

Editorial preface

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The papers collected in this special issue of Conservation Genetics are the outcome of the final meeting of the European Science Foundation Research Networking Programme “*Integrating population genetics and conservation biology: merging theoretical, experimental and applied approaches*”. The research network, in short known as ConGen, aimed at providing a venue for concerted scientific action in the field of conservation genetics and to combine and integrate different perspectives. The ConGen network has been supported by 15 ESF countries and was chaired by Kuke Bijlsma and Volker Loeschcke. In the last 5 years, the network has supported many workshops, science meetings and exchange grants, particularly supporting young scientists (see www.esf.org/congen or www.congen.biz). This undoubtedly has helped the field of conservation genetics to mature fruitfully at a European scale.

The final meeting of the network on “*Integrating Population Genetics and Conservation Biology*” took place in Trondheim, Norway from May 23–27, 2009, with more than 150 participants and was organized by a local team of the Norwegian Institute of Nature Research and the Norwegian University of Science and Technology chaired by Kjetil Hindar (for a more detailed meeting report see *Biol. Lett.* (2010) 6:3–6). We have asked the plenary speakers and participants of the meeting to submit manuscripts for this special issue. After the submitted manuscripts

underwent the usual process of critical peer-reviews, with Kuke Bijlsma, Volker Loeschcke and Joop Ouborg acting as guest editors, it resulted in the 28 papers collected here. Clearly the papers cover the different research areas, approaches and perspectives in the field of conservation genetics and in many cases integrate different approaches. We have also asked a few scientists that have a long-standing experience in the field to write a future perspective of what they consider as being important issues in the field and how the field is expected to develop (these can be found at the end of the issue). Both during discussions at the meeting itself, and in several contributions to this special issue, one clear development emerges, namely that conservation genetics is heading towards conservation genomics. There is little doubt that genomic approaches will open new exiting avenues for future research in the field of conservation genetics.

We considered the journal Conservation Genetics as an obvious platform for publishing the contributions and were very pleased that this was met with enthusiasm of both the editor, A. Russ Hoelzel, as well as the staff members of the editorial office responsible for production of the journal. We hope this collaboration has resulted in a high quality issue.

We hereby want to thank Kjetil Hindar and his team for organizing the meeting so smoothly, the editor A. Russ Hoelzel for his confidence and allowing us to edit this special issue as guest editors, and the staff members of the Springer Journals Editorial Office, Catherine Cotton, Catherine S. Murphy and Gayathri Balasubramanian, for fast and helpful editorial support. Last but not least, we thank all the authors and reviewers; without their help this special issue would have been impossible to produce.

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