

Integrating genomics into conservation management

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Captive populations play a vital role in conservation, supporting both in situ and ex situ conservation projects. A healthy, self-sustaining captive population serves as valuable insurance against extinctions and a source of individuals for reintroduction into the wild. Genetic and genomic data can advance conservation and management across a range of scenarios. Although expanding, genomic data do not exist for most captive populations and there remain few examples of how these data can be integrated directly into conservation efforts. In this issue of *Molecular Ecology Resources*, Humble et al. (2020) present a chromosomal-level genome assembly for the extinct-in-the-wild scimitar-horned oryx (*Oryx dammah*), and resequencing data to survey genetic variation across captive populations. These data are exciting for reintroduction planning by offering guidance for selecting source populations to maximize global genetic variation and valuable resources for effective post-release monitoring. The genomic resources generated also are valuable tools with the power to yield novel and important insights into the evolution of scimitar-horned oryx and other antelope species.

KEYWORDS

bioinformatics/phyloinformatics, captive populations, conservation genetics, genomics/proteomics, wildlife management

Reintroductions are a powerful tool in species conservation. Hundreds of species have benefited from reintroductions, and they have been effective in curbing the accelerating loss of biodiversity (Soorae, 2018, Brichieri-Colombi and Moehrenschrager 2019). The ultimate goal of a reintroduction is to attain long-term persistence without human intervention. Genetic diversity is central to this goal, contributing to a species' adaptive potential and promoting biodiversity and ecosystem integrity. Seeded with abundant genetic diversity, a reintroduced population can grow and become self-sustaining.

Initial sampling of founders is a critical component of population establishment. Founding a reintroduction with a large number of unrelated individuals maximizes genetic diversity and provides a solid foundation for a successful reintroduction. Mixing founders from genetically differentiated source populations can better represent species-wide genetic variation (McLennan, Grueber, Wise, Belov, & Hogg, 2020; Ralls et al., 2018). To identify valuable source populations and develop a plan to sample them, it is necessary to survey

potential source populations. Surveys naturally include any remnant populations in the wild, and frequently incorporate studbook-managed captive populations (e.g., in zoos). Zoo-based captive breeding programmes aim to maintain gene diversity in populations over the long term through prioritized pairings that minimize mean kinship and thus sustain a valuable reservoir of genetic variation. Broadening our view to consider the entire in situ/ex situ spectrum reveals the potential value of semicaptive populations in private collections or ranches. These animals are typically managed using less stringent (or no) genetic management practices compared to zoo breeding programmes, yet they conceivably represent an untapped reservoir of genetic variation for conservation management.

Humble et al. (2020) apply a genomics approach to survey genetic variation in source populations of the scimitar-horned oryx (*Oryx dammah*), a species declared extinct in the wild (Figure 1). Captive populations exist in European, North American and Australian zoos, but most remaining animals are held within



FIGURE 1 A female scimitar-horned oryx (*Oryx dammah*) with her calf in the Ouadi Rimé-Ouadi Achim Wildlife Reserve in central Chad, one of the largest protected areas in the world. This reserve was the last major stronghold of scimitar-horned oryx before it was declared Extinct in the Wild by the IUCN in 2000. The ambitious reintroduction programme has successfully released animals into the Reserve, and recorded the first wild-born calves in decades. Future reintroductions will benefit from genomic data to select source populations. Image courtesy of Justin Chuvén

unmanaged private collections in the United Arab Emirates and the southern USA. A comprehensive reintroduction project has been under development since 2014, and the first animals arrived in Chad in 2016. Founder selection is key to the success of this large-scale reintroduction effort, and was a principal motivation for the Humble et al. (2020) study. The authors surveyed studbook-managed zoo populations of scimitar-horned oryx in Europe and the USA, and the largest private collection held by the Environment Agency of Abu Dhabi. By developing strong partnerships throughout the reintroduction planning process, the authors were able to survey across the spectrum of remaining ex situ populations to identify source populations that could be sampled to maximize global variation and increase adaptive potential in scimitar-horned oryx as they are reintroduced back into their native range in North Africa.

Collecting whole genome resequencing data offered unprecedented resolution for assessing genetic diversity in prospective source populations. Despite theoretical predictions that ex situ populations would harbour low levels of genetic variation, Humble et al. (2020) reveal surprisingly high levels of genetic diversity in scimitar-horned oryx populations, attributable to successful husbandry leading to rapid population growth in captivity. This result confirms earlier work using molecular markers with less resolution (Iyengar et al., 2007; Ogden et al., 2020). Humble et al.'s (2020) results also uncover the possibility that the semicaptive private collection was founded with a larger number of animals than previously thought, especially encouraging news for conservation.

In addition to high-resolution genetic diversity data, the chromosomal-level genome assembly generated by Humble et al. (2020) also facilitates the development of single nucleotide polymorphism (SNP) genotyping arrays for effective post-release

monitoring. Humble et al. (2020) used a combination of chromium sequencing (10X Genomics), which uses linked-read sequencing to create the base assembly, and Hi-C contact mapping, which generates long-range genomic position information using chromosome conformation capture. This combination of approaches greatly improves the scaffold N50 (to 100.4 Mb in Humble et al., 2020), and shows promise for studies of nonmodel species because it requires comparatively little template DNA (although the DNA should be of high quality). The robust chromosomal-level assembly provides a reference to develop powerful SNP arrays that can be used to genotype even low-quality samples, facilitating studies of inbreeding, relatedness, admixture and locally adaptive variation to improve post-release monitoring (Flanagan, Forester, Latch, Aitken, & Hoban, 2018).

The value of the quality oryx reference genome assembly extends beyond applied conservation benefits to provide a resource for evolutionary and comparative genomics. Chromosomal synteny found between the scimitar-horned oryx and cattle are relevant to the study of genome evolution and the analysis of homologous gene families. For example, cattle could be used as a model to predict putative functional genes in scimitar-horned oryx that could advance research, conservation and breeding programmes. Comparing genomes across Bovidae would also help better resolve phylogeny in this clade, in particular the muddled relationships among antelope species. Humble et al. (2020) also use their data to reconstruct historical demography in the scimitar-horned oryx, finding that the dynamic patterns of past population disturbance coincide with periods of known climatic change in North Africa, and are similar to trajectories for other North African grassland species. The pairwise sequential Markovian coalescent (PSMC) approach used by them has low power to detect recent demographic changes, but the data presented provide a foundation for future work to sequence additional individuals to reliably estimate recent demographic changes, for example using approximate Bayesian computation (ABC).

The future is bright for scimitar-horned oryx conservation. Genome-enabled founder selection benefits reintroduction efforts by increasing representation of global genetic variation and boosting adaptive potential. Ex situ populations, in particular those in studbook managed programmes, harbour more genetic variation than expected. In both zoos and private collections, populations can be more effectively managed through integrated management strategies informed by genomic data and modelling (Giglio, Ivy, Jones, & Latch, 2016; Wildt et al., 2019). As the scimitar-horned oryx reintroduction programme continues and populations become established, SNP arrays developed from the genomic resources presented in Humble et al. (2020) can be used to effectively monitor wild populations. Conservation is never more pressing than for a species that has gone extinct in the wild, and Humble et al. (2020) highlight how a better understanding of a species' genome can enhance applied conservation.

AUTHOR CONTRIBUTIONS

E.K.L. wrote and edited the manuscript.

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