

A deep dive into evolutionary genomics and its use in conservation science

Conservation and the Genomics of Populations. 3rd edition. Allendorf, F. W., W. C. Funk, S. N. Aitken, M. Byrne, and G. Luikart. 2022. Oxford University Press, Oxford, UK. 746 pp. US\$60.00 (paperback). ISBN 978-0-198-85657-3.

Conservationists usually face the problem of shrinking populations of endangered wildlife. In such cases, contemporary conservation management can greatly benefit from the genetic background of threatened populations that conservation genetics can provide (Allendorf, 2017; Hohenlohe et al., 2021). Undoubtedly, better-informed decisions can be made if conservation practitioners have access to information on genetic structure, genetic diversity, and other population genetic characteristics of populations requiring management. The genetic rescue of European adders (*Vipera berus*) in an isolated Swedish population has become a textbook example of a successful genetic management. High levels of inbreeding were identified as a potential source of the severe decline in that population, but after the temporal introduction of males from genetically more diverse populations, the isolated population successfully recovered and started to grow (Madsen et al., 2004). The case of this isolated adder population is a good example of how evolutionary genetics can turn the fate of threatened populations if population genetic information is available for management planning.

Conservation practitioners should ideally have access to population genetic information on endangered populations and, at least during their training, they should have the chance to learn about the toolkit of evolutionary genetics, which can deliver such information. And if we apply evolutionary genetics to address questions in conservation, we arrive at conservation genetics, the science of studying evolutionary genetics of usually small, fragmented populations that are on the brink of extinction. Luckily, there are textbooks on conservation genetics dedicated to advanced undergraduate and graduate students and a few targeting professionals in conservation as well. Two of these are the first and second editions of *Conservation and the Genetics of Populations*. As the title implies, these editions provide a detailed overview of population genetics and its implications for conservation biology. However, there has been a major leap in technology since their publication.

The recent revolution in obtaining high-throughput DNA sequence information from virtually any nonmodel organisms has made it possible to use genomic approaches in wildlife preservation and opened a new avenue in conservation genet-

ics: conservation genomics (Allendorf et al., 2010). The application of genome-wide variability in conservation does not only increase the resolution power of molecular genetic tools, but also opens a new avenue for asking exciting microevolutionary questions that can strongly influence conservation management decisions (e.g., by revealing adaptive variation) (Hohenlohe et al., 2021). Until now the relatively new field of conservation genomics had not been introduced to the conservationist reader through a comprehensive textbook. This gap is filled by the third edition of Allendorf et al.'s work, which really is a significant upgrade compared with the previous editions. It carries over most of the topics from the second edition, but there are newly included parts on genomics.

The third edition, however, is not just about genomics, and this is with a clear purpose. As emphasised by the authors, the use of genomic data requires a thorough understanding of the underlying theory of population genetics. Therefore, the book heavily builds on the previous editions and provides the reader with information on the basic principles of population genetics (e.g., the Hardy–Weinberg equilibrium, natural selection, effective population size, population subdivision), quantitative genetics, and the methods of studying genetic variation in natural populations. It also keeps an eye on anthropogenic challenges, including hybridization, invasion, exploitation of populations, and climate change. The book would not be a conservation genetics textbook without a strong focus on conservation and management, where the reader can learn about critical characteristics of endangered populations (e.g., inbreeding, population sizes, population connectivity), management units, and practices in conservation genetics.

The text is easy to comprehend by one with a basic understanding of graduate-level ecology and population genetics and achieves the goal of balancing theory, empirical evidence, and statistical analyses. As such, the book does not provide molecular genetic protocols to conduct the relevant laboratory analyses, but it does provide guidance to select the most suitable evolutionary genetic or genomic approach via well-chosen examples of a given conservation problem. These are illustrated by self-explanatory figures that in general are slightly modified from original research papers to highlight the main message of the text without getting lost in details otherwise important in a scientific paper. The study of conservation genetics and genomics is assisted by a comprehensive glossary, which even sheds light on such unusual terms as *gnomics* (see p. 582 for a surprising

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REFERENCES

- Allendorf, F. W. (2017). Genetics and the conservation of natural populations: Allozymes to genomes. *Molecular Ecology*, 26, 420–430.
- Allendorf, F. W., Hohenlohe, P. A., & Luikart, G. (2010). Genomics and the future of conservation genetics. *Nature Reviews Genetics*, 11, 697–709.
- Hohenlohe, P. A., Funk, W. C., & Rajara, O. P. (2021). Population genomics for wildlife conservation and management. *Molecular Ecology*, 30, 62–82.
- Holderegger, R., Balkenhol, N., Bolliger, J., Engler, J. O., Gugerli, F., Hochkirch, A., Nowak, C., Segelbacher, G., Widmer, A., & Zechos, F. E. (2019). Conservation genetics: Linking science with practice. *Molecular Ecology*, 28, 3848–3856.
- Madsen, T., Ujvari, B., & Olsson, M. (2004). Novel genes continue to enhance population growth in adders (*Vipera berus*). *Biological Conservation*, 120, 145–147.
- Theissinger, K., Fernandes, C., Formenti, G., Bista, I., Berg, P. R., Bleidorn, C., Bombarely, A., Crottini, A., Gallo, G. R., Godoy, J. A., Jentoft, S., Malukiewicz, J., Mouton, A., Oomen, R. A., Paez, S., Palsboll, P. J., Pampoulie, C., Ruiz-López, M. J., Secomandi, S., ... European Reference Genome Atlas Consortium. (2023). How genomics can help biodiversity conservation. *Trends in Genetics*, <https://doi.org/10.1016/j.tig.2023.01.005>

definition). The book ends with a useful appendix on probability, statistics, and coding and an extensive list of references. The appendix and references are unfortunately not available in all printed copies, but all readers can access them online at the website of the publisher at www.oup.com/companion/AllendorfCGP3e.

Genomics is seen in application in a brand-new chapter on population genomics, which presents an overview of genomic methods in nonmodel organisms. Besides this novel chapter, several studies are included from recent literature to exemplify the use of genomic approaches in conservation research. Another novelty is the inclusion of a chapter on practical conservation genetics, which helps bridge the long-recognized gap between conservation geneticists and conservation practitioners (Holderegger et al., 2019). I was especially happy to see new subchapters in the appendix on the use of Linux, coding in bioinformatics, and data filtering, which are key in several aspects of genomics. I felt disappointed, however, by the relatively little information on genome assembly in the book, which, considering how beneficial reference genomes in conservation are (Theissinger et al., 2023), could have been introduced in more detail, including information on different sequencing approaches and how to use them in the assembly process. This is one part of contemporary genomics that should be considered for inclusion in more detail in a future edition of this otherwise comprehensive textbook.

This book provides conservation biologists with an ideal way to get acquainted with evolutionary genetics and the use of genomics in conservation science. It will help readers gain insightful understanding of the theory of population genetics that underpins conservation genetics. If you are using or planning to use a genomic approach in conservation, go for this edition; it will be invaluable.

