

Microbial diversity*

The microbial world is the largest unexplored reservoir of biodiversity on the Earth. It is an important frontier in biology under intensive investigations. Interest in the exploration of microbial diversity has been spurred by the fact that microbes are essential for life since they perform numerous functions essential for the biosphere that include nutrient cycling and environmental detoxification. The vast array of microbial activities and their importance to the biosphere and to human economies provide strong rationale for understanding their diversity, conservation and exploitation for society.

In her inaugural address, Manju Sharma (Former Secretary, DBT) laid emphasis on the importance of microbial diversity in sustainable development by citing the serendipitous discovery of penicillin by Alexander Fleming and subsequent research efforts that led to development of several other bioactives which have revolutionized treatment of infectious diseases. She cited another example of the discovery of *Thermus aquaticus* by Thomas Brock, the source of thermostable DNA polymerase used in PCR that has changed the face of modern biology. Sharma released a book *Microbial Diversity: Current Perspectives and Potential Applications*. This book contains contributions from nearly 60 experts from India and abroad, in 1133 pages. The inaugural session was followed by four keynote addresses to set the tone for the ensuing discussions. B. N. Ganguli (Agharkar Research Institute, Pune) explained how understanding the diversity of Actinobacteria has led to the discovery of several novel antibiotic compounds. Shivaji (CCMB, Hyderabad) and his coworkers have discovered many new species of bacteria belonging to the genera such as *Planococcus*, *Leifsonia*, *Kocuria*, *Psychrobacter*, *Marinobacter* and others, which are psychrophilic and oligotrophic. Modulation of membrane fluidity is found to be crucial for survival of these microbes at low temperatures. Bharat Patel (Griffith University, Bris-

bane, Australia) reported that a halophilic and thermophilic anaerobe, *Halo-thermothrix orenii* produces an amylase with unique structural adaptation towards thermo-halophilicity based on protein crystallization and 3D studies. Girish Sahni (IMTECH, Chandigarh), on the other hand, described how his group has been successful in designing a new clot-specific streptokinase derivative through recombinant DNA and protein engineering approaches for the first time in India.

B. N. Johri (G.B. Pant University, Pantnagar) provided a glimpse of the developments in the realm of microbial diversity, based on his experience, of bird's nest fungi, thermophilic moulds, AM fungi and rhizobacteria, and concluded that the diversity developments have moved in circles with the difference that current tools permit a deeper look at the structure-function relationship. S. P. Singh (Saurashtra University, Rajkot) described the occurrence of haloalkalophilic bacteria in saline habitats of Gujarat, and the biotechnological applications of their enzymes such as proteases active at alkaline pH and high salt concentrations. Y. Kawarabayasi (National Institute of Advanced Industrial Science and Technology, Ibaraki, Japan) demonstrated the possibility of recovering useful genes from uncultivable microbes of geo- and hydro-thermal environments through genomic technique. Direct sequencing of environmental DNA was shown to provide information on phylogeny, gene resource and community structure of the uncultured microbes. Following this current theme of unculturables, Rakesh Sharma (Institute of Genomics and Integrative Biology, Delhi) explained efforts in accessing genes encoding novel biocatalysts from unculturable bacteria by preparing metagenomic libraries directly from environmental DNA. Yogesh Shouche (National Centre for Cell Science, Pune) described how his group has been able to analyse the diversity of microbiota of wild *Culex quinquefasciatus* mosquitoes by culture-dependent as well as culture-independent approaches that have resulted in recovery of a new species, *Aeromonas culicicola* from the midgut. The majority of bacteria, however, in this milieu belonged to the class Proteobacteria. Three hundred *Bt* isolates obtained from soils collected

from various locations in India were shown, by S. Kaur and her coworkers (IARI, New Delhi), to have a highly conserved ITS region of the 16-23S rDNA.

K. Natarajan (Madras University, Chennai) described the diversity of agarics in Nilgiri biosphere reserve. Members of Tricholomataceae dominated in all the forest types surveyed, and were followed by the members of Agaricaceae. The dominant fungal species belonged to *Agaricus*, *Lepiota*, *Marasmiellus* and *Marasmius*. The work of M. S. Reddy (Thapar Institute of Engineering and Technology, Patiala) on the diversity of ectomycorrhizal fungus *Pisolithus* from India by analysing ITS region of rDNA revealed considerable genetic variation in the isolates of the so-called *P. tinctorius* and confirmed the occurrence of two species, *P. albus* and *P. indicus*. R. K. S. Kushwaha (Christ Church College, Kanpur) reported the occurrence of considerable diversity in the genus *Chrysosporium*, and stressed on the need to study keratinolytic abilities of the species. The role of microbial culture collections in preserving world's microbial diversity was highlighted by G. S. Prasad (MTCC, IMTECH, Chandigarh). He informed the audience that MTCC was recognized as an International Depository Authority by World Intellectual Property Organization (WIPO) under the Budapest treaty.

Ashok Pandey (RRL, Thiruvananthapuram) discussed the microbial fermentation technologies for the production of phytaes, the manufacturing companies and their commercial prospects. P. Gunasekaran (Madurai Kamaraj University, Madurai), on the other hand, observed that the whole genome sequence of *Zygomonas mobilis* was made up of 2.056 megabase pairs with 1998 predicted coding ORFs covering 87% of the genome. This bacterium has several advantages over conventional yeasts for ethanol production which includes 12% ethanol tolerance, higher volumetric sugar uptake and ethanol productivity, and amenability for genetic manipulations. S. C. Taneja (RRL, Jammu) described the potential applications of oxidoreductases (dehydrogenases) in the form of whole cells, in diastereoselective transformations, whereas K. Isobe (Iwate University, Japan) described that oxidases and oxidase-producing microbes such

*Based on an International Conference on Microbial Diversity: Current Perspectives and Potential Applications, held at the Department of Microbiology, University of Delhi South Campus, New Delhi during 16-18 April 2005.

as *Alcaligenes* sp. GOX 373 and *Aspergillus japonicus* were useful in the production of aldehydes and organic acids. Oxidases have prosthetic groups, and therefore, do not require an additional cofactor regeneration system.

Marcio Pocas-Fonseca (University of Brasilia, Brazil) informed that they have cloned and expressed cellobiohydrolase, endoglucanase and β -glucosidase genes of the thermophilic mould *Humicola grisea* var. *thermoidea* in *Saccharomyces cerevisiae*. The recombinant yeast was grown in 3000 L fermentors, and the culture supernatants containing cellulases have been shown to be useful in biostoning and biopolishing processes. Datta Madamwar (Sardar Patel University, Vallabh Vidyanagar) described immobilization of *Candida rugosa* lipase by his group in polyvinyl alcohol cross-linked with boric acid in the presence of calcium alginate, and its application in the esterification of alcohol and fatty acid. Other enzyme-directed presentations included those of B. S. Chadha (Guru Nanak Dev University, Amritsar) and coworkers on the existence of multiple xylanases in several thermophilic moulds with approximately 75 diverse xylanase isoforms. R. P. Singh (IIT Roorkee, Roorkee) discussed that the thermostability increased by replacing Arg¹⁵⁶ with glutamic acid in the xylanase of *Streptomyces lividans* 1326. V. S. Bisaria (IIT Delhi, New Delhi) presented the applicability of xylanases produced by *Melanocarpus albomyces*, a thermophilic mould, in paper bleaching. The prebleaching of paper pulps with xylanase at 50°C and pH 6.5 for 2 h brought down chlorine requirement by 15% with concomitant gain of 3 per cent points in the pulp brightness. Xylanase-based prebleaching also reduced the toxicity of the bleach effluent. P. Prema (RRL, Thiruvananthapuram) reported production of acidic and neutral polygalacturonases by a *Bacillus* sp. BAP-11, which were useful in juice clarification and pulp biobleaching, respectively. E. M. Papamichael (University of Ionnina, Ionnina, Greece) described that his group has isolated a halo-alkaliphilic *Bacillus* sp. 17N-1 that produced novel proteases of biotechnological interest. The mechanism of action of the novel protease was understood using proton inventory method, Arrhenius curves and kinetic parameters.

In the area of nanotechnology, Absar Ahmad (National Chemical Laboratory, Pune) described a novel biological method

that is developed for synthesis of intracellular/extracellular gold, silver and cadmium sulphide nanoparticles using fungi such as *Verticillium* sp. and *Fusarium oxysporum*, and species of *Thermoactinomyces* and *Rhodococcus*. The enzymes and proteins were found to be involved in the reduction of metal salts and capping of the reduced metal and metal sulphides at nanoscale. Gopal Reddy (Osmania University, Hyderabad) showed the possibility of producing lactic acid from starch in single step fermentation by *Lactobacillus amylophilus* GV6. This bacterial strain appeared to produce lactic acid in high yields from cheap renewable starchy substrates. P. K. Sarkar (University of North Bengal, Siliguri) described the diversity and role of microbes in the production of fermented soybean, kinema with *Bacillus subtilis* playing a predominant role in processing. Kinema was shown to be devoid of soy oligosaccharides that are a potential source of flatulence.

In the area of heterologous expression of bioactives, Gotthard Kunze (IPK, Gatersleben, Germany) described *Arxula adenivorans*, a dimorphic Ascomycetous yeast with considerable potential. His group has successfully cloned and expressed genes encoding glucoamylase, tannase, invertase, xylitol dehydrogenase and PHB-synthesis in *A. adenivorans*. The yeast was shown to utilize *n*-alkanes and degrade tannins, phytates and purines. S. R. Dave (Gujarat University, Ahmedabad) isolated *Acidithiobacillus ferrooxidans* and *Leptospirillum ferrooxidans* from Chitradurga acid mine drainage water and used them in extracting copper from chalcopyrite concentrate. These isolates were tolerant to toxic heavy metals. P. Maruthi Mohan (Osmania University, Hyderabad) described development of metal-resistant and hypersensitive strains of *Neurospora crassa* which were shown to have excellent potential in bioremediation of toxic metal ions in simulated environmental conditions. In order to improve the efficiency further, several genes encoding high-affinity metal transporter genes have been identified and PCR amplified for expression in bacterial systems. Arundhati Pal (University of Calcutta, Kolkata) reported isolation of nickel resistant bacterium, *Wautersia paucula* which contained a major uptake system involving magnesium transporters and a minor energy dependent pathway for Ni uptake.

I. S. Thakur (JNU, New Delhi) reported development of a consortium comprising six bacterial strains with very high de-

colorization potency and utilization of chlorinated phenols. H. S. Saini and his coworkers (GND University, Amritsar), on the other hand, developed a consortium of *Stenotrophomonas acidaminiphila*, *Pseudomonas putida*, *P. fluorescens* and *Bacillus cereus* with a significantly high rate of decolorization of textile processing industries. R. K. Jain (IMTECH, Chandigarh) found 45 different phylotypes in the bacterial community of a pesticide contaminated site; further analysis suggested that the bacterial community consisted of Proteobacteria and Actinobacteria. The pesticide-contaminated site was remediated using *Arthrobacter protophormiae* RKJ100. Rup Lal (University of Delhi, Delhi) described his group's efforts in dissecting *lin* genes involved in the degradation of hexachlorocyclohexane in *Sphingobium japonica*, *S. indica* and *S. francensis*. He reported that bacteria isolated from different continents contained identical *lin* genes. C. Manoharachary (Osmania University, Hyderabad) threw light on the diversity of aquatic fungi and their role in recycling of organic matter in aquatic bodies and observed that since these fungi formed a part of food chain, at least some species are good bio-indicators of water quality, and play a role in the maintenance and conservation of aquatic systems. S. N. Bagchi (R.D. University, Jabalpur) described the structure, mechanism of action and regulation of the production of natural herbicidal algicides of cyanobacteria such as *Oscillatoria laetevirens*.

In the area of plant-microbe interaction and sustainable plant development, Michel Aragno (University of Neuchatel, Switzerland) highlighted that the rhizosphere competent bacteria most probably resulted from a long coevolution with plants, and the soil acted as a reservoir of these microbes. The signalling compounds produced by plants may act either as attractants or repellants of bacterial populations. R. G. Kapooria (University of Zambia, Zambia) reported that VAM flora of Zambian soils was rich in species of *Acaulaospora*, *Gigaspora* and *Glomus*. The greenhouse and field experiments showed that VAM inoculation controlled the incidence of tomato wilt and *Septoria* leaf spot of tomato. Appa Rao Podile (University of Hyderabad, Hyderabad) described cloning of glucose dehydrogenase gene by his group from *Escherichia coli* and its expression in *Azotobacter chroococcum* with an eye on its sustainability in phosphate solubilization. Sheela Srivastava (University of Delhi

South Campus, New Delhi) described an IAA-overproducing strain of *Azospirillum* that improved root proliferation in sorghum. Anita Pandey (G.B. Pant Institute of Himalayan Environment and Development, Almora) reported development of microbial inoculants by her group that enhanced growth and vigour of seedlings of *Cedrus deodara*. This group has also been successful in developing efficient inoculants for tea gardens. B. Ramakrishnan (Central Research Institute, Cuttack) informed that different management practices appeared to have different effects on soil microbial characteristics, which were reflected more in microbial biomass content and utilization patterns of substrates when examined by cluster analysis. Anil Tripathi (BHU, Varanasi) described the colonization of rice by bacterial endophytes such as *Herbaspirillum* sp., *Serratia* sp., *Bradyrhizobium* sp., *Pantoea* sp., *Pseudomonas stutzeri*, *Azoarcus* sp., *Acetobacter diazotrophicus*, *Azorhizobium caulinodans* and *Rhizobium leguminosarum* and showed their close association throughout the growth cycle. Radha Prasanna (IARI, New Delhi) reported that considerable diversity of cyanorhizobacteria existed in the rhizosphere, and suggested that the association may play a key role in the nutrient cycling and improving the vigour of the crop. Sunil Pabbi (IARI, New Delhi) dwelt on the intergeneric and intrageneric variations in pigments, cell constituents and enzymes of cyanobacteria collected from different regions of the country.

Based on his extensive studies on the molecular analysis of the viruses, Indranil Daspupta (UDSC, New Delhi) reported that geminiviruses of cassava were highly

diverse in India. M. V. Rajam (UDSC, New Delhi) dealt with the use of polyamine biosynthesis as a potential target for controlling plant fungal diseases. He discussed that his group has recently initiated work on knocking out the expression of fungal ornithine decarboxylase gene using RNAi technology.

Navin Khanna (ICGEB, New Delhi) in his lecture described the work that his group is carrying out in the area of designing and expression of novel recombinant protein antigens by assembling key immunodominant, linear and dengue virus-specific epitopes (chosen on the basis of pepscan analysis, phage display and computer predictions) with the aim of developing inexpensive diagnostic tests with high degree of sensitivity and specificity. N. Mishra (IVRI, Bhopal) highlighted that the organization of viral genome in the region of C-E2 of Indian isolates of bovine viral diarrhoea virus was similar to that in Osloss strain. S. Maan and her associates (Haryana Agricultural University, Hisar) studied genomic diversity in Orboviruses of Reoviridae, and found them to undergo a high rate of mutation and exhibit a high level of genetic variability. Nirmala Bardiya (Inha University, South Korea) reported purification of recombinant HBs antigen from methylotrophic yeast *Pichia pastoris* by adsorption-desorption on aerosol followed by ion-exchange and gel permeation techniques. D. V. Singh (Institute of Life Sciences, Bhubaneswar) reported that clinical isolates of *Vibrio cholerae* were similar to environmental isolates in their genetic patterns, and he concluded that the aquatic environment was indeed a reservoir for *V. cholerae*. J. S. Virdi (UDSC, New Delhi)

highlighted that the ribotyping showed uniform pattern of strains of *Yersinia enterocolitica* isolated from food, water, pigs and diarrheic human subjects. Molecular fingerprinting, however, revealed heterogeneity in the stains.

In his valedictory address, S. Ayyappan (ICAR, New Delhi) described the diversity of microbes in aquatic environments, and their importance in aquaculture. He further suggested to the microbiologists to develop appropriate networked programs on microbial diversity in the context of environmental and sustainable perspectives where considerable funding is likely.

Besides 60 oral presentations, over 200 posters were presented during the three days of conference. Young scientists including PG students and research scholars took part enthusiastically in poster presentation. There were limited presentations on marine microbial diversity, in-depth taxonomy and Archaeobacteria, and a general view was that these components required greater research thrust in future. That microbial diversity is indeed in the forefront of microbial teaching and research was proven by the general awareness depicted through both oral and poster presentations. The quality and range of topics presented at this conference was not only large but representative of areas of topical interest and was appreciated by the participants from India and abroad.

T. SATYANARAYANA

*Department of Microbiology,
University of Delhi South Campus,
Benito Juarez Road,
New Delhi 110 021, India
e-mail: tsnarayana@vsnl.net*