



VIEWPOINT

Conservation genetics: 50 Years and counting

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It has been 50 years since the landmark paper by Frankel highlighted the importance of genetic variation for continued evolution in the conservation of species. Despite major technological and theoretical advances in the analysis of genome data, we have failed to fully integrate genetics into conservation practice. The IUCN does not incorporate genetic data into their Red List assessment of species, and the relatedness of individuals in the studbooks of zoos are still only assessed by using pedigree records that contain uncertainty and error. Several obstacles have been responsible for the slow uptake of genetics in conservation: (1) the primary objectives of our activities differ across the conservation community; (2) inequality in exposure to advanced sequencing technologies and analytical tools has created a communication gap; and (3) most money in research has been allocated to funding scientific advances rather than their applications in the real world. These obstacles are more important than other alleged problems, such as the costs or complexity of genetic analyses, or scepticism about the relevance of genetic variation in species conservation. Fortunately, once acknowledged, these obstacles can be redressed so that real progress can be made in conservation.

Conservation biology is a “mission-oriented crisis discipline” that aims to evaluate human impacts on biodiversity and prevent the extinction of species. It is a multidisciplinary approach that integrates theories from the fields of ecology, ethology, demography, taxonomy, and genetics. The insights gained from these disciplines underpin many management decisions taken by conservation practitioners. Crucially, however, two parties in the conservation community—that is, the “geneticists” and the “practitioners on the ground”—have prioritized different

outcomes. The latter group consists of NGO conservation professionals—supported in various degrees by local government bureaucrats—and they have been working tirelessly on saving species from extinction by stopping habitat loss and/or mitigating its consequences. On the other hand, the geneticists and bioinformaticians have been improving their methods to quantify genetic variation and assess the mutation load in populations, developing evermore integrated and advanced analyses. These scientific endeavors have been fuelled by the funding environment in academia, which tends to evaluate the quality of research by the number of papers published in high impact journals, the number of citations, and patents. Less value has been given to the actual impact of the research on real-world problems, such as saving a species from extinction. Although this is gradually changing, this longstanding difference in values has further increased the divide between both parties. The drive for advancing technology and methods also meant that the understanding of the analyses has moved even further out of reach of non-experts. Indeed, in this fast-moving field, methods became obsolete even before they could be learned or applied in practical conservation. Sadly, our quest for increasingly advanced analytical tools may have steered us further away from what should have always been our primary objective—saving species from extinction and protecting their habitats. Do we really need a handheld sequencing machine to conduct meaningful conservation work? Rather than a Star-Trek-like tricorder, what the conservation community really needs are some nails and hammers to save the rocking ship from sinking.

For conservation genetics, the past 50 years have shown that “*the perfect is the enemy of the good.*” Yes, we have come

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a far way, and what can be done now with genomics we could not have imagined 50 years ago. However, the biggest advance we can make now is to stop tinkering with our tools. We must decide on a standardized set of summary statistics that can be extracted from genome data in a routine fashion. Those statistics need to be simple so that they can be understood by the whole conservation community. The statistics need to assess the severity of genomic erosion that impairs the fitness of individuals and the viability of populations: (1) the loss of genetic variation due to inbreeding and drift; (2) the introgression of genomes by the hybridization of species (rather than admixture); and (3) the accumulation and expression of deleterious mutations. So much can be learned by analyzing the genome of just a single individual of a population or species. It captures the signatures of past selection and the demographic history of an entire species, dating back to events from far before the current population decline. Those past events are important because the potential scars they may have left in the genome will affect the future viability of populations and species. Hence, these data are critical to help direct conservation management.

Furthermore, the statistics will need to conform to a universal standard to ensure that they are comparable across (closely related) species. The development of a "gold standard" approach is already underway for genome sequencing; the conservation genetic community now will need to adopt a similar approach for the downstream analyses. Once a set of robust statistics has been decided, they can be included in the IUCN Red List assessment as an addendum for each species. With the Earth BioGenome Project and many whole-genome sequencing projects underway, genomic data are rapidly being generated for many species. Conservation biologists can now post samples of their species to these sequencing consortiums to obtain high-quality reference genomes. The next step is to develop a service that can perform the downstream analyses to calculate and report these genomic summary statistics in an internationally accepted universal standard. I believe the insights gleaned from these statistics will significantly enhance conservation practice. First, they will improve the

assessment of the long-term extinction risks of species in the Red List, highlighting trends across taxonomies that may have thus far gone unnoticed. Although this may not be of immediate use to conservation on the ground, it could help to inform wider conservation policies and strategies relevant to the 2030 Agenda for Sustainable Development of the United Nations. Second, those statistics can also be calculated for a larger number of individuals of a species or population in resequencing projects. Such data are valuable for conservation on the ground, for example to assess the impact of different management strategies, and to inform ex situ conservation and genetic rescue programs.

Conservation practitioners have applied crucial "first aid," saving many threatened species from imminent extinction. It is now time to provide "second aid" to ensure that the small populations continue to thrive. This requires the integration of population genetic theory and genomic know-how into conservation; this must be done now, rather than pondering for another 50 years.

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Cock Van Oosterhout wrote the paper.

CONFLICT OF INTEREST

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