

Editorial

Biological diversity or biodiversity – the web of life – includes diversity within species, between species and of ecosystems. A healthier biodiversity is of fundamental importance as it delivers a variety of natural services, *viz.*, ecosystem services, biological resources and social benefits, completely free of charge to the human society. According to the convention of biodiversity, 40% of the world's economy and 80% of the needs of the poor are derived from biological resources. A rich biodiversity also ensures a greater ability of the ecosystems to withstand natural disasters more efficiently. Biodiversity acts as both the measure of variety of life and an indicator of overall health of our planet. In the recent decades, interest in biodiversity has grown immensely as a consequence of the rapid loss of it, as well as due to the increasing realization of its biological and commercial importance to human society and the environment. In 2010, the International Year of Biodiversity, worldwide attention was renewed to factors that threaten biodiversity, and to needs/concerns/challenges being faced globally for physical/functional characterization, efficient management and conservation of biodiversity. It led the United Nations to announce 2011 to 2020 as the Decade of Biodiversity with a view to contribute to the implementation of strategic plan for biodiversity conservation. As India is one of the mega centres of biodiversity, these concerns assume paramount importance warranting urgent efforts to catalogue, conserve, manage and utilize our national wealth.

Since genome plasticity is basal to the evolution of life and thus to biodiversity in nature, decoding the prolific information embedded in the genome (which is now easily amenable through modern genome-wide molecular techniques and tools) can help us devise efficient and timely approaches to characterize and manage biodiversity/genetic resources. Hence, the idea of bringing molecular biologist, naturalist, ecologist and conservationist on one platform to focus on the recent advances in genomic strategies and tools that aid in characterizing, utilizing and conserving biodiversity was conceptualized, which led a three-day international symposium on 'Genomics and Biodiversity' in Hyderabad, India, from 23 to 25 February 2011. The symposium (<http://www.ccmb.res.in/adnat15/index.html>) was jointly organized by ADNAT (Association for Promotion of DNA Fingerprinting and Other DNA technologies; <http://www.adnat.in>) and CCMB (Centre for Cellular and Molecular Biology; <http://www.ccmb.res.in>), as part of the 15th Annual Convention of ADNAT at CCMB.

Justifying the theme of the symposium, talks covered a rich diversity of research areas, organized into six sessions, namely, Genomics Platforms and Technologies, Characterization of Biodiversity, Genomics for Harnessing Biodiversity, Genomics for Diversity, Disease and Health, Conservation of biodiversity, and Biodiversity Studies in Challenging Scenarios. Overall, there were 23 invited talks by eminent scientists from India and eight other countries (Germany, UK, Australia, Singapore, Republic of Korea, USA, Colombia and Kenya); six short presentations by young researchers, and a panel discussion by scientists and social stakeholders on 'Genomics, Untapped Biodiversity, GMOs and Socio-Environmental Concerns'. The meeting was attended by a large number of researchers and students from across the country and also by the members of the ADNAT society.

The keynote address was by Victor Smetacek, Alfred Wegener Institute, Germany, who intriguingly exposed our ignorance about ocean biodiversity and brought us face to face with the damaging effects of huge anthropogenic pressure on oceans. His wonderful talk is already published as a perspective paper in the September 2012 issue of *Journal of Bioscience*. Robert J Henry (QAAFI, Australia), Richard Hodgson (Illumina Agrigenomics, Singapore), Scott Jackson (Purdue University, USA), Martin Ganai (TraitGenetics GmbH, Germany) and Rajeev Varshney (ICRISAT, India) presented the great strides taken in the next-generation sequencing platforms based emerging high-throughput genomic approaches for molecular markers discovery, genotyping, and the immense potential/opportunities that these offer for biodiversity characterization and more importantly its utilization. Sridhar Sivasubbu, (CSIR-IGIB, India) walked us through the genomic landscape of zebrafish, which has become an ideal model system to have insights in vertebrate evolution. Lalji Singh and K Thangaraj (CSIR-CCMB, India) traced the genetic diversity and ancestry of Indian populations using nuclear and mtDNA markers, and showed how endogamy



has resulted in formation of many small, isolated population groups characterized by their private genetic disorders. Jürgen Kun (Institut für Tropenmedizin, Germany) showed how population genetic studies could help identify genetic polymorphisms in immunorelevant NOS2 genes that confer protection against the severest form of malaria among children of Gabon. There were several interesting talks that succinctly brought out the immense potential of high-throughput genomic approaches in agricultural research; these included genomics-driven management and utilization of *planta* diversity available in *ex-situ* gene banks for desirable genes (Andreas Graner and Andreas Boerner, IPK, Germany; BM Prasanna, CIMMYT, Kenya; Hari Upadhyaya, ICRISAT, India); understanding domestication of soybean (Suk Ha Lee, Seoul National University, Korea), and evolution of legume genomes (Douglas R Cook, University of California, USA) by comparative genomics; conservation and utilization of indigenous livestock resources (Olivier Hanotte, The Frozen Ark, UK); and understanding genetics of disease causing organisms of livestock (Damer Blake, The Royal Veterinary College, University of London, UK). Similarly, a number of eminent speakers highlighted the challenges and opportunities proffered by genomic approaches in the field of wildlife conservation, from DNA-barcoding-based monitoring of faunal biodiversity under modifying habitat pressure (Andrew J Crawford, Universidad de los Andes, Colombia); population structure and phylogeography of bird species (TA Burke, University of Sheffield, UK), to ways and means to peep into the evolutionary past of vertebrate species through mitogenomes and genomics (Axel Janke, LOEWE Biodiversity and Climate Research Center, Germany; Jan K Janecka, Texas A&M University, USA). S Shivaji (CSIR-CCMB, India) presented the microbial biodiversity in extreme cold environments of Antarctica and the Arctic and discussed how genomics has helped understanding their adaptations to such climates.

Excellent science, strongly emphasizing the important role the emerging/enabling genomic approaches promise in addressing the challenges involved in managing the global biodiversity, and the fact that we were entering the Decade of Biodiversity (2011–2020), suggested us the need to chronicle the talks for the benefit of various stakeholders in biodiversity. We are happy that the *Journal of Bioscience* accepted our request to bring out a special issue, and ten of our speakers agreed to contribute to the same, which resulted in this issue of peer-reviewed full-length articles providing a broad glimpse of the variety of scientific enquiry into various facets of biodiversity exploration. The first three articles discuss the advancement in recent genomic platforms that aid in the discovery and development of molecular markers, which in turn are expected to dramatically shift the efficiency of molecular breeding to a higher level in plants. These should serve as simple primers for young researchers venturing into the field. The article by Rajeev Varshney *et al.* provides the success story of the development of genetic resources (thousands of SSRs and SNPs) in legume crops through next-generation sequencing, and their use in developing comprehensive genetic maps and identification of candidate markers linked to agronomically important traits with the help of high-throughput genotyping methods. The next two articles (Ganal *et al.* and Henry *et al.*) provide simple but comprehensive reviews of the genomic approaches that have greatly accelerated the pace of ‘molecular marker discovery’ and the development of large genome-wide SNP arrays, followed by their potential applications in characterization of genetic resources, creation of high-density linkage maps and also in association studies. As a step forward, the next three articles inform us about how the genomics approaches/molecular markers can help us in understanding the origin/evolution of the vast germplasm resources, and also in their meaningful management, preservation and utilization. The article by Prasanna traces the centre of origin of maize and migratory routes of maize domestication using molecular markers on diverse germplasm, and emphatically brings out the need for high-throughput precision phenotyping as prerequisite to exploit the genetic resources for desirable variability. In their article, Kim *et al.* describe how whole genome sequencing of diverse germplasm can aid in identifying QTLs governing complex traits by comparative genomics approach, exemplifying it with their identification of 118 genes involved in flowering pathway in soybean. In the following article, Bomer *et al.* discuss the fate of genetic integrity of long term stored germplasms that differ in their modes of reproduction, and highlight the need for integrating molecular markers in the management of large *ex situ* genebanks. In concert with crop plants, there is an equal need for healthy livestock for sustainable agriculture. In the following article, Emily and Damer reviews the genomics based population-level approaches that have accelerated the pace of mapping genomes of parasitic organisms, taking the example of coccidial protozoans that causes diseases of severe importance in both medical and veterinary fields (the genomic information of protozoans is expected to help in developing vaccines using reverse-genetic tools). The next two articles turn the focus from plant/agriculture biodiversity

to faunal biodiversity. In the first of these articles, Paz and Crawford discuss the use of DNA-barcoding-based rapid inventories of sympatric diversity among frogs, and highlight the importance of sampling approach (from clade-based sampling to geographically focused sampling) to answer questions related to macro-ecology and community phylogenetics. Subsequently, Janecka *et al.* throw light on the astonishing fact that the rates of molecular and morphological evolution is highly decoupled and suggest from their findings that insertions and deletions in the functional regions (that brings about phenotypic divergence) probably arise and fix faster than the rate of neutral substitution in the genome. In the end, the focus shifts to the most studied animal species, *Homo sapiens*, which has diversified extensively since it originated in Africa about 200,000 years ago. In this last article, Tamang *et al.* review the complex genetic origin of Indian populations and the driving forces that led to the current high-level diversity, as revealed by mitochondrial, Y-chromosomal and autosomal DNA marker analysis of around 20,000 individuals across India. The review highlights the fact that the contemporary Indian populations are the descendents of the very first modern humans who ventured the journey of Out-of-Africa about 60,000 years ago. It is hoped that this special issue will initiate many youngsters in the area of applied genomics to conserve/manage our natural biological resources/wealth.

We would like to thank all the speakers, who readily accepted our invitation to attend the symposium, and all those who willingly contributed their articles to this special issue. We also take this opportunity to thank A Veerabhadra Rao, and all the members of RKA group at CCMB, especially Jagath Janani, Richa, Satrupa, Shalini, Pratyusha and Phanidranath, who worked untiringly to make the symposium a success, and also helped in bringing out this issue. We thank all the reviewers for their valuable inputs, suggestions and critical comments in shaping the manuscripts. We will also like to put on record our words of appreciation for DP Kasbekar, the Editor of *Journal of Bioscience*, for accepting our request to bring out this special issue, and Sushila Rajagopal and Jai Benjamin from the Editorial Office of the journal for all their help, cooperation and patience in bringing out this issue. We hope that you will enjoy reading the articles.

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