Invited Review

Systematics and biodiversity research in the era of genomics

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The symposium ‘Systematics and Biodiversity Research in the Era of Genomics’ was opened with a warm welcome to all participants by Mats Tilset, chairman of the DNVA’s Natural Sciences Division. Afterwards, Per Sundberg, chief editor of the Zoologica Scripta, gave a brief review of the history of the journal since it started with the first volume in 1971. Actually, the history of the Zoologica Scripta can be traced much longer back in time, in fact to the founding of the Swedish Royal Academy of Sciences in 1739, and its series of publications that appeared under different names such as Arkiv för Zoologi. The focus and the scope of the Zoologica Scripta has changed over the years; while in the 1970s and 1980s, large morphology-based taxonomic papers were published, today’s focus is on systematics, phylogeny, evolutionary ecology, phylogeography and conservation biology. Along with the changing scope, Zoologica Scripta has developed into a leading journal in the field (Fig. 1) and ranks currently number 12 in the category Zoology of the ISI Journal Citation Reports© Ranking. The DNVA and the editors are particularly pleased that the Zoologica Scripta offers a profound and highly reputed outlet for advanced original research in Animal Systematics.

The scientific part of the symposium included eight invited keynote talks that explored the opportunities and challenges for the field that came along with the development of high-throughput laboratory method and the generation of huge data sets (please find the detailed symposium programme as Data S1). These excellent cutting edge presentations triggered many enthusiastic discussions during the breaks and provided scholars in the field with new ideas.

The editors of the Zoologica Scripta are pleased that we now can provide papers of six of the invited speakers that summarize their presentations for this special issue (section) of the Zoologica Scripta.

Dunn and Munro, Brown University, USA, discuss the increasingly important role of phylogenetics in genomics. They point at the power of descriptive genomics to test key questions in biology but also take up the challenges that will arise, for example the breakdown of the current nomenclatural systems for describing gene homology.

Gonzalo Giribet, Harvard University, USA, discusses in his paper some major controversies, such as whether Ctenophora or Porifera is sister group to all other animals and poorly resolved deep nodes in the animal tree of life. He also explores how some of the conflicts relate to the nature of phylogenomic data.

Richmond, Sinding and Gilbert, University of Copenhagen, Denmark, address the state of the art of de-
extinction methods that aim at one-day literally reviving now extinct species. They discuss the outstanding challenges for these methods and explore what might constitute the definition of success of de-extinction.

Haarsma, Siepel and Gravendeel, Radboud University Wageningen and Naturalis Biodiversity Centre Leiden, Netherlands, focus on the added value of metabarcoding, that is taxon identification from complex mixtures using a standard DNA region, in evolutionary studies. The authors explore how caveats of the approach such as false negatives and skewed abundances can be overcome when metabarcoding is combined with traditional methods such as microscopy.

Alexander Suh, Uppsala University, Sweden, explores the reproducibility of the phylogenetic hypotheses currently contributing to the avian Tree of Life. He argues that the onset of the neovarian radiation is most likely irresolvable. He also cautions against bootstrapping in the era of genomics and suggests to instead use reproducibility as support for phylogenetic hypotheses.

Scott Edwards, Harvard University, USA, discusses phylogenomic subsampling, a method for studying the stability of phylogenetic analyses to investigate the consistency and stability of various methods of phylogenetic analysis of multilocus data sets, including so-called species tree methods. He reports that concatenation exhibits the common pattern of oscillating among conflicting tree topologies with high support, even within single replicates. Guidelines for analysing and reporting the results of phylogenomic subsampling are provided that should become a routine part of phylogenetic analysis in the next-generation era.

The invited papers compiled in this issue that present the authors’ views on important topics of Animal Systematics can hopefully to some extent convey the essentials of the Oslo symposium to the readership of the Zoologica Scripta.

Last but not least, we wish to express our uttermost gratitude to The Norwegian Academy of Sciences and Letters who sponsored the symposium and the current special issue of the Zoologica Scripta, and without their support, the symposium could not be held.

Supporting Information

Additional Supporting Information may be found in the online version of this article:

Data S1. The program of the symposium ‘Systematics and Biodiversity Research in the Era of Genomics’, November 5, 2015, Oslo, Norway.