

MOLECULAR ECOLOGY

Upcoming special issue: Conservation Genomics - making a difference.

Call for contributions to be open soon. For questions or queries please email Michael Hansen (mmh@bio.au.dk) or Ben Sibbett (bsibbett@wiley.com)

The title of this special issue could be read as either a statement or as a question. Conservation genetics is an established discipline with numerous examples of the use of molecular markers in conservation and management. When integration and use of genomic data in conservation became a realistic possibility, it was particularly highlighted how conservation genomics could shed light on crucial questions and problems that could not be answered by analyzing few genetic markers. This included issues such as understanding the genomic basis of inbreeding depression and the genetic architecture of functional traits and how this would be affected by anthropogenic pressure (Allendorf *et al.* 2010; Ouborg *et al.* 2010). Nevertheless, concerns were soon raised that an important gap existed between academic research in conservation genomics and translation into practical conservation (Shafer *et al.* 2015). There was an issue of resources: were the added costs of genomic methods justified by the information provided? Were genomic resources like reference genome sequences available for species of conservation concern? There were also equally important issues of applicability of methods, obtaining clear-cut results that could be communicated to conservation managers and overall bridging the gap between academic research and practical conservation needs (Shafer *et al.* 2015). Even though at the time some cases of successful application of conservation genomics were available, they mostly concerned commercially important or charismatic species (Garner *et al.* 2016; Shafer *et al.* 2016).

The overarching aim of this special issue is to explore the state of conservation genomics now several years after these important discussions. A lot has happened with respect to developments of sequencing techniques and decreased prices, and high quality genome assemblies are increasingly becoming affordable and available for non-model species. Also, user-friendly methods, pipelines and programs are continuously being developed. Several of these should have direct application in conservation, with Runs of Homozygosity for estimating inbreeding being a particularly illustrative example (Ceballos *et al.* 2018; Kardos *et al.* 2018). It is telling that the newest edition of a leading textbook in the field has changed title to "Conservation and the Genomics of Populations" (Allendorf *et al.* 2022). In reality, however, is it just the academic field of conservation genomics that has matured? Have we come closer to bridging the gap between research and its translation into practical conservation? The conservation genetics gap is a well described phenomenon (reviewed by Klütsch & Laikre (2022)); does genomics add to this gap or help diminish it?

We invite empirical papers that use genomics approaches to target questions of importance to conservation and either discuss or demonstrate the practical conservation relevance of results (keeping in mind that relevance should also extend beyond the studied species). We

also welcome opinion papers and reviews, critical and visionary alike, along with theoretical contributions towards implementing genomics in conservation. Please note: If you are interested in contributing a review or opinion piece, please contact the editors to discuss your proposed topic.

Specific topics could include - but are not limited to - the following:

- Detecting inbreeding and inbreeding depression in wild populations
- Fitness effects of deleterious mutation load and management decisions based on deleterious mutations
- Genomics in planning and/or monitoring assisted migration for genetic and evolutionary rescue
- Climate change adaptability and vulnerability
- Genomics of harvested populations
- Demographic histories of endangered populations
- Genomics and the definition of conservation units
- Introgressive hybridization from introduced or domestic species and populations into native populations
- Genomics for monitoring trends in genetic diversity
- Genetics or genomics? Matching methods and conservation needs
- Frameworks and experiences for translating conservation genomics research into practical conservation, and use of genomics to implement conservation policy

Allendorf FW, Funk WC, Aitken SN, Byrne M, Luikart G (2022) *Conservation and the Genomics of Populations* Oxford University Press.

Allendorf FW, Hohenlohe PA, Luikart G (2010) Genomics and the future of conservation genetics. *Nature Reviews Genetics* **11**, 697-709.

Ceballos FC, Joshi PK, Clark DW, Ramsay M, Wilson JF (2018) Runs of homozygosity: windows into population history and trait architecture. *Nat Rev Genet* **19**, 220-234.

Garner BA, Hand BK, Amish SJ, *et al.* (2016) Genomics in Conservation: Case Studies and Bridging the Gap between Data and Application. *Trends in Ecology & Evolution* **31**, 81-83.

Kardos M, Akesson M, Fountain T, *et al.* (2018) Genomic consequences of intensive inbreeding in an isolated wolf population. *Nature Ecology & Evolution* **2**, 124-131.

Klüttsch CFC, Laikre L (2022) Closing the Conservation Genetics Gap: Integrating Genetic Knowledge in Conservation Management to Ensure Evolutionary Potential. In: *Closing the Knowledge-Implementation Gap in Conservation Science* (eds. Ferreira CC, Klüttsch CFC), pp. 51-82.

Ouborg NJ, Pertoldi C, Loeschcke V, Bijlsma R, Hedrick PW (2010) Conservation genetics in transition to conservation genomics. *Trends in Genetics* **26**, 177-187.

Shafer ABA, Wolf JBW, Alves PC, *et al.* (2015) Genomics and the challenging translation into conservation practice. *Trends in Ecology & Evolution* **30**, 78-87.

Shafer ABA, Wolf JBW, Alves PC, *et al.* (2016) Genomics in Conservation: Case Studies and Bridging the Gap between Data and Application Reply. *Trends in Ecology & Evolution* **31**, 83-84.

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