively novel insights. However, the generation of genomic data and subsequent analyses and interpretations remain challenging and largely confined to academic research in ecology and evolution. This generates a gap between basic research and applicable solutions for conservation managers faced with multifaceted problems. Before the real-world conservation potential of genomic research can be realized, we suggest that current infrastructures need to be modified, methods must mature, analytical pipelines need to be developed, and successful case studies must be disseminated to practitioners.

Conservation biology and genomics

Like most of the life sciences, conservation biology is being confronted with the challenge of how to integrate the collection and analysis of large-scale genomic data into its toolbox. Conservation biologists pull from a wide array of disciplines in an effort to preserve biodiversity and ecosystem services [1] and genetic data have helped in this regard by, for example, detecting population substructure, measuring genetic connectivity, and identifying potential risks associated with demographic change and inbreeding [2]. Traditionally, conservation genetics (see Glossary) has relied on a handful of molecular markers ranging from a few allozymes to dozens of microsatellites [3]. However, for close to a decade [4] genomics – broadly defined as high-throughput sampling of nucleic acids [5] – has been touted as an important advancement in the field, a panacea of sorts for the unresolved conservation problems typically addressed with genetic data [6,7]. This transition has led to much promise but also hyperbole, where concrete empirical examples of genomic data having a conservation impact remain rare.

Under the premise that assisting conservation of the world's biota is its ultimate purpose, the emerging field of conservation genomics must openly and pragmatically discuss its potential contribution toward this goal. While there are prominent examples where genetic approaches have made inroads influencing conservation efforts (e.g., Florida panther augmentation [8,9]) and wildlife enforcement (i.e., detecting illegal harvesting [10]), it is not immediately clear that the conservation community and society more broadly have embraced genomics as a useful tool for conservation. Maintaining genetic diversity has largely been an afterthought when it comes to national biodiversity policies [11,12] and attempts to identify areas that might prove to be essential for conserving biological diversity rarely mention genomics (e.g., [13,14]). An obvious reason for this disconnect is that many of the pressing conservation issues (e.g., [15,16]) simply do not need genomics but instead need political will.

The traditional use of genetic data in conservation biology has been historically demarcated into two interrelated areas [3]: (i) understanding how evolutionary processes such as genetic drift, selection, and migration shape genetic and phenotypic variation of natural populations and determine population structure; and (ii) more specifically, describing the effects of low effective population size on genetic variation and population viability. Nested within these are more general conservation issues such as resolving taxonomic uncertainties, preserving local adaptation, and offsetting inbreeding depression (Table 1). Whether genome-scale data can improve inferences within these two areas and better inform conservation initiatives remains up for debate. Furthermore, there are a plethora of uncertainties that practitioners need to be aware of, and considerable obstacles that need to be overcome, before genomics can make the transition to applied conservation science. Many of the qualitatively novel aspects of genomic analyses, which include monitoring of epigenetic markers [17], environmental DNA approaches to assay species communities [18], and transcriptome assays [19], are still at an exploratory stage and are far from seeing use in real-world conservation issues.

Here we focus first on how traditional applications of genetics in conservation can benefit from scaling up to genome-wide data. In particular, we highlight two key areas that have received attention in the literature:

Glossary

Adaptive locus: a region of the genome under selection that encodes a phenotype (or is closely linked to a causative locus) with fitness consequences in a particular environment.
Annotation: the process of delineating and assigning function to genetic sequences.
Background selection: the loss of genetic diversity at neutrally evolving sites that are linked to sites under purifying selection.
Candidate genes: genes putatively underlying variation in a certain phenotype.
Coalescent theory: a retrospective population genetics framework that traces genetic variants of a locus to the most recent common ancestor. Used to infer demographic parameters of population histories.
Conservation genetics: uses genetic markers to help conserve biodiversity and manage species and populations. Traditional genetic markers include allozymes, microsatellites, and targeted gene sequences.
Conservation genomics: uses genome-wide information to help conserve biodiversity and manage species and populations. Genomic data is derived from high-throughput sequencing technology. Relevant examples are whole genome resequencing and targeted approaches like exome sequencing, GBS, SNP genotyping, and transcriptome sequencing.
Effective population size: a population genetics convention describing the number of breeding individuals in an ideal population that would lose genetic variation at the same rate as the observed population.
Environmental DNA: DNA found in environmental samples (e.g., water, soil) that can be used in genetic or genomic analysis. This contrasts with traditional approaches that target a specific organism or tissue.
Genetic drift: the loss of genetic variants due to random sampling from one generation to the next.
Genome assembly: the process of ordering and orienting sequencing into a contiguous consensus sequence of the genome.
Genotyping by sequencing (GBS): the sequencing of a repeatable subset of the genome seeded by restriction enzyme recognition sites. Restriction site-associated DNA sequencing (RAD-seq) is another commonly used term.
Haplotypes: particular combinations of alleles at collinear positions along a stretch of DNA.
Inbreeding: the increase of genomic segments in identity by descent due to mating between closely related individuals. Results in an increase in homozygosity, potentially revealing detrimental recessive alleles with negative fitness consequences.
Linkage disequilibrium: the non-random association of alleles at two or more loci.
Orthology: homologous DNA sequence descended from a shared common ancestor.
Outlier locus: a region of the genome that, based on user-defined criteria (often extreme population differentiation), deviates from the rest of the entire genome.
Recombination: the process of genetic exchange between homologous chromosomes, often resulting in a new combination of alleles.
Transcriptome: the set of all RNA molecules transcribed from a DNA template.

Table 1. Main areas traditionally addressed by conservation genetics [3], current status of genetic and genomic approaches, and the contribution that genomics can potentially make

Category	Status of conservation genetics	Possible contribution of conservation genomics	Required for transition from basic to applied[a]
Evolutionary genetics of natural populations			
Demographic inference – population history	Regularly used Moderate resolution	Improved accuracy and precision Finer-scale population structure Less limited by sample size	Clear understanding of limitations and biases User-friendly software
Adaptive genetic variation	Minimally used Based on population correlations [77] or candidate gene approaches	Improved detection of adaptive loci Management frameworks proposed [28] Methods still emerging Interpretations unclear	In-depth validation studies Genome annotation
Quantitative genetic variation	Limited resolution Often dependent on pedigrees or targeted gene approaches	Improved detection of quantitative trait loci Active application (e.g., genome-wide association studies)	Ecological studies Genome annotation
Taxonomic identification and general diagnostics	Regularly used Moderate resolution Restricted to single individuals	Assay species simultaneously [78] Improved hybridization detection Improved detection of pathogens	Defined pipelines (Box 3) Repeatability
Effects of small population size			
Inbreeding detection	Regularly used Limited resolution [34]	Improved estimates of inbreeding [34,62] Novel genomic metrics [79] Assess impact on specific genomic regions or adaptive loci	User-friendly bioinformatics Genome annotation Practitioner demand
Population viability	Minimally used [80]	Improved estimates of inbreeding metrics used in viability models [80]	Practitioner demand
Additional applications			
Genetic monitoring	Minimally used [11]	Improved sampling regimens [63] More powerful biodiversity surveys	Practitioner demand Compliance [11]
Population census	Regularly used	Higher-throughput screening	Practitioner demand
Maternity, paternity, and kinship analysis	Regularly used	Useful when microsatellite power is limited [81]	Practitioner demand

[a]Steps required before genomics research can regularly be applied to conservation issues.

identifying adaptive loci and the increased resolution afforded to genomic tools. Although the attention is warranted, part of our goal is to highlight the current limitations associated with the analysis and interpretation and suggest how conservation practitioners should best deal with the uncertainties arising from the novel possibilities that genomic data offer. We argue that both of these areas remain a largely academic pursuit and, compared with conservation genetics, conservation genomics is far from seeing regular application. We discuss why the uptake of genomics in conservation has been, and is likely to continue to be, difficult for practitioners and propose solutions to overcome the gap between basic genomics research and conservation practice.

Scaling up: what can genomics do for conservation genetics?

From a conservation geneticist's viewpoint, the genomic approach offers a dramatic increase in the number of variable genetic markers used (generally SNPs). This advance should in principle improve the precision of estimating diversity and population demographic parameters (e.g., effective population size) of conservation relevance [6,20]. Whole-genome sequencing, sequencing targeted portions of the genome [21], and direct genotyping of a random subset of the genome [generically referred to as genotyping by sequencing (GBS)] [22] permit the assaying of genomic diversity at many orders of magnitude above the traditional number of predesigned genetic markers. These approaches, GBS in particular, bypass the laborious process of marker characterization, primer development, and genotyping required for microsatellites and can be compared and combined across laboratories (which is difficult for microsatellite loci). Genomics further opens up the possibility of screening individuals and populations for adaptive loci, which is suggested by some to be the biggest potential contribution of genomics to conservation [5]. While targeting candidate genes (presumed adaptive) or serendipitously finding neutral markers linked to adaptive loci has not been uncommon in the conservation genetics era, given the low linkage disequilibrium often seen in natural populations [23] and the polygenic nature of many traits [24], screening the entire genome holds considerably more power. Importantly, experimental systems have given us clues about the signatures that adaptive evolution leaves on the genome [25] and academic interest in using genomics to explore local adaptation in the wild has grown considerably (e.g., [26,27]). Conservation genomics is directly impacted as it draws from the methods and models developed in this basic research.

Numerous reviews have covered these advances in relation to conservation in detail [6,20,28–33] and novel applications and analyses are still emerging (Box 1). It is fair to say, however, that to date conservation genomics and the broader fields of ecological and evolutionary genomics are far from mature. While much praise and promise

Box 1. An emerging area stemming from ancient DNA technology

Genomic analysis of ancient samples – considered anything from a museum specimen to archaeological specimens [84] – can establish baseline levels of genetic parameters in ancestral populations before demographic declines [85]. This concerns both the amount of genetic variation that might have been lost over time and the origin of contemporary population structure. The timing of population fragmentation and how this is related to past changes in the environment (e.g., anthropogenic impact, climate change) can provide valuable insight into current processes influencing population viability. For example, determining whether low effective population size or high population structure is inherent to the biology of a species or a direct result of recent anthropogenic disturbance is useful information to have when factoring genomic data into conservation planning.

Ancient DNA and genomic approaches provide another advantage in that they are less constrained by sample quality. The latter is illustrated by the fact that entire genomes have been reconstructed using optimized genomic approaches on 400 000-year-old samples of early hominids [86]. Sample quality is of direct concern to conservation biology, since sample collection and quality become increasingly difficult when the species of interest is rare or elusive in the wild. Conservation biologists often need to resort to museum samples or noninvasive sampling (e.g., scat, hair, scales) of poor quality. Utilizing genomic techniques often employed for ancient DNA studies (e.g., [85,87]) not only has potential for the recovery of genetic information from the species of interest, but additionally reveals aspects of pathogens (e.g., [88]) that might prove relevant to conservation and management.

has come with adding genomics to the conservationist's toolbox, challenges and uncertainties that do not exist with conservation genetic data have also arisen.

Detection of adaptive loci

Almost every review of conservation genomics has discussed the potential of emerging genomic tools to identify and study genetic variation with fitness consequences that are potentially involved in local adaptation [6,20,28,33]. The inclusion of markers that reflect local adaptation would augment the identification of conservation units and improve detection of genomic regions causing inbreeding depression [6,28,34]. Identifying adaptive markers would also be useful for conserving evolutionary processes (e.g., [35,36]) and genes associated with increased relative fitness could be propagated via human assistance, possibly including purposeful hybridization to maximize adaptability to changing environments [37,38]. This facet of conservation genomics clearly has the potential to provide information on the species, population, and individual level that was inaccessible using traditional genetic markers.

However, the detection of adaptive loci is challenging and interpretations are often vague. Screening genomes for loci under selection, let alone providing clear evidence for adaptive variation, remains an active area of academic debate and research [39,40]. It is becoming increasingly clear that many genes with small effects underlie phenotypic variation of fitness relevance [41,42], which makes their detection difficult. A further challenge is that the loci underlying adaptation need not exhibit clear signals of recent selection [43], and while studies have shown genomes under pervasive selection with many loci linked to adaptive genetic variation [27], others have documented virtually homogeneous genomes with only a few regions of presumed fitness significance [26]. Thus, while genome-wide data provide access to the adaptive genomic landscape, the signatures of adaptation vary on a case-by-case basis and could simply go undetected. In current practice, adaptive loci are often equated with outlier loci showing extreme population differentiation [39,44]. However, outlier loci often fall within areas of low recombination and are often the result of nonadaptive processes [39]; in such cases, the outlier regions could simply be reflective of demography, background selection in areas containing genomic features (i.e., centromeres), or sequence assembly artifacts. For example, in a genomic study on flycatchers (*Ficedula* spp.) almost all outlier peaks were likely not the result of selection imposed by the environment but instead reflected areas of low diversity generated by linked purifying selection [39,45]. Signals, perhaps prematurely associated with local adaptation, could instead be caused by numerous other processes such as mate choice, selfish alleles, or background selection acting on a heterogeneous recombination landscape [26,46–49]. Most genome datasets of wild populations will have neither a genome assembly to assess the spatial distribution of putative adaptive variation [50] nor the necessary information on recombination rates to avoid false-positive and false-negative inferences of local adaptation.

Given the multitude of uncertainties surrounding the detection and interpretation of adaptive loci, how can they best be implemented into a conservation framework? In his seminal essay, Michael Soulé [1] discussed the need for conservation biologists to tolerate some degree of uncertainty, and this will be the case for adaptive loci for the foreseeable future. While explicit conservation frameworks incorporating adaptive loci have been proposed [28], empirical examples and case studies of their application remain lacking. Where clear ecotypes exist, diagnostic outlier loci can be a valuable tool for monitoring stocks (e.g., salmon fisheries [51]) regardless of their adaptive significance. In less clear cases, the framework of Funk *et al.* [28], which advocates for a hierarchical approach using a combination of outlier and neutral loci to manage populations, is a valid approach. As there is likely to be a trade-off between genetic uniqueness and genomic diversity [52,53], we do not advocate managing only outlier loci; instead, where putative genetic contributions to adaptive variation can be identified, it should remain standard practice to incorporate additional information in the form of neutral markers or phenotypic data.

This still leaves a broader question unanswered: how much weight should be given to putatively adaptive variation that appears important at present but holds no information about future adaptive potential? As the proportion of gene sequences with functional annotations grows, the value of individual loci for conservation will increase (e.g., detecting disease susceptibility [54]) and it is conceivable that loci of known function could be managed and propagated under certain conservation scenarios (e.g., disease outbreak in a small population; see also Box 2). In most cases functional annotation can be borrowed from related species [55] and databases (e.g., the Gene Ontology

Box 2. Conservation genomics and translocations

Endangered species are often vulnerable to pathogen outbreaks, both in captive-breeding populations and in small, isolated natural populations. With high-throughput sequencing approaches even trace amounts of pathogen or parasite DNA can be detected in various types of sample (e.g., environmental DNA [18]) and host species can be readily identified [89]. This technology provides a rapid and cost-efficient way to identify and monitor pathogen load in populations at risk. Translocation and reintroduction programs could benefit from rapid genomic testing of pathogen load before release and select individuals based on desired criteria. Genomic screening could also allow the selection of individuals according to specific genetic signatures or simply maximum variation. For the purpose of conservation interventions such as the founding of captive populations, genetic rescues (i.e., restoring positive growth [90]), or assisting migration, these data could be vital and the ability to monitor the outcomes after such interventions would be enhanced (e.g., Figure I [83]).

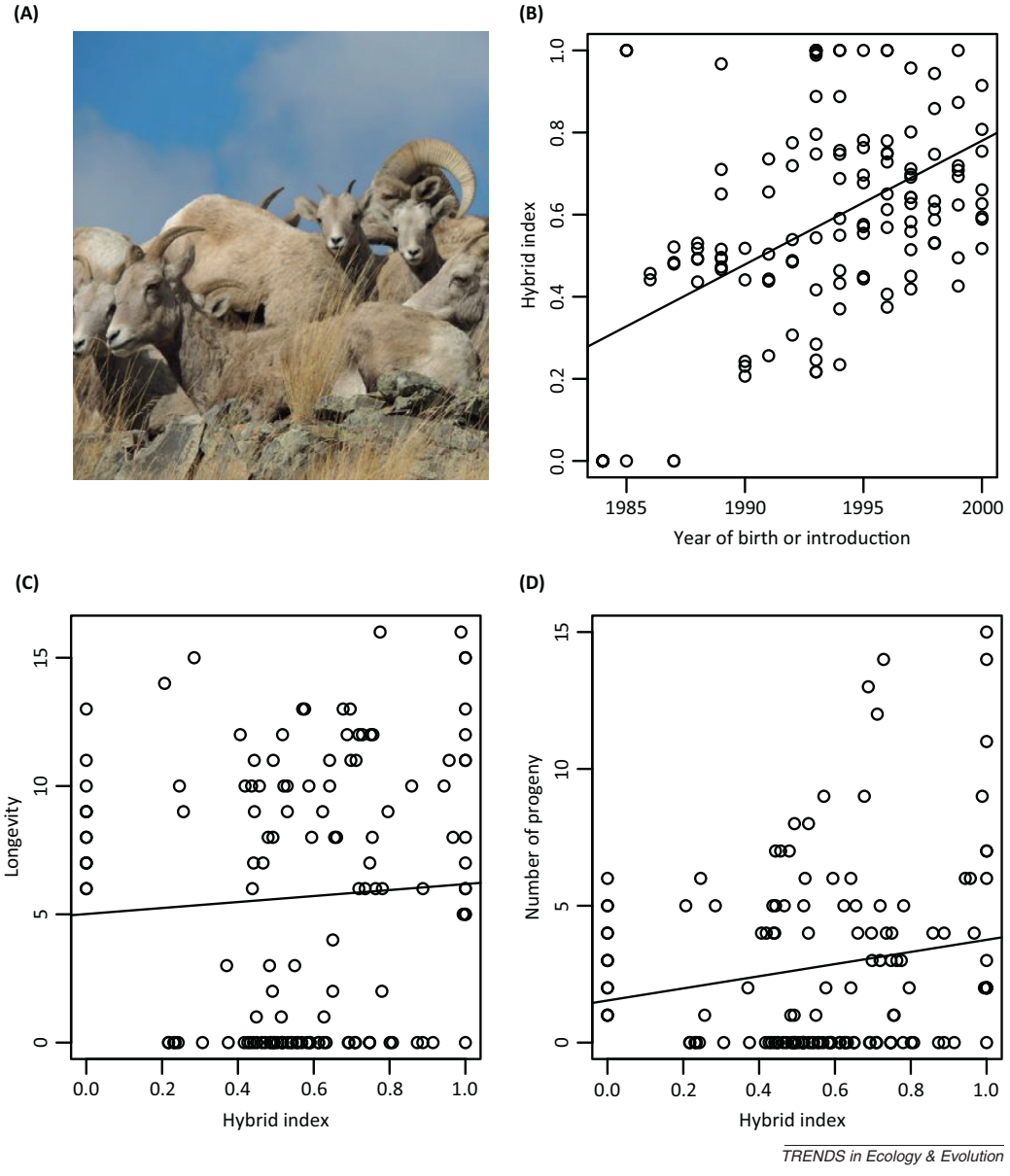


Figure I. Genetic rescue of a population of **(A)** Bighorn sheep (*Ovis canadensis*) at the National Bison Range, MT, USA. Two separate introductions successfully increased genetic diversity and reversed the negative effects of inbreeding [82]. Miller *et al.* [83] used population monitoring and genome-scale data to document the demographic impact of the introductions. **(B)** The hybrid index based on genome-wide data showed that migrant alleles (from translocated individuals) increased over time, and life-history traits including **(C)** longevity and **(D)** number of offspring both increased with migrant ancestry.

Consortium) under the assumption of orthology, although with unclear implications for the organism in question [56]. However, caution is warranted here for one reason: using human genetics as the example, even with whole-genome sequencing efforts on large sample sizes success in uncovering the genetic basis of rare recessive diseases – and it is those that will be exposed by inbreeding – remains limited [57]. Similarly, almost a decade of genomic work on the endangered California condor (*Gymnogyps californianus*) [58] has yet to uncover the genetic basis for chondrodystrophy, a recessive and lethal form of dwarfism. These examples, combined with the above arguments, suggest

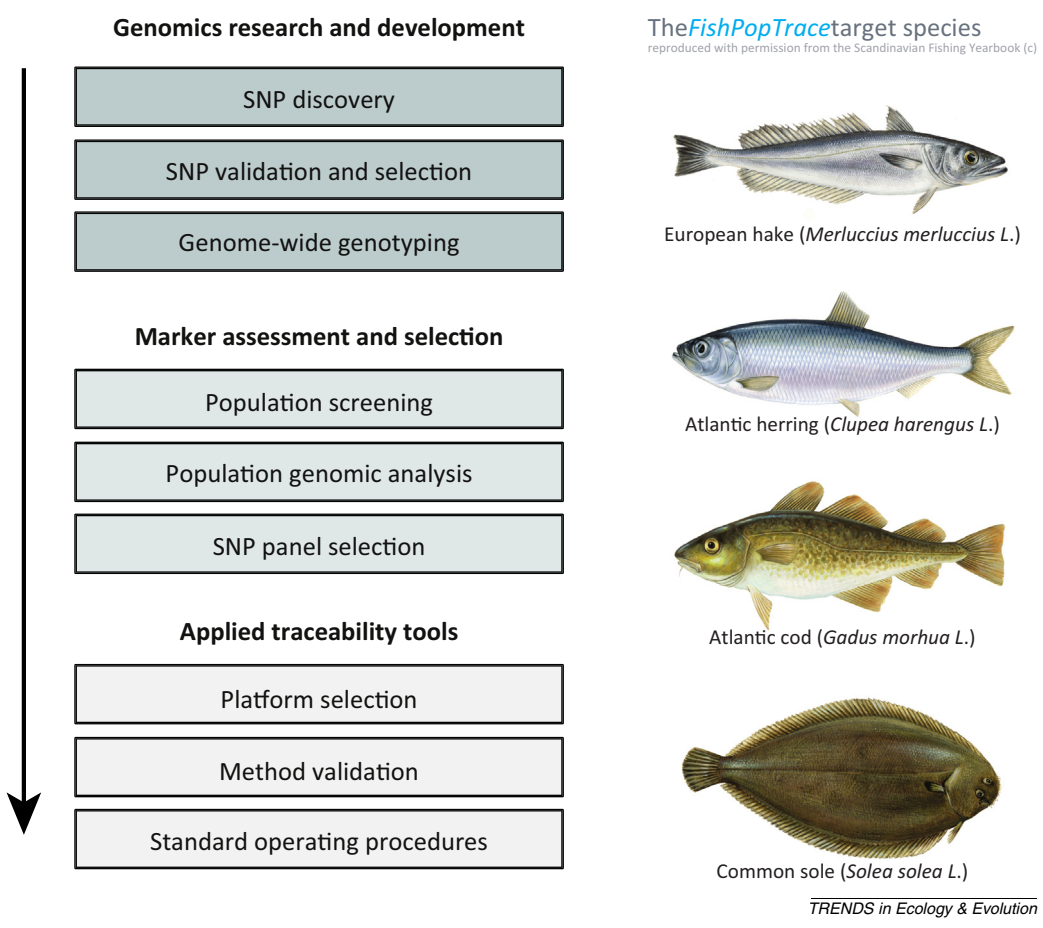
that we should not expect to detect, or invest a large effort in detecting, single adaptive genes of real consequence for conservation. Even if detected, the overall impact of individual loci on conservation and management will remain tangential (e.g., through population models and projections [54]) until genotype–phenotype correlations of the focal species can be inferred with a high degree of certainty.

Increased population genomics resolution

In the realm of population genetics there are clear advantages that come with ample genome-wide data. Notably, genomic data should improve estimates of population demography [44], which are becoming increasingly amenable to model-based inference using Approximate Bayesian Computation or composite likelihood models [59,60]. The characterization of processes such as inbreeding will be more precise [34,61,62] and genomic data can be a useful monitoring tool [63] or reveal subtle population structure that is relevant for stock management (Box 3). Novel analytical approaches using haplotype information [64] or long stretches of homozygous sites [65] to infer population demographic histories have produced particularly exciting results. However, similar to adaptive loci, using genomic data to infer demographic parameters is still an area of active academic research [66,67]. User-friendly software that accommodates genomic data – a key for practical application – remains limited (e.g., [67–69]) and high-performance computer clusters are generally required for data storage and analysis. Demographic studies that have explicitly tested the utility of genomic data have shown that essentially whole-genome sequencing should be used [60], estimates can be biased [39,70,71], and some parameters simply cannot be estimated [71]. While genomics does offer increased resolution for addressing many outstanding conservation genetic problems (Table 1), we must still accept some, perhaps large, degree of uncertainty in the estimates produced.

Box 3. From the laboratory to law: FishPopTrace

The step change afforded by genomic techniques and the transition from fundamental research to application can both be demonstrated by the development of genomic tools for fisheries management in Europe. The FishPopTrace project funded by the EU Framework 7 program utilized genome-wide technologies to identify and genotype SNP markers in four species of commercial fish: cod, herring, hake, and sole. These data were used by fishery geneticists to describe populations within species and subsequently to identify minimum SNP panels of maximum power to trace the geographical origin of fish in trade. FishPopTrace revealed population structure at a geographical scale not previously recognized, leading directly to tools for applied conservation (e.g., identification of illegal trade and mislabeling). The UK government and the Marine Stewardship Council are now using the stock traceability information in a regulatory and authenticity verification framework. The challenge for applied conservation laboratories will be to develop similar pipelines and apply this level of rigor to less charismatic or economically valued species.



Here, we propose that conservation practitioners are best served by focusing on broad-scale population genetic patterns that might be relevant to conservation issues of interest. From a practical viewpoint, the difference between three and five migrants per generation is not important, but three versus 500 is. Explicit formulation of the role that genomics can play in achieving 'conservation priors' – meaning a predetermined objective aimed at improving population viability – is a useful model in this regard [5]. If maintaining genetic connectivity were set as a conservation prior, for example, differentiating low- versus high-migration scenarios with genomic data would clearly be informative. We stress, however, that even with more precise estimates the organism's biology still must be taken into account. If there is undetected family or population substructure represented in the genomic data, the estimated demographic parameters, which generally rely on coalescent models, will reflect some hierarchical level (i.e., the region or species) instead of the population of interest at its current state. This effect is illustrated in a conservation study on Chinook salmon (*Oncorhynchus tshawytsca*), where effective population size estimates inferred with genomic data were occasionally higher than the census size [70]. While this is a conceptual issue that also influences conservation genetics, it is an important consideration that will impact the utility of the parameters estimated from genome-scale data that might otherwise be overlooked by naively expecting not only increased precision, but also higher accuracy.

The gap between genomics research and conservation application

We are approaching the $1000 genome [72], meaning that generating genomic information has become increasingly accessible even for non-model organisms with large genome sizes [50]. The pursuit of improved resolution and adaptive loci will transform many conservation genetics laboratories. Additionally, as life science companies dismantle old instrumentation, discontinue software, and support only the new high-throughput instruments, many conservation genetic applications will simply be forced into using genome-wide approaches [5]. However, gaps remain in the transfer of fundamental genomic research to end-user conservation application. The scientific and policy-practitioner communities operate in largely separate spheres (Figure 1) and we feel that introducing genomics into the equation will increase the gap. In the pre-genomics era of microsatellites and Sanger sequencing, individual laboratories could start with sample collection and proceed all the way to data analysis and application. With high-throughput sequencing, data generation is predominately outsourced and

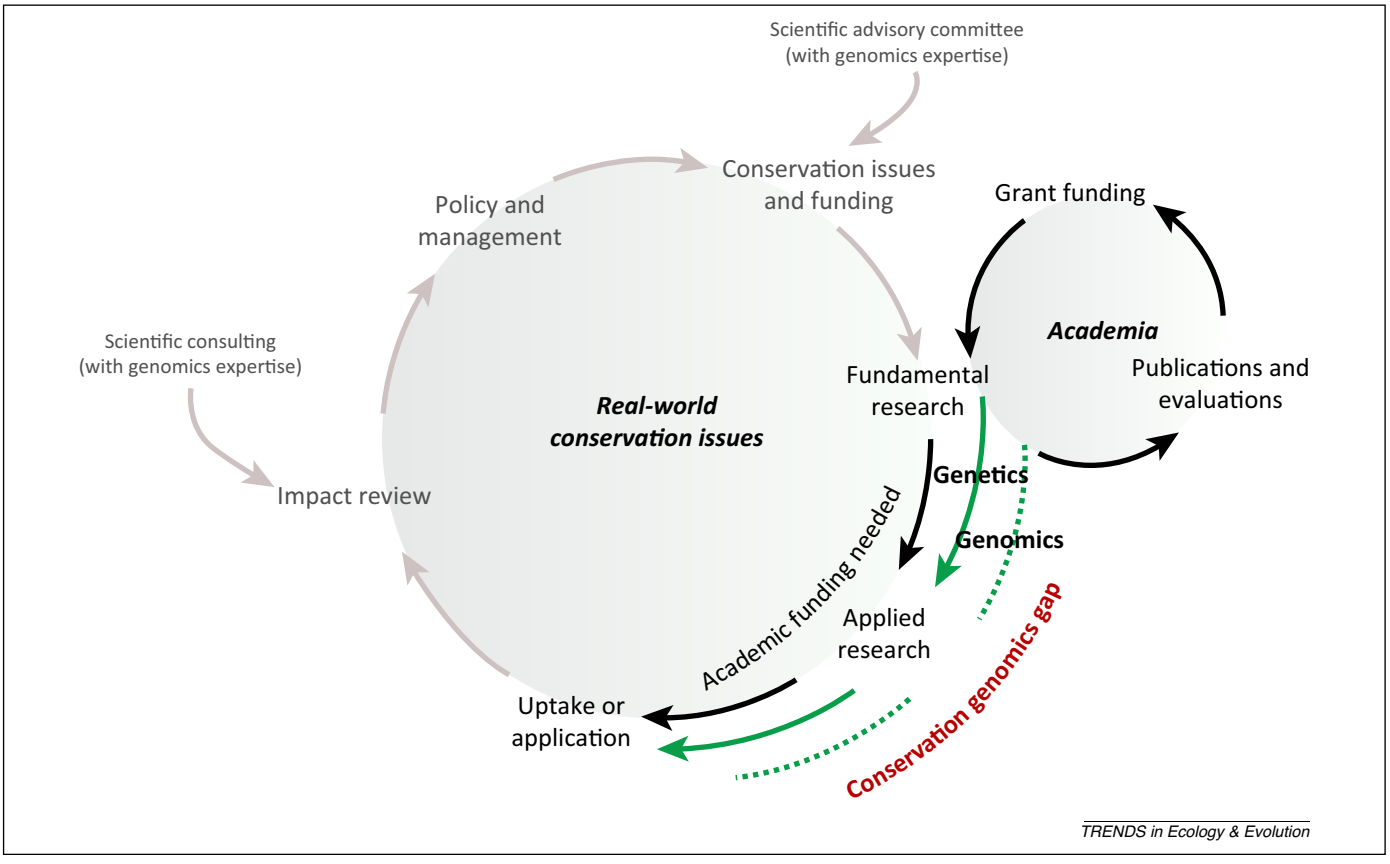


Figure 1. Schematic for the translation of conservation genomics research to conservation policy and action. Currently there are two largely separate spheres of applied and basic research. The black lines represent basic research to applied workflow, with the green lines reflecting the extent to which conservation genetics and genomics currently fit into this scheme – note that conservation genetics has integrated into the applied sphere. The broken green line represents the gap we see between the academic groundwork readily embracing genomic technology and on-site conservation needs. The gray lines are reflective of the larger framework we envision (and that is emerging) where conservation questions directly fund conservation genomics research and feed into management and biodiversity policies. Importantly, the applied component maintains a firm link to the conceptual advances driven by basic research.

data cleaning and analysis often require expert consultation, creating multiple layers that do not exist with conservation genetics. Thus, advances in genomic methods might contribute to an increasing gap between research and application without a concerted effort on the part of both scientists and conservation practitioners to build effective bridges. Broadly speaking, these gaps can be described in terms of the knowledge, tools (i.e., standardized methods and user-friendly analytical pipelines), finances, and communications needed to link fundamental research with applied science. Funding to the basic and fundamental research institutions is often not compatible with frontline conservation actions and will aid in biodiversity conservation only if applied research – which is often seen as repetitive and incremental from a basic research perspective – is supported (Figure 1).

Concluding remarks: bridging the conservation genomics gap

In our view, it seems most fruitful in the current academic and conservation frameworks to encourage genome scientists to communicate their research to practitioners and stakeholders and apply their techniques to conservation issues where appropriate. We stress that, for the conservation practitioner, it is not important to differentiate genetic from genomic methods; rather, it is sufficient to convey that we can now address a broader range of questions than before. The uncertainty in the new approaches should be clearly acknowledged. In the long term, it will be crucial to develop a range of laboratory protocols (e.g., [73]) and fail-safe tools that support conservation genomic applications and deliver tangible benefits to conservation managers (Box 3).

However, there is a more systemic problem with the current state of conservation genomics, in that there is little incentive for academic researchers – whom in many ways lead the conceptual debate and the development of genomic tools vital to application – to engage fully in applied conservation. Applied conservation genomics research is generally not reinforced in current funding schemes and some academic research is branded as conservation (perhaps only as a selling feature for publication), even when it has little real-world conservation value. Developing a genomic tool or framework that can be implemented by practitioners requires a level of rigor and repetition that is not conducive in the 'publish-or-perish' climate. Thus, we must rethink how the academic and conservation community funds conservation genomics research. In particular, we envision a research-policy framework analogous to translational medicine, or colloquially 'bench to bedside', that enables basic research to have an applied impact [74]. Here the funding is partly driven by designated conservation questions and application and uptake are the measured currency, not (just) publications (Figure 1). The applied output, evaluated by experts, leads directly into policy and ultimately cycles back to the funding body. Emerging examples, like the UK's research evaluation framework that specifically evaluates impact beyond academia and Sweden's split governmental funding bodies with one emphasizing a link to stakeholders, should encourage bridging of the gap.

The key for conservation genomics will be for the academic and policy spheres to communicate in an effort to maintain a firm grasp on conceptual advances (driven by academic research) and on-site conservation needs (recognized by practitioners). We are not so naive as to think that we can restructure the current academic funding and political climate, but recognizing how the current system fails to deliver tangible results is a starting point. Identifying the critical gains from genomic analysis in relation to drivers like conventions [e.g., the Convention on International Trade in Endangered Species (CITES)] or extinction risks [e.g., the International Union for Conservation of Nature (IUCN) Red List] will be vital in this regard. In other words, if the IUCN or CITES requests specific information to inform their conservation decisions, can genomics be the tool to provide it? We would be remiss not to note that some progress has been made in overcoming these barriers. The IUCN recently formed a Conservation Genetics Specialist Group that evaluates such critical gains and over the past 3 years the EU Framework 7 Support Action Project 'ConGRESS' [75,76] has engaged over 300 stakeholders in Europe and canvassed their opinions on the use of genetics in practical conservation. While a need for the application of genetic technologies could be demonstrated to ConGRESS, a clear link to genomics was not (yet) evident. Thus, conservation genomics still must prove its worth; explicit examples of realized gains from genomics need to be disseminated to the conservation community.

Genomics is not a substitute for biological replication or good experimental design; more sequencing will not provide an answer *per se* and the resolution required to address the question at hand or conservation prior needs serious consideration. We acknowledge that genomics can, and probably will, play a part in resolving future conservation issues but caution against unrealistically high expectations, call for a more open discussion of limitations, and express the need to identify a clear niche for genomics in conservation practice. With time, methods will mature, user-friendly analytical pipelines will be developed, and case studies will emerge; hopefully, this will promote an integrated research-to-application framework that will bridge the conservation genomics gap.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.tree.2014.11.009.

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