

Abstracts from the 8th International Barcode of Life Conference in Trondheim, Norway

The 8th International Barcode of Life Conference is held in Trondheim, Norway, 17–20 June 2019, marking the second occasion this biennial conference series is hosted on the European continent. Building upon a community history of meetings in South Africa (2017), Canada (2015), China (2013), Australia (2011), Mexico (2009), Taiwan (2007), and the UK (2005), the 8th Conference will bring together 384 presenting authors from 57 countries to discuss the latest developments in DNA barcoding-enabled biodiversity research and nature management. The latest methodological advances in molecular techniques and bioinformatics, socio-economically relevant applications of DNA barcoding and metabarcoding, as well as legislative frameworks and regulatory practices will be covered.

Spotlight on Norway and the North

The 8th Conference naturally features strong representation of the Norwegian Barcode of Life Network (NorBOL, www.norbol.org), a research and infrastructure network that has linked researchers from across Norway for the past 12 years (Ekrem et al.). NorBOL, along with several other especially well-developed national networks (e.g., Mexico, Germany), serves as a valuable model for nations building their own Barcode of Life Networks. With a diverse research program, NorBOL is notable in maintaining its momentum in building DNA barcode reference libraries. NorBOL has led the generation of an increasingly comprehensive DNA barcode reference library for the animals, plants, and fungi of northern Europe as well as for the Arctic region more broadly, including in challenging marine groups (e.g., annelids: Bakken et al., Budaeva et al.; echinoderms: Kongshavn et al.; bivalves: Skahjem and Bakken; invertebrates and fish: Willassen et al.). These efforts serve as a valuable foundation for both fundamental research and diverse applications.

Targeted reference library building is being combined with methodological developments for working with ancient DNA from lake sediment cores (“sedaDNA”), resulting in novel insights into the history of Northern (e.g., Epp et al.) and Alpine (e.g., Garcés-Pastor et al.) regions. Moreover, NorBOL researchers and collaborators are at the forefront in the continued expansion of genomic representation beyond a few marker genes. Alsos and colleagues highlight “plant barcode 2.0”, whereby shot-

gun sequencing is used to increase the genomic data available for >1000 species of plants from Norway and neighbouring countries. This effort is creating a resource for genomic and evolutionary study. Moreover, through using environmental shotgun sequencing, some limitations relating to PCR bias and taxonomic resolution can be overcome for studies of spatial and temporal patterns in plant communities. Understanding the interrelationship between climate change, anthropogenic stressors, and biological diversity is of paramount contemporary relevance given the rapid rate of environmental change in polar regions.

Methodological advances: environmental DNA and genomics

Multiple exciting contributions use DNA captured directly from the environment (water, soil, air), i.e., environmental DNA (eDNA), to detect organisms. Research directions include whole-community analysis through eDNA metabarcoding as well as sensitive, species-specific detection using quantitative PCR (qPCR). The study of eDNA is opening new avenues for the non-invasive monitoring of endangered species (e.g., Bracken et al.; Troth et al.); for the detection of invasive species (e.g., Lin et al.; Loeza-Quintana and Hanner); and for exploring the diversity and ecosystem health of soils (e.g., Ariza et al.), freshwaters (e.g., Beentjes et al.; Majaneva et al.), and marine waters (e.g., Baillie et al.). An intriguing new perspective involves the use of eRNA in biodiversity science and conservation as a means of reading concurrently the taxonomic and transcriptomic profiles of complex, metabolically active biological assemblages (Cristescu; Kagzi et al.).

The 8th Conference also showcases methodological developments in DNA metabarcoding and biodiversity genomics. The plant research community is trending towards metagenomics approaches, in which shotgun sequencing is used (e.g., Alsos et al.; Bell et al.), as well as plastid genomes (e.g., Fu et al.; Schroeder et al.; Sheng et al.). Animal researchers are also increasingly exploring mitochondrial genomes (mitogenomes) as superbarcodes (e.g., Jiang and Liu; Yang et al.) and genomic shotgun sequencing methods (e.g., Nie et al.). However, Singer and colleagues draw attention to the incompleteness of reference databases for whole-community aquatic metagenomics. Therefore, targeted sequencing

of selected marker genes will likely remain an important method for biodiversity detection and taxonomic annotation over the coming years. Important contributions in the area of DNA metabarcoding methodological development will be presented, including a large test of PCR primer performance for benthic freshwater invertebrates (Elbrecht et al.). Experimental manipulations in mesocosms advance our understanding of how fine-scale taxonomic resolution from metabarcoding yields new knowledge of the response of biotic communities to multiple stressors (e.g., Beermann et al.). Development and testing of molecular biology protocols and bioinformatics approaches remain active areas of research in metabarcoding (e.g., Bohmann and Carøe; Brandt et al.). Metabarcoding routines are now being rolled out for specific national and international-scale biomonitoring projects for aquatic and terrestrial biodiversity (e.g., deWaard et al.; Meissner et al.; Knowlton).

While recent advances in high-throughput sequencing technology open new avenues for large-scale biodiversity analysis, the increasing usage of large sequence datasets also highlights the persistent limitations in taxonomic reference databases. Taxonomic annotation of DNA sequence reads remains a challenge, particularly in understudied habitats, geographic regions, and taxonomic groups. Several contributions on diverse taxonomic groups point out such deficiencies and call for more attention towards populating reference databases and for further developing taxonomic assignment algorithms (e.g., Meyer et al.). High-quality taxonomic assignments are essential for taxonomic groups of medical concern and for species regulated internationally, such as invasive species and agricultural pests (Hanner). By contrast, Cordier and Pawlowski use supervised machine learning methods to estimate indices of biotic ecosystem health, without relying on taxonomic assignment. With further acceleration in applications of metabarcoding and metagenomics, including using ultra-deep sequencing platforms (e.g., Fahner et al.), it is expected that further development of taxonomy-free analytical methods will be of interest.

Humanity, biodiversity, and the Barcode of Life

The conference proceedings capture a cross-section of the myriad ways in which humans interact with biodiversity. Pervasive themes include the DNA barcoding of medically important species and an increase in the variety of academic, governmental, and private-sector users of DNA barcoding and associated techniques. For exam-

ple, in a unique contribution in this conference series, Smits et al. describe their work on DNA barcoding insect species that can serve as disease vectors in geographical regions where the Belgian military is deployed. The authentication of commercial products—including fisheries species (e.g., Falcão et al.), herbal medicinal products (e.g., Priya et al.), and timber products (Radanielina and Rakotonirina)—remains a significant area of focus across nations. Efforts continue to characterize insect communities in agricultural landscapes and to develop efficient pest monitoring systems (e.g., deWaard et al.).

The 8th Conference will also host the launch of the BIOSCAN project (<https://ibol.org/projects/bioscan>), a major initiative to bring nations together to expand DNA barcoding and biodiversity research (Hebert). A major and important development is increasing participation of researchers from hyper-biodiverse nations in the International Barcode of Life community. Varied national and institutional priorities are apparent among the conference proceedings, showcasing how the methodological advances and databases built by the International Barcode of Life community can be leveraged in diverse ways to understand, sustainably use, and preserve biodiversity.

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Torbjørn Ekrem, Elisabeth Stur, Torkild Bakken, Michael D. Martin, and Sarah J. Adamowicz

T. Ekrem, E. Stur, T. Bakken, and M.D. Martin. NTNU University Museum, Norwegian University of Science and Technology, NO-7491 Trondheim, Norway.

S.J. Adamowicz. Department of Integrative Biology & Centre for Biodiversity Genomics, University of Guelph, Guelph, ON N1G 2W1, Canada.