

Advancing the science of taxonomy in India*

As our scientific surmises on evolution, ecology, biodiversity and molecular biology are less robust than we assume, today we are losing species faster than they are evolving or discovered. The implications are vast and serious for all human enterprises ranging from forestry to food production to medicine. High quality taxonomic research is vital for poverty reduction through sustainable agriculture, forestry, fisheries, combating insect pests and human diseases and for sustainable national and international trade in biological products without endangering indigenous plant and animal species. Though India is extremely biodiverse, with about a million species of living organisms, fewer than 100,000 of these have been formally described. Guided by the United Nations' Millennium Development Goals, India agreed to quantify and protect the existing biodiversity. This has been critical in meeting targets and obligations of international treaties and conventions such as the Convention on Biological Diversity and national legislations such as the Biological Diversity Act. In observance of the International Year of Biodiversity 2010, under the aegis of the National Biodiversity Authority (NBA), the Ashoka Trust for Research in Ecology and the Environment (ATREE) organized a National Consultation.

The prime objective of the workshop was to assess the present status of taxonomy and biodiversity loss in the country. The group addressed issues pertaining to current trends, responsibilities and potential roles Indian taxonomists can play nationally as well as globally. Simultaneously, the discussants underscored the limitations and obstacles faced by Indian taxonomists and outlined steps to lever-

age national and international expertise, networks and relevant stakeholders to strengthen the science of taxonomy in India.

Madhav Gadgil (Agharkar Research Institute) in his keynote address, spoke on the history of taxonomy in India and identified a few core issues that needed to be deliberated at the consultation. He urged that we need to think of new ways of exposure and networking. He stressed upon the fact that organizations dealing with taxonomy and other disciplines of systematic biology need to integrate the new range of developments specifically in the Indian context. K. N. Ganeshiah (University of Agricultural Sciences (UAS), Bangalore) and Madhav Gadgil both elaborated that we have to generate demand and opportunities for systematic biology in the country. Professionals should reach out to people on a large scale at every level from the grassroots to higher echelons and in different languages. Only such a large scale effort will create awareness and ultimately contribute to the growth of taxonomy and conservation of the biodiversity. Kamaljit Bawa (ATREE, Bangalore) pointed out that if prime centres of taxonomic research continue to be isolated, there could be no growth in taxonomic research. Multiple centres of excellence need to be set up to facilitate growth and development besides free exchange of scientific ideas and information. C. A. Viraktamath (UAS) commented that it is imperative that we agree to exchange information and collaborate nationally and internationally. Kamaljit Bawa and Mohan Ram (Delhi University) opined that there needs to be a shift in focus to revisionary studies to answer many questions and younger people need to be trained in the best institutions with adequate resources to promote systematic biology. Ramakrishna (Zoological Survey of India, Kolkata) stressed that national institutions such as the ZSI and Botanical Survey of India (BSI) need to prioritize tasks and regions that need to be inventoried in the near future. He emphasized the need to expand our taxonomic research to a pan-Asian realm than confining to the Indian subcontinent.

The participants also discussed the rapid strides that taxonomy is making by assimilating developments in molecular and computational techniques. These developments will offer unprecedented opportunities to Indian taxonomists to enlarge the scope of their work and practise citizen science. P. L. Gautam (NBA) commented that the consultation has provided a good synthesis of information on taxonomy and biodiversity conservation in India. He recognized the need for national and international collaborations, networking of national institutions and agreed that the NBA and other relevant stakeholders need to work together to ensure growth and development in the field of taxonomy.

The participants acknowledged that taxonomy is crucial to meet the challenges of biodiversity conservation in the 21st century. To successfully achieve the targets of international treaties such as the Convention on Biological Diversity, the scientific community submitted a set of recommendations that needs immediate consideration by the Ministry of Environment and Forests, Ministry of Science and Technology and the Ministry of Human Resources Development.

- Strengthen the science of taxonomy in India by establishing centres of excellence in systematic biology in the universities and other knowledge based institutions. Such centres should incorporate conventional and modern molecular, digital, and computational tools and approaches to taxonomy. The centres will also: (i) facilitate the completion of inventories of the country's flora and fauna and compilation of people's biodiversity registers; (ii) train systematic biologists in national and international institutions of repute, with financial support to visit international natural history museums and collections to facilitate revisionary/monographic studies; (iii) offer basic systematic biology courses in the curriculum for undergraduate biology students; (iv) facilitate the use of information technology to organize and disseminate taxonomic data, and support biodiversity portals to engage civil society in collating highly dispersed but immense biodiversity information, and

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(v) encourage publication of field guides to identify our flora and fauna to draw students and young people to the study of taxonomy, and to create awareness on the importance of biodiversity.

- Enable free access for researchers to natural habitats for study and collection of specimens for comprehensive taxonomic revisions of our flora and fauna following modern systems of classification.

- Establish state-of-the-art national and regional repositories for preserving type specimens and other valuable biological material for posterity at suitable locations.

- Encourage national and international collaboration in taxonomic research and free exchange of specimens for basic, non-commercial research and promote fundamental research in biology

by suitably amending the Biological Diversity Act, 2002.

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MEETING REPORT

Asia-Pacific bioinformatics conference 2010*

Every year, since 2003, the Asia-Pacific Bioinformatics Conference (APBC) has been held with an aim of 'exploring research, development and novel applications of bioinformatics'. The first conference was held at Adelaide, Australia. The 2010 edition of the conference held in Bangalore, India, was the first APBC to be held in South Asia region and was attended by around 600 participants. Industry tracks, tutorial sessions, keynote lectures, and student presentations were held. Selected articles were also published in the open-access *BMC Bioinformatics* journal.

The first industry track was chaired by Vijay Chandru (ABLE and Strand Life Sciences, Bangalore) during which Vijayanti Gupta (Strand Life Sciences) gave a talk on 'Personalized medicine in breast cancer'. She said, 'one therapy does not fit all and one treatment could have various outcomes'. For cancer, the choice of therapy is dictated by its subtype. She discussed two problems – identifying potential targets in tumour necrosis cancers and ranking breast cancer subtypes by prognosis. This work was a collaborative effort of Kidwai Memorial

Institute of Oncology, Bangalore (provided samples and carried out histopathology studies), Indian Institute of Science (conducted microarray studies), and Strand Life Sciences (analysed data).

Prashant S. Naik (Jubilant Biosys, Bangalore) gave an overview of curated pathway databases, Jubilant's PathArt tool and its use in drug discovery, and the challenges faced in drug discovery. Vamsi Veeramachaneni (Strand Life Sciences, Bangalore) described the method of detecting heteroplasmy in mitochondrial genome of the same individual using next-generation/end sequencing technique. Alpan Raval (D. E. Shaw Research, Hyderabad) presented 'An information theoretical framework for genomic island detection'. A genomic island is a cluster of genes acquired through a single horizontal gene transfer event. Genomic islands are used as markers and for studying antibiotic resistance.

In the second session, chaired by Ramesh Hariharan (Strand Life Sciences), Maya Krishnan (Persistent Systems, Pune) described laboratory information management system (LIMS) for improving lab efficiency. LIMS can only capture data but caters to data on receiving samples, performing tests and reviewing results. It provides for a paperless laboratory solution but a single LIMS does not work for all domains. Current and future trends in biocuration were discussed by Usha Mahadevan (Molecular Connections, Bangalore). Curation is essential because there is a huge amount of data available that needs to be analysed while pursuing biological

and biomedical research. Data is of three kinds – pathways, reactions and enzymes and is highly heterogeneous and complex. Srinivasan Parthiban (Reverse Informatics, Chennai) raised the question 'Are you ready for "in-litro" drug discovery?' Parthiban emphasized the use of literature for searching drug targets to reduce cost and time consumed otherwise. An example of a drug discovered using *in-litro* method is Cozaar (Merck).

Each day of the four-day conference began and ended with a keynote lecture. Pinakpani Chakrabarti (Bose Institute, Kolkata) elaborated upon protein-protein interactions, their structural features, residue conservation and energy distribution, and location of binding sites. Two proteins interact based on the nature of the interacting surfaces. Crystallography is not the ideal way to determine quaternary structures of proteins; they have to be studied in solution form and homodimer has been found to be the most common symmetry in these structures. Structural databases have been created representing different types of protein-protein interactions.

To fully understand the regulation of any gene, one must identify all binding sites and understand their functions. This is one of the challenges faced apart from gene naming and consensus sequence bottleneck problems. Sorin Istrail (Brown University, USA) described the CYRENE project on gene regulatory networks. A database named 'cis-lexicon' has been created for storing the location and function of all experimentally-found and validated binding sites (*cis* sites). Miklós Csűrös (Université de Montréal, Canada)

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