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BioTech NEWS

Newsletter of the Department of Biotechnology, Government of India

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CONTENTS

Department of Biotechnology,
Ministry of Science and Technology,
Government of India

Reader's mail

Response

It is only recently that I chanced on four back issues of bio-tech news, including the latest December 2006 issue. I was pleasantly surprised and actually amazed by the high quality of content in all the newsletters despite it being a government publication. I am impressed by the design of the newsletter… terrific feature articles by outstanding scientists, pieces by industry leaders, cutting edge articles, technical updates and profiles. Indeed the newsletter is well conceived.

From the perspective and interests of organizations like Foundation for Revitalisation of Local Health Traditions (FRLHT), Bangalore, I would like to read, once in a while, features on trans-disciplinary research between India's profound traditional health sciences and western science. Dr. M.S. Valiathan's recent initiative in "Ayurvedic biology", covering fields like pharmaco-genomics, points to the exciting possibilities in this cross cultural field. Dr. G. Padmanabhan, IISC, in the June 2006 issue of Biotech News also talks about traditional medicine as another niche area (Indian Biotech: Today and Tomorrow). I do believe trans-disciplinary research bridging the genius of East and West should be one of the USPs of Indian biotechnology given the richness of the country's knowledge heritage. It needs an attitude of self respect and pride amongst knowledge leaders and a conscious obliteration of the prejudices sown by colonizers 200 years ago.

Darshan Shankar, Director, FRLHT, Bangalore.

As a student of biotechnology, I have found Biotech News a major source of current information, apart from what is offered on the internet. After reading the profiles of institutions working in the field of biotechnology and the Newsdesk column, I feel more confident about opting for a career in biotechnology. You could, of course, help students like us by providing information on careers in biotechnology based on recent educational experiences in India and abroad of young Indian biotechnologists.

Vasudha Agarwal, La Martiniere Girls' College, Lucknow.

To the readers

The Department of Biotechnology had relaunched Biotech News - its official newsletter - with reorganized content, fresh attire and with increased periodicity around a year back. The earlier version, you may recall, was published twice a year at six-monthly intervals. In order to maintain currency, and bring to its readers a flavor of the various developments in biotechnology as seen from DBT, the Newsletter is now appearing six times a year at 2-monthly intervals, both in hard copy and e-format versions.

As mentioned earlier, we have reorganized the content to make it more informative and user friendly. Each issue has one or more 'Feature' articles written by eminent life science experts. 'Cutting Edge' focuses on critical analysis of a frontier area of life sciences/biotechnology. 'Tech Update' highlights recent developments from institutions and industry. 'News Desk' brings you a round up of various scientific meetings, brain-stormings, international collaborations etc. 'Tech Transfer' keeps you informed of latest technology transfers to industry and other user groups of biotech products, processes as well as launch of these in the market. 'Profile' seeks to provide snapshots of an institution active in biotechnology. Finally, 'Notice Board' alerts you to DBT's call for proposals, forthcoming meetings, positions vacant at DBT and its autonomous institutions, recent publications etc.

With all these changes, we aim to reach out to a larger section of the society, particularly, schools, colleges and post-graduate institutions, as well as industry and voluntary organizations interested in life sciences and biotechnology.

This is the first issue of year 2007. I urge readers to send in their views and suggestions on what they would like to see in Biotech News.

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Organic Boost

Biofertilizers: Are they here to stay?

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Feature

Fertilizers supply essential plant nutrients, mainly Nitrogen (N), Potash (K) and Phosphorous (P) as they are removed in large quantities from the soil by each successive harvest. Increasingly high inputs of chemical fertilizers for high yield agriculture during the last 150 years has not only left our soils degraded, polluted and less productive but also posed severe health hazards.

For instance, in South-East Asia, decline in productivity of major cereals, particularly rice, has been observed due to decrease in effective N-supply and adverse changes in organic content in soils due to over dependence on nitrogenous chemical fertilizers. Attempts to increase N-supply by excessive application of fertilizers lead to poor utilization of the same by target crops resulting in passage of the excess N to water bodies, nitrates to ground water and green house gases to the atmosphere. In soils with general nutrient deficiency such as red, laterite and mountain soils, the deficiencies of P, S & Zn is accelerated due to excessive N-induced dry matter. This leads to further decline in crop yield.

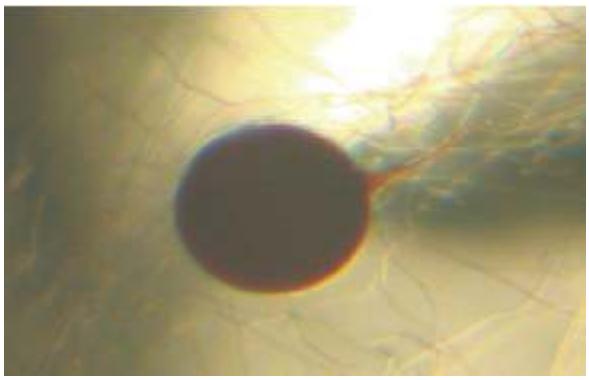
Increasing awareness in this regard has gradually brought about a major shift in consumer preferences towards organic food grown without use of any chemicals whatsoever. This is particularly so in the developed countries but the trend is beginning to catch in other countries as well, including India. The global market for organic food and natural products is on the upswing and is expected to have touched USD 40 billion by 2006 (actual figures awaited). Demand for organic food has seen a steady increase both in developed and developing countries. Worldwide, over 130 countries are producing certified organic products in commercial quantities today.

India is the third largest producer and consumer of fertilizers in the world (after China and USA) accounting for 12% of world production of N & P nutrients and 12.6% of world consumption of NPK nutrients.

Table 1. Fertilizer Consumption (NPK) in India (million tonnes)

Year	Food grain production	Fertilizer Consumption	Per hectare Consumption
1999-2000	209.80	18.07	95.23
2001-2002	212.02	17.36	91.49
2006-2007 (Target)	234.29	23.55	115.23
2011-2012 (Target)	320.00	37.92	168.99

Out of the total of 329 Million Ha of India's geographical area, about 114 Million Ha is under cultivation. With India hurtling towards overtaking China as the most populous country, meeting the increasing demand for food shall continue to be major challenge. Further increase in food production will depend on either increasing the productivity of existing areas or by bringing additional lands, presently under fallow or wasteland categories, under cultivation. Around 56.29 million hectares of the land area is currently categorized as wasteland or fallow land that can be brought under cultivation in the future. Thus, the total area under cultivation can rise to a total of 170.29 million hectares. Given the fact that all additional areas visualized as above will be largely rainfed, bio-fertilizers have the potential to play a major role in making agriculture a viable proposition here.



In vitro Mycorrhiza spore

Bulk of India's fertilizer usage is concentrated in areas where irrigation facilities are available and this accounts for just 30% of arable land. Rainfed areas that account for 70% of the balance land hardly see any fertilizer usage. Farmers in these areas often use organic manure made from locally available biomass to meet incremental nutrient requirements of their agricultural crops. These regions of India provide considerable opportunity for organic farming due to very low utilization of chemical inputs.

The holistic strategy presently gaining ground is the Integrated Nutrient Management (INM) program that aims at achieving harmony in the conjoint use of all resources like chemical fertilizers, organic manures, green manures, biofertilizers, crop residues and other non-conventional sources of plant nutrients. This is complemented by efforts to maximize nutrient use efficiency of crops and minimization of nutrient loss and leakage from cropping system. The objective is to meet the three goals of Integrated Plant Nutrient System (IPNS) viz. maximization of crop yield, sustenance of the natural resource base of agriculture (soil, water and air quality) and improvement of the socio-economic conditions of the farming community.▶▶

> "Given the fact that all the waste or fallow land which can be brought under cultivation in future will be largely rainfed, bio-fertilisers have the potential to play a major role in these additional areas"

Feature

"The Integrated Plant Nutrient System (IPNS) aims to maximize crop yield, sustain the natural resource base of agriculture (quality of soil, water and air) and improvement of the socio-economic conditions of the farming community"

Biofertilizers: Indian Scenario

The Gazette of India (2006) defines biofertilizer as a product containing carrier based (solid or liquid) living micro-organisms which are agriculturally useful in terms of nitrogen fixation, phosphorus solubilization or nutrient mobilization, so as to increase the productivity of the soil and/or the crop. These broadly include the nitrogen fixers (symbiotic and non-symbiotic bacteria), phosphate solubilizing fungi and bacteria and the mycorrhizal fungi that are capable of mobilizing non-labile nutrients from soil and transporting them to and across plant roots. A recent addition is the plant growth promoting rhizobacteria (PGPR), specifically the fluorescent Pseudomonads, which stimulate plant growth and repress root diseases by a variety of mechanisms.

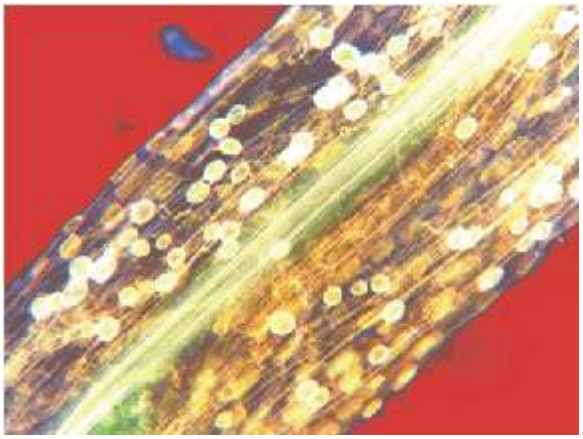
So far emphasis has been given only to certain types of biofertilizers such as *Rhizobium, Azotobacter, Azospirillum* and Phosphate solubilizing bacteria (PSB). Usually carrier material such as peat, lignite, peat soil, humus, wood charcoal or similar material favoring the growth of microorganisms is used. However, in practice a large variety of microbial inoculants are available and being used as biofertilizers. These include *Azolla, Trichoderma, Frankia* and Vesicular Arbuscular Mycorrhiza (VAM).

Table 2. Important micro organisms constituting biofertilizers

Microorganism	Nutrient fixed (Kg/ha/year)
Actinorrhizae (Frankia sp.)	150 kg nitrogen/ha
Algae	25 kg N_2/ha
Azolla	900 kg N_2/ha
Azospirillum	10-20 kg N_2/ha
Rhizobium	50 to 300 kg N_2 / ha
Azotobacter	0.026 to 20 kg N_2 / ha
Mycorrhizae	Solubilize food phosphorus (60%)
Phosphate solubilizing bacteria and fungi	Solubilize about 50-60% of them fixed phosphorus in the soil

Phosphorus deficiency is one of the major limiting factors in crop growth and nitrogen fixation in the tropical regions. Phosphorus is a non-renewable costly input, often in short supply. Phosphate fertilizers also have pollution problems associated with them. In soils with high pH, a major portion (75% phosphatic fertilizer) of the fertilizer applied becomes non-usable (fixed) through chemical reactions and gets converted to a form that is inaccessible to plants. Presently in India, there is an annual demand of approximately 47.98 lakh tonnes of phosphatic fertilizers for agriculture application of which only 33.48 lakh tonnes is supplied by domestic chemical fertilizer industries, and the remaining 14.5 lakh tonnes is procured from other countries.

Mycorrhiza based biofertilizer technology is one such successful technology capable of wasteland reclamation and beneficial in agriculture because it provides phosphorus nutrition to the plant. Mycorrhizal fungi can utilize phosphorus from extremely low concentrations, even from unavailable sources, and provide an alternative to offset the high cost of phosphate fertilizer input. Mycorrhizal technology is an innovative invention offering a partial substitute to chemical fertilizers as it enables plants to thrive better and offers better establishment and enhanced yield in nutrient poor conditions. This fungal microbe, which forms a symbiotic, non-pathogenic, permanent association between the roots of land plants, is an appropriate partial substitute to phosphatic fertilizers and promotes yields significantly. This is extremely beneficial to almost all cultivated plants as it has a broad host range in contrast to other products available. It is easy in application, quite similar to chemical fertilizers. Its cost of production is also highly competitive as compared to chemical fertilizers. Thus, biofertilizers offer a huge potential for widespread use offering both economic and environmental advantage to farmers/growers and commercial viability to production units.



Colonised roots with vesicles

There are several types of biofertilizers now being marketed in India. Some of the prominent ones are *Rhizobium, Azatobacter* and *Azospirillum*. The Indian Council for Agriculture Research and Department of Biotechnology have actively encouraged application of rDNA technology for better quality Rhizobium and Azatobacter. In order to help the industry, DBT has established certain repositories to keep micro organisms. In the case of biofertilizers, the established repository for microbes is the National Facility for Rhizobium Culture Collections, Division of Microbiology, IARI, New Delhi. The others are the National Centre for Conservation and Utilization of Blue-Green Algae, IARI, New Delhi, the Microbial Type Culture Collections, Institute of Microbial Technology, Chandigarh, the National Facility for Marine Cyanobacteria, Bharatidasan University, Tiruchurapalli and the Facility for Mycorrhizal Culture Collections, The Energy and Resources Institute (TERI), New Delhi.

A number of entrepreneurs in India have now established facilities for the production of mycorrhiza. The constructed area requirement is 5,000 square feet to produce 200 ton/annum and 12,000 square feet to produce 1000 ton/annum. In India, a ▶▶

centralized production facility for a product like arbuscular-mycorrhizal fungi (AMF) is feasible. However, at this stage business is in the concept selling stage and effective demonstrations are very necessary for product penetration at regional levels. Once the product potential is demonstrated in various agro climatic zones in the country, consolidation may occur.

Quality Control and Regulation of biofertilizers

Most of the microbial bio-inoculants and organic fertilizers available in the market would have to address a common problem: quality control and its regulation. It is necessary to ensure that these products are of standard quality. In India and comparable countries, most commercial organic fertilizers are not covered by national or international standards, such as those which govern the quality of chemical fertilizers. It is important to evaluate the produced inoculum from commercial units with certain reference values to ensure strict adherence to protocols and methodologies recommended by recognized and independent laboratories. This is most vital as several handling errors may occur during technology adoption and industrial production resulting in poor product quality. This may lead to dissatisfaction of both end users and producers. Thus, specific protocols for quality control of microbial biofertilizers need to be developed and standardized for application. This is essential not only as a guarantee for producers and users but also for the protection of ecosystems. Moreover, this would also help in quality management and assessment of inoculum potential with every batch of inocula produced. Unless quality control is achieved, the full potential of biofertilizers may remain untapped.

For mass production of biofertilizers, critical benchmarks at all stages of inoculum development covering all possible parameters desirable for ensured production, are required to be identified. These include viability checks from the processing stage till the formulation stage, ranging from the colonization of host roots, weight of dried inoculum at harvest, propagule estimations, infectivity potential of crude and formulated diluted inoculum, formulation conditions like temperature and suitable storage conditions. Such benchmarks also help to institutionalize process efficiency at the production level. Once the commercial launch of the formulation is achieved, both the developer of the technology and the distributing industries share equal responsibilities for the authenticity and performance of commercialized products, and must continue to work together to evaluate responses obtained from the field. This would ensure confidence building and continuous use of these products over the years. Thus, it is important to monitor the effectiveness of the inoculum to regularly validate product performance and customer satisfaction.

The responsibility of the laboratory developing biofertilizers should be to consider the following features as desired by the end user:

- Compatibility with local indigenous microbial isolates for prompt and effective plant growth
- Ability to survive, and stability in the carrier system
- Ability to survive while seed-coated, even under adverse climatic conditions
- Wide-range of host applications
- Ability to maintain genetic stability
- Absence of harmful contaminants
- Prolonged shelf life

Quality standards have been notified by BIS and regular testing is also done by NBDC/RBDCs and State Government Laboratories. The Government of India, vide its Gazette extraordinary [part II-section3-subsection (ii)] dated 24 March, 2006, released the specifications for biofertilizers, alongwith their tolerance limit and method of analysis. However, this is limited to Rhizobium, Azotobacter, Azospirilum and Phosphate solubilizing bacteria (PSB) only and there is a need to bring other types of biofertilizers under its ambit.

The Government has been providing non-recurring grant-in-aid up to Rupees 20 Lakhs for setting up of biofertilizer production units of 150 MT annual capacity by industry, cooperatives, PSUs/NGOs etc. National Project on Organic Farming (NPOF) has been approved for implementation during the 10th Plan with an outlay of Rs. 57.05 crores for the production, promotion, market development and certification of organic farming in the country. Current production of bio-fertilizers in the country is 10,000 mt/annum against the production capacity of 18,000 mt/annum. Average annual consumption of bio-fertilizers in the country is 64 g/ha.

Biofertilizers have shown great potential as a supplementary, renewable and environmental friendly source of plant nutrients and are an important component of INM and IPNS. However, existing production units do not have the capacity to meet present requirement. Most of the production units lack in instrumentation, production techniques, skilled staff etc. for production of superior quality bioinoculants. The result is the production of poor quality products which is in turn responsible for the poor response of farmers towards biofertilizers. Keeping in view the changing scenario of production systems and environmental concerns associated with chemical fertilizers, it is necessary that biofertilizers play a more significant role in production systems and maintain ecological equilibrium and sustainability as well. What is most needed is a business driven approach that delivers commercially feasible results which attracts the attention of business houses and policy makers. ■

"Quality control of commercial microbial inoculants is extremely important for developing faith among the user community"

Cutting Edge

Diversity Arrays Technology (DArT)

Low Cost, Generic Molecular Markers for Breeding and Research

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Andrzej Kilian, DArT, P/L, Canberra, ACT, Australia
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"DArT technology is not dependent on having DNA sequence information, is expandable based on user's needs, and is high-throughput with low cost"

The use of molecular markers has been shown to be a powerful approach for the genetic dissection and manipulation of many traits of importance in agriculture. However, their full impact, especially in breeding, is yet to be realized. This is due to a number of limitations such as the time and resources required to discover a large number of polymorphic markers for a species, requirements for sequence information for marker development, and the cost and time for scoring the markers (average per datapoint cost of over US$1.00).

With the advent of Restriction Fragment Length Polymorphisms (RFLP), genetic maps were developed for many species, including many crops of agricultural importance. While various strategies were employed to reduce the costs and increase the throughput of RFLP detection, the lengthy and elaborate procedures of Southern blotting and probe hybridizations greatly limited the number of samples that could be analyzed, thus maintaining high per sample costs. The discovery of microsatellites (or simple sequence repeats, SSRs) in many species provided much simpler protocols based on PCR amplification and gel-or sequencer-based detection. However, there are large costs and time required to develop primers that detect SSRs in a species, although once developed, SSR assays are relatively simple, low-cost and can be automated for moderately high-throughput. An often overlooked limitation of SSRs is the lack of an efficient automated analysis system to detect the specific SSR allele in a sample, and to convert this into usable data for mapping or characterization (software does exist but still often requires significant user input for interpretation).

Recently, systems that detect single nucleotide differences between DNA samples (single nucleotide polymorphisms, SNPs) are being developed as these can be assembled into large-scale, low-cost detection platforms such as the Illumina Bead Arrays (www.illumina.com). For species where extensive sequence information exists (e.g., maize and rice), the development of SNPs is relatively easy, although overall costs can be high. For other species, the requirement for extensive sequencing is a limitation, although such sequencing is becoming more achievable with recent developments in extremely high-throughput sequencing strategies (e.g., Life Sciences 454 DNA Sequencing, www.454.com).

Diversity Arrays Technology (DarT)

A marker platform that offers certain advantages, especially in the breeding context, is based on array hybridization technology and has been termed, Diversity Arrays Technology (DArT). Developed by Dr. Andrzej Kilian and his team, this technology provides a cost-effective and whole-genome genotyping tool (see references and the DArT P/L web site: www.diversityarrays.com). The technology is not dependent on having DNA sequence information, is expandable based on the user's needs, and is high-throughput and low cost (per datapoint costs below US$0.10). DArT analysis requires the assembly of a "genotyping array" that contains genomic clones that show variable hybridization intensities across the individuals under study. Such arrays have been developed by Dr. Kilian and his team for several species, including sorghum, rice, barley, wheat, chickpea, pigeonpea and many others including animal species. The "genotyping array" is hybridized with an individual DNA sample using microarray technology, the hybridization signal measured and converted into a genotype score. DArT P/L bioinformaticians have developed specialized software for automated data extraction, storage and analysis.

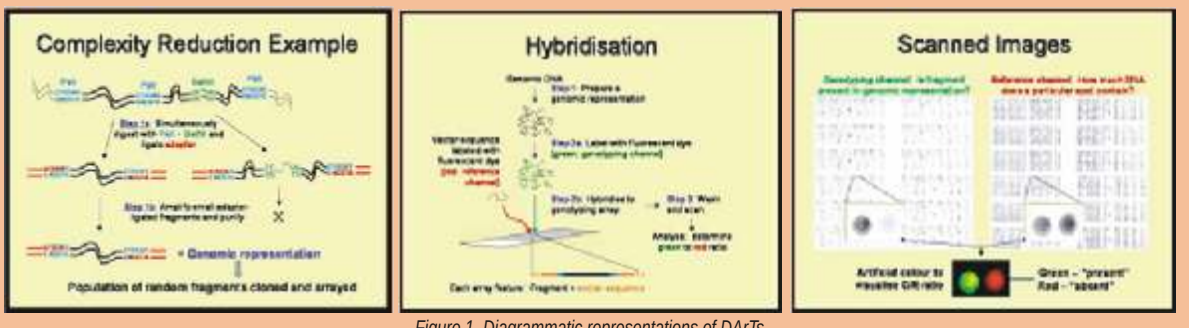

Figure 1. Diagrammatic representations of DArTs.
In the top panel, DNA samples are reduced in complexity by restriction digestion and selective amplification before cloning and arraying.
In a typical DArT analysis (middle panel), DNA is extracted from a sample, reduced in complexity, labeled and hybridized to the 'genotyping array'.
The hybridized arrays are scanned and the images converted into a binary matrix (1's and 0's) for further analysis (bottom panel).
[Diagrams reproduced from the DArT P/L web site with the permission of the author.]

Diversity Arrays Technology (DArTs) Low Cost, Generic Molecular Markers for Breeding and Research

DArT Development

A DArT marker is simply a segment of DNA that has been determined to be polymorphic across a range of germplasm of interest. Such markers are most easily scored as dominant (presence/absence) loci, although many can be scored in a hemi-dominant manner. Like all marker systems, a marker discovery phase is required to identify the most polymorphic and useful markers for large-scale genotyping. Unlike most other marker systems, no sequence information or DNA synthesis is required, and the same platform is used for both discovery and routine genotyping.

Figure 1. *(on page 6)* presents the basic steps in a DArT analysis. To develop a genotyping array for a species, genomic DNA is isolated from a number of individuals that represent the diversity to be studied (e.g., genebank accessions, breeding lines, parental lines). The pooled DNA is then reduced in complexity by one of several methods that involve digestion with one to three restriction enzymes of various cutting frequencies, followed by adapter ligation and PCR amplification. The 'representation' produced following amplification is then cloned and individual inserts (markers) are arrayed on a microarray. The production of markers via cloned DNA provides a rapid and simple method for generating the sequence of any specific DArT marker in the future. Labeled genomic DNA from the original individuals is then hybridized to the array and polymorphic clones (DArT markers) are identified that produce hybridization signal intensity differences for different individuals. The selected markers are then used to produce a 'genotyping array' for large-scale genotyping. Several thousand markers can be screened on a single array to discover the most polymorphic markers that are then used on 'genotyping arrays' to detect several hundred loci in parallel using only small quantities (ng) of sample DNA.

For routine DArT genotyping, sample DNA is reduced in complexity using a similar protocol used in the discovery phase, labeled, and hybridized to one or more genotyping arrays. The hybridization signals are measured and specialized software (DArTsoft) used to convert the signals into genotypic scores (usually 1's and 0's). The genotypic scores can then be analyzed in a manner similar to other molecular marker genotypes (e.g., SSRs, SNPs) using statistical software packages for diversity, genetic and/or breeding applications.

The infrastructure required for high-throughput DArT analyses is not extensive, but does require a dedicated molecular biology laboratory with certain basic equipment for DNA extraction, cloning and microarray hybridization, along with more specialized equipment for microarray printing and scanning (Figure 2. *on page 8*). In addition, adequate computing support is required to handle the large datasets that are produced.

DArT Applications

Dr. Kilian and his team at DArT P/L have made excellent progress in applying DArTs in a number of plant, animal and pathogen species. For plants, these include important agricultural species such as rice, barley, wheat and sorghum, among other important crop and model species. Applications of DArTs are essentially the same as for other marker types. DArT arrays can be extremely useful in assessing the diversity of genetic resource collections and breeding germplasm. The ability to genotype an individual at relatively low per datapoint costs means that a much larger set of individuals (accessions) can be studied, thus often eliminating the need to identify subsets of the materials due to cost and technology constraints. By analyzing the entire collection, a complete understanding of the diversity is obtained, greatly reducing the risk of missing critical germplasm accessions in the study.

The generation of molecular maps that form the basis to locate genomic regions (Quantitative Trait Loci, QTLs) involved in the expression of important agronomic traits has been and will remain an important application of molecular technology. To obtain even a reasonable level of genome coverage and a fairly complete genetic map of a species, requires a few to several hundred molecular markers. In some species (e.g., rice, maize, Arabidopsis), markers are abundant and polymorphic so that the identification of sufficient quantity of molecular loci is easy. In most other species, there is still a lack of sufficient numbers of polymorphic loci. While DArT markers may not be any more polymorphic than other marker types, the fact that several thousand can be screened very rapidly means that DArTs provide an efficient marker type for whole genome mapping. Once a few hundred DArT markers are available for a species, the development of a molecular genetic map for a segregating population becomes a matter of days, rather than months or years that other marker types can require. In fact, by using DArTs, the major limitations in the genetic analysis of most traits are the availability of segregating populations and/or cost-effective phenotyping protocols.

Association mapping is becoming an option in many species, especially for those where the development of genetic populations is restricted or time consuming. Effective association mapping requires fairly dense coverage of a genome with molecular markers. Again, the large number of DArTs that can be screened in a single assay provides an attractive option for such studies. Once particular associations are identified, the same DArT array can then be used in backcrossing the associated segments into elite breeding and farmer varieties. ▶▶

> "The ability to genotype an individual at relatively low per datapoint costs means that a much larger set of individuals (accessions) can be studied"

Diversity Arrays Technology (DArTs) Low Cost, Generic Molecular Markers for Breeding and Research

Of particular importance is the application of DArTs to breeding programs, especially for use in marker-assisted selection (MAS). A major limitation for the use of markers in breeding is often the lack of a large number of markers, both linked to the trait(s) of interest, and for selection of the background (or non-linked) genomic segments (e.g., in a backcrossing program). Beyond just the number of markers, the cost of, and time needed to, produce a datapoint is often prohibitive. Given the extensive genome coverage, high-throughput and low-cost, DArTs provide a very attractive marker system for such breeding applications. Costs of below US$0.10 per datapoint mean that a single individual in a backcrossing program could be genotyped for several QTL segments (using two flanking markers) for around US$1. By including 100 additional DArT markers on the array to detect random loci throughout the remainder of the genome, an entire genotype of the backcross individual would be determined for around US$10.00. Such complete genotypic information would allow the breeding program to select those individuals that not only have the QTLs of interest, but also contain the maximal amount of recurrent parent genome greatly accelerating the conversion of elite lines. All of this selection can be accomplish well before the breeder makes the actual crosses in the field, e.g., at the seed and/or seedling stage.

"Given the extensive genome coverage, high-throughput and low-cost, DArTs provide a very attractive marker system for breeding applications"

A simple application of DArTs for MAS is in the backcrossing of individual or multiple transgenes into new varieties. Given the difficulty to produce a highly effective transgenic event and the fact that most regulatory policies consider each 'event' as unique, once an 'event' has been developed that will be released in a country, it will be necessary to introgress this 'event' into a range of elite varieties. This is accomplished in most crops by backcrossing for several (4+) generations followed by selfing for 2-3 generations to fix the transgene in the final product. At each generation, the presence of the transgene is determined by various methods ranging from phenotpying, to ELISA, to DNA detection. While such methods are simple and inexpensive, most backcross programs are not able to make any selection on the recurrent parent genome as this would require extensive genome analysis at a number of loci. A single DArT genotyping array with ~100 markers would provide a low-cost method to determine how similar a particular backcross individual is to the desired recurrent parent. This could result in obtaining the desired new variety in 50% or less of the time required if DArTs were not used.

Given the advantages offered by DArTs and the desire to provide a generic technology that could be applied to any species of interest, The Center of Excellence on Genomics (CEG) recently approved by the Department of Biotechnology (DBT) to be established at ICRISAT, will implement DArT technology as one of its flagship marker services for research and breeding in India. A partnership with DArT P/L in Australia will provide the required technology transfer and training to ensure that DArTs are effectively established and operating systems provided in the most timely fashion. Initially, DArT systems will be available for a number of important crop species in India. Other species will be added through collaborations with Indian institutes and scientists interested in using DArTs in their research.

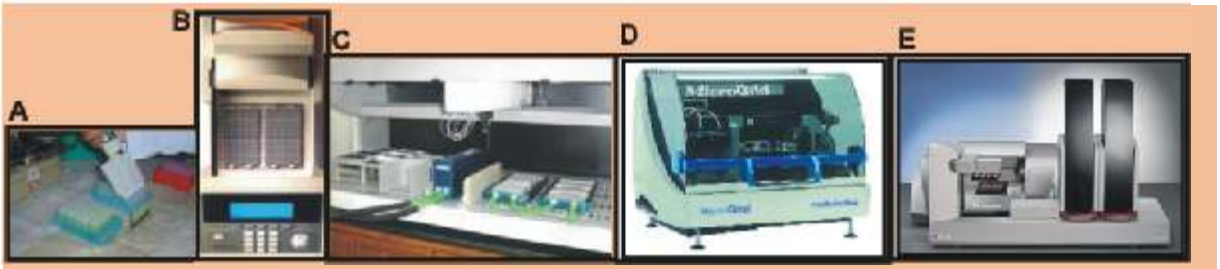

Figure 2. Examples of the major infrastructure required for DArT analyses. In addition to a basic molecular biology laboratory equipped for DNA extraction (A) and PCR amplifications (B), the use of a robotic pipetting station (C) for more automated DNA extractions and PCR setup can be useful. The two major pieces of equipment required are a microarrayer (D) to print the arrays contained the DArT markers and a scanner (E) to detect the signals following hybridization with sample DNA.

While the CEG will be providing DArTs as a major marker service, other technologies such as DNA sequencer-based SSR detection, TILLING and EcoTILLING detection via LiCOR systems, and high-capacity phenotypic analysis for abiotic stresses will also be available at the CEG. High-capacity data storage and analysis will be established to provide the necessary data handling for the large datasets produced by the CEG and to ensure that these are made available to the researchers in a timely and effective manner. The ultimate goal of the CEG is to make molecular markers available as an effective tool for all researchers and breeders in India.

(More details and references are available on the DArT P/L website, www.diversityarrays.com

National Centre for Plant Genome Research

Aruna Asaf Ali Marg, P.O. Box No. 10531, JNU Campus, New Delhi - 110 067, http://ncpgr.nic.in/

Profile

The National Centre for Plant Genome Research (NCPGR) was established in 1998 as a frontline autonomous research institution in Genomics research under the Department of Biotechnology, Government of India with a small and dedicated group of scientists working out from its interim premises in Jawaharlal Nehru University. NCPGR was dedicated to the nation by none other than his Excellency, Dr. A.P. J. Abdul Kalam, the President of India, on November 28, 2005, after which the activities of NCPGR became operational from its own tastefully designed and developed campus in South Delhi. The current mandate of NCPGR is:

- To promote basic and applied research in plant molecular biology;
- To identify important genes/factors and manipulate those for generating transgenic plants with improved agronomic characters and pathogen/stress resistance;
- To develop molecular markers for monitoring important traits.

NCPGR is the only national research centre of its kind in the country that is entirely dedicated to core research in advanced areas of Plant biotechnology including molecular biology, genetic engineering and genomics with an applied emphasis. It aims to generate new knowledge about the genetic composition of plants, assimilate it with all other current knowledge and utilize the genomic knowledge in the construction of new varieties of plants and crops. In line with its mandate, the NCPGR is actively contributing to the understanding of gene structure and function, genome organization, gene expression and gene manipulation to breed improved varieties of food and industrial crops. Over the years it has also created a niche to provide the requisite infrastructure for the country to take its due place amongst the nations that are in the forefront of genome research.

NCPGR is widely recognized for its transgenic work using AmA1 and OXDC genes on nutritional improvements of potato and tomato. The value added AmA1 transgenic potato, in terms of nutritional quality has now undergone satisfactory field trials for its agronomic performance. Expression of AmA1 gene in other staple crops is in progress. Also, low oxalate, fungal tolerant OXDC tomato varieties have been developed and promising lines have been selected. Development of few▶▶

> "R&D work in the area of plant genomics will open great opportunities for crop improvement which is of paramount national interest"

What was the background and rationale which led to the genesis of the NCPGR ?

The idea of establishing a national R&D institution such as NCPGR was conceived in late nineteen ninety six due to several motivating factors. Molecular Genetics had already made spectacular advances in our understanding of the gene expression in the life cycles of viruses and bacteria. Genome sequences of many microorganisms had been revealed and advances were being made towards sequencing of genomes of fungi, plants and primates, including man. Serious biotechnological interventions had begun for industrial production of useful biomolecules. On the other hand, agricultural productivity had become stationary in India thereby compromising the food and nutritional security of the country. It was evident that strengthening of plant biology research with the tools and techniques of genomics, proteomics and metabolomics will be helpful in understanding the molecular details of the key processes that determine field and quality of produce from plants. There were strong indications that R&D work in the area of plant genomics was to open great opportunities for crop improvement and would be of paramount national interest.

What role and contribution do you envision for the institute in the coming decade?

NCPGR aims to fulfill its multifarious role as the premier national laboratory for plant genomics and transgenic research. NCPGR will also train scores of postgraduates and academicians from sister laboratories in its research areas. The doctoral degree program in collaboration with Jawaharlal Nehru University will be continued. New knowledge will be generated about physical organization and functional expression of plant genomes/genes. Some of the most important genes connected with tolerance to high temperature, drought, diseases, photosynthesis, flowering and maturity and secondary metabolism will be defined, cloned and manipulated for crop improvement.

What are the pioneering areas of research in plant genome which is exciting the minds of young scientists in India and elsewhere?

A large number of areas in plant genomics are exciting and some of these will engage the interest of NCPGR scientists in coming years. Let me list some of the challenges which immediately come to my mind: What are the genetic mechanisms for origin of new plant species? How do genomic segments/genes get silenced or activated in plants? What are the determinants of mitotic and meiotic cell divisions? What are various levels of interactions between nuclear, mitochondrial and chloroplastic genomes for engineering better energy efficiency and growth profiles in larger fruits? How to increase the photosynthesis rate and capacity of sinks in C3 and C4 crop plants? How to manipulate hormonal regulation for short life cycles, higher productivity, fruit maturity/ripening, seed composition and prolonged seed viability? How to introduce nitrogen fixation ability in the above and below ground parts of plants? Please understand that this is only a short list of the important and exciting questions regarding plant biology.

A Ph.D. in Biochemistry from Calcutta University Dr. Asis Datta, Padma Shree, began his career in 1973 at JNU's School of Life Sciences, eventually to serve as its Vice Chancellor (1996-2002) before moving to NCPGR as its Director. Winner of the prestigious Shanti Swaroop Bhatnagar Award (1980) and Life Time Achievement Award of INSA (2005), he is associated with several prestigious international scientific institutions, and has more than 100 scientific papers in international journals to his credit, in addition to 3 Indian and 4 US patents. Dr. Datta spoke to Biotech News about the history and future vision of NCPGR.

more transgenic vegetables and legume crops with OXDC gene is in progress. In addition, as a long-term goal to develop transgenics with increased shelf life, candidate genes have been identified.

The search for dehydration inducible genes in chickpea has led to the identification of DREB-2 that is also induced by salinity. The single copy intron-less DREB-2 expresses in root, resides in the nucleus, binds to dehydration responsive element(s) and has transactivation potential. Its tobacco transgenic has improved seeding growth, root branching and salinity and dehydration tolerance. DREB-2 is thus of agronomical importance.

A proteomic approach towards identifying and cloning of novel osmotic stress responsive genes from legumes and cereals has also been initiated by NCPGR. A number of environmental stress and hormone responsive proteins in legumes have thus been identified.

Field trials of value added AmA1 transgenic potato

Substantial progress has also been made in the area of functional genomics of Chickpea/Ascochyta interactions and nearly two hundred genes involved in defense/resistance have been isolated. Modulation of expression of a number of genes like Lipid transfer protein (nsLTP), a Ser-Thr protein kinase (CaArPK) and resistance gene homolog (CaAr(131) by defense-signaling molecules like SA, JA and ABA has been examined. Also, several hundred genes involved in fungal wilt disease response have been identified by DNA array technology. A framework linkage map of chickpea has been developed and the putative resistance gene against fungal wilt has been tagged.

So far, the Centre has developed 302 microsatellite markers and 31 EST-SSR markers for chickpea genome. Also, an anchor linkage map has been developed on which traits such as Desi/Kabul seed type, seed size, pod number, flowering time and flower color are being placed.

Considerable progress has been made in the transcript profiling of certain terpenoid indole alkaloid (TIA) pathway genes in callus and suspension cultures of periwinkle plant Catharanthus roseus that is known to be unique for its heterochromatic imprints distinguishable from Arabidopsis thaliana, vertebrates and fungi.

In Arabidopsis thaliana, a ligand binding screening has led to the identification of several Z-Box specific transcription factors, viz. ZBF1 and ZBF2. While ZBF1 encodes for a bHLH transcription factor involved in crosstalk between light, ABA and JA signaling pathways; ZBF2 encodes for a bZIP protein. ZBF1 assumes agronomic significance as its mutants show hyper-photomorphogenic growth. Over and under expression of ZBF1 in tomato and carrot are in progress.

In rice, eight members of MAPK family along with the representative reporter genes in source, sink and defense related pathways have been cloned and sequenced. The MAPKs were found to be differentially regulated by cold, heat and drought stresses. Also, a few members of *wrky* and AP2/EREBP transcription factors have been cloned and sequenced.

Besides strengthening its existing network program, and as a part of the international SOL initiative, NCPGR has already completed sequencing and annotation of three of the BACs (374Kb) of chromosome 5 of tomato allocated to it in the Solananaceae Genome Network (SGN) project.

The overall quest of NCPGR's activities is to speculate with genomic knowledge gained, test the formulated idea, test the hypothesis experimentally and apply the results to real life problems in agriculture.

NCPGR has, under affiliation to the Jawaharlal Nehru University, undertaken postgraduate research programs for Ph.D. degree since 2001. Currently about fifty-five students are enrolled. The Centre also accepts a large number of young researchers under various other categories and organizes periodic short-term training programs for scientists from various universities/institutions. Through its infrastructural base for academic-industry interactions and knowledge-cum-material resources, NCPGR is poised to significantly contribute towards understanding of plant cell differentiation, development, morphogenesis, growth and regeneration, photosynthesis, plant microbe interaction, plant breeding and genetic engineering.

"The overall quest of NCPGR's activities is to speculate with genomic knowledge gained, test the formulated idea, test the hypothesis experimentally and apply the results to real life problems in agriculture"

Roaring Counts

Genotyping faecal samples of Bengal tiger for population estimation

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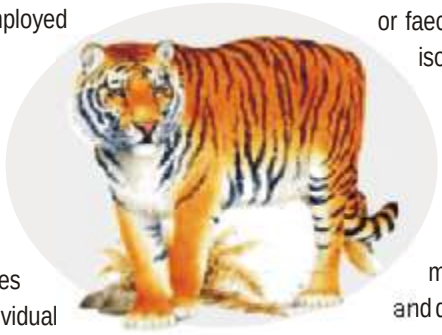
Everybody knows that there are alarming reports pouring from all over India documenting the loss of tigers. There is no doubt that the threat of extinction is hanging over these animals. Though widespread in the earlier part of the last century, the number of tigers in the wild all over the Indian subcontinent dwindled to a figure of 4500 in 1998 as per an educated guess by tiger researchers. The chief cause of this decline of tiger populations is habitat fragmentation, depletion of prey and extensive hunting.

Population estimation and monitoring of an endangered species is important for conservation planning. Tigers are difficult to count visually because they are elusive, nocturnal, territorial and cryptic animals. Therefore indirect and non-invasive methods have been employed for population estimation.



The traditional method of estimating tiger populations is called the "pugmark" method. It has been in use for three decades now for estimating tiger populations in India. The pugmark method assumes that the paw-print of each tiger is individual specific. Therefore, during a tiger census plaster casts and tracings of the left hind paw-prints of a tiger are made wherever encountered in forests and tiger numbers arrived at on the basis of the paw measurements. However, each and every paw-print of all the tigers in an area may not be available at the time of census. Moreover, the pugmarks would change in shape and size based on the substrate that a tiger walks upon; thus a single tiger could possibly be counted as several individuals. Also, this method is prone to human errors during tracing or casting the paw-prints. Therefore, the veracity of this method has been questioned by tiger researchers.

The DNA or deoxyribonucleic acid of all living organisms is unique to each and every individual, which is why no two individuals (except identical twins) are completely alike. DNA is composed of four bases called Adenine (A), Thymine (T), Cytosine(C), and Guanine (G). Certain combinations of these four bases called short tandem repeats or STRs [for instance CACACACACA] are interspersed all over the mammalian DNA. The STRs are important because they can help to uniquely identify one individual from another based on their copy number which varies from individual to individual. It is now possible to preferentially target these unique STR regions of the DNA because of the development of a recent technology called Polymerase Chain Reaction (PCR). Thus one can identify each and every individual animal because of the unique arrangement of repetitive DNA, popularly called 'DNA fingerprint'. Therefore, if one could generate 'DNA fingerprints' of endangered animals like tiger, one can uniquely identify one tiger from another and therefore arrive at reasonable estimates of tiger populations.

However, this is easier said than done! The primary problem in generating unique 'DNA fingerprints' of tigers would be the procurement of biological material. Genetic studies of free-ranging animals are carried out by collecting shed hairs or faecal samples from forests from which DNA is isolated. Thus DNA can be extracted from the animal that one is studying without even catching it. This is called non-invasive sampling. Once individual 'DNA fingerprints' are obtained for the animals, it is possible to estimate populations using mathematical models that can predict population abundance and density.

The source of DNA in faecal samples is the sloughed-off intestinal epithelial cells. However, generating 'DNA fingerprints' from tigers living in the wild is beset with problems. DNA isolated from faecal samples is of very poor quality since they are subject to a variety of environmental conditions, insect attack and/or fungal degradation, particularly so in sub-tropical countries like India. There are several technical difficulties involved with working with such miniscule and poor quantities of DNA. Therefore before one embarks upon long term DNA based population studies of tigers covering the entire country, it was necessary to conduct a pilot study in order to check whether it is feasible at all to use DNA based methods to count the animals.

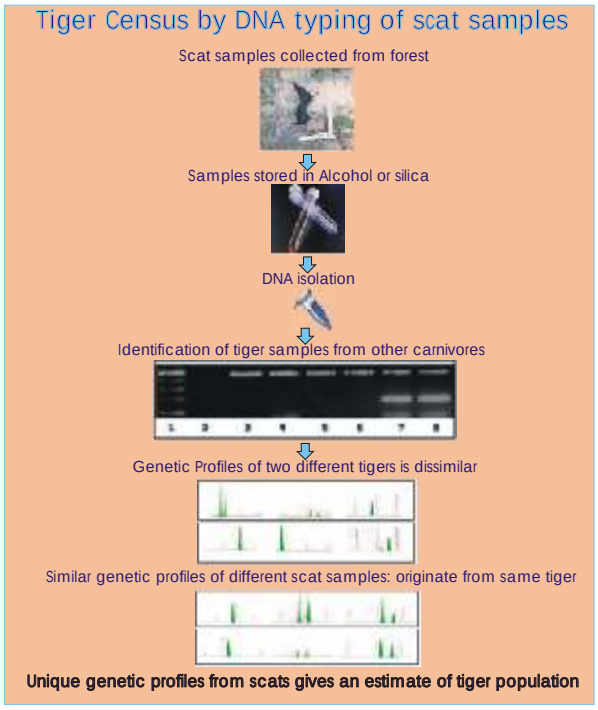
The Centre for Cellular and Molecular Biology has carried out such a pilot study with faecal samples collected from two protected areas to check the possibility of carrying population studies in tiger populations by non-invasive genetic methods. The primary goal of our study was to *identify individual tigers with unique DNA fingerprints and whether these unique DNA fingerprints can be used for identifying individuals in a protected area so that tiger population estimates can be generated.* ▸▸

"If one could generate 'DNA fingerprints' of endangered animals like the tiger, one can uniquely identify one individual from another and therefore arrive at reasonable estimates of species population"

Roaring Counts
Genotyping faecal samples of Bengal tiger for population estimation

"With the unique short tandem repeats (STR) it is possible to distinguish between even closely related animals with a 99% certainty„

In our study we identified the unique STR regions in tigers for identifying individuals and calculated the probability of obtaining similar fingerprints in closely related individuals. It was found that with these STRs it is possible to distinguish between even closely related animals with a 99% certainty. This part of the study was confirmed with captive tigers before embarking on DNA analysis of samples collected from the forest.

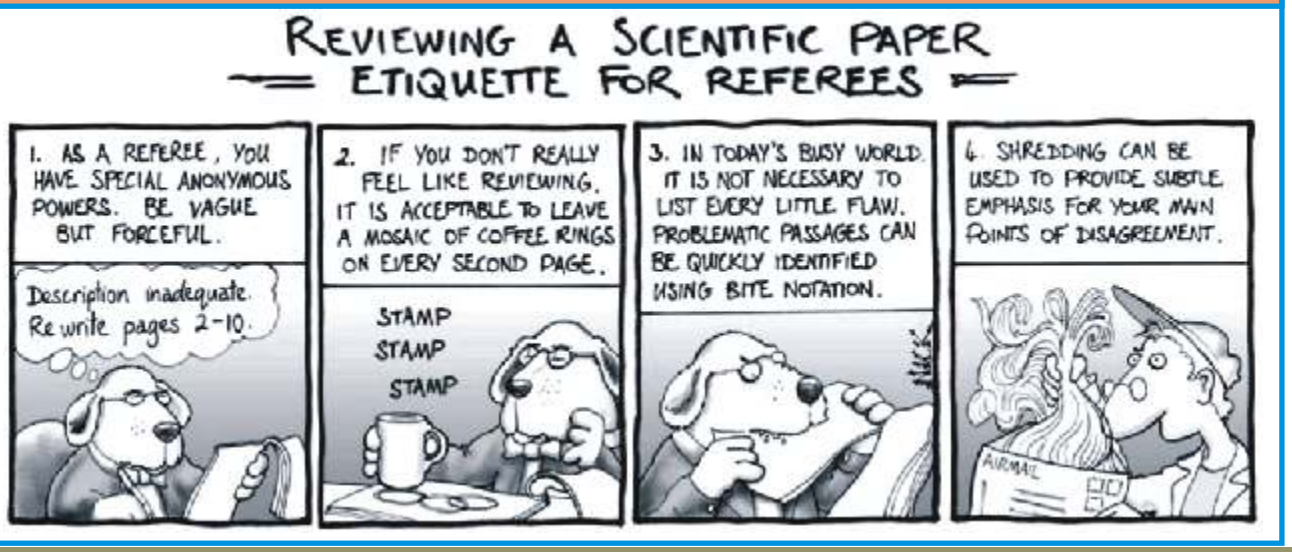


Field work was conducted at two locations in southern India namely, Mudumalai Wildlife Sanctuary in Tamil Nadu and at Biligiri Rangan hills Temple (BRT) Sanctuary in Karnataka.

Scat samples were collected randomly and preserved in alcohol or desiccant silica. At this point, we were confronted by yet another difficulty. The tiger shares its habitat with two other carnivores, namely the leopard and dholes (wild dogs). As the biological material for our study was faecal samples, there was no room for confusing the faecal samples of tigers from those of the other two carnivores. Morphological features of the faecal samples have traditionally been used for distinguishing the faecal samples of these carnivores. Though it is easier to differentiate the scats of wild dogs from those of the tiger and leopard, it is difficult to distinguish between the faecal samples of the tiger and leopard. Moreover, such identification procedures are often subjective. Therefore we developed a DNA-based method for identifying the scat samples of tigers from those of other carnivores. This can identify the scats of tigers with greater certainty than the morphological methods that are generally used. DNA was isolated from the scats that were collected from the study areas. Samples were positively identified as tiger with the DNA-based assay that we developed. Samples are then subject to 'DNA fingerprinting'. DNA-based sex identification of the samples was also done. The results of the DNA profiling show that samples collected from forests could be assigned to individuals. As we followed a random sampling method in our pilot study, we could give an estimate of the Minimum Number Alive (MNA) at the time of sampling.

The results of our study indicate that it is indeed possible to conduct such surveys on a large scale and that it would be possible to estimate tiger population under appropriate sampling designs in protected areas in India. DNA fingerprinting through genotyping faecal samples could therefore become the method of choice for counting tigers in the future.■

On the lighter side



News and Happenings

Second ASEAN-India Bioinformatics HRD Program

The second ASEAN-India Bioinformatics Workshop, supported by Ministry of External Affairs, Department of Biotechnology, Ministry of Science & Technology and the ASEAN Secretariat was organized in Delhi by Sri Venkateswara College, University of Delhi, from December 14-16, 2006. The workshop was inaugurated by Shri Anand

Distinguished Guests on the Inauguration of the 2nd ASEAN India Bioinformatics HRD Programme, December 14-16, 2006, New Delhi. (Seating from L to R) Dr. T. Madhan Mohan, Prof. Ashok S Kolaskar, Prof. Dinesh Singh, Shri Anand Sharma, Prof. Tan Tin Wee, Dr. A. Sankara Reddy and Dr. Donald Thambunan

Sharma, Hon. Minister of State, Ministry of External Affairs. Prof. Ashok S. Kolaskar, former Vice Chancellor, University of Pune, delivered the keynote address on "Bioinformatics: Current Status in India". Prof. Dinesh Singh, Director, University of Delhi (South Campus), in his address emphasized the need to integrate mathematics and Statistics in Biology teaching at the university level.

The focus of the workshop was to introduce the discipline of Bioinformatics to 20 delegates from ten ASEAN member countries (Brunei, Cambodia, Lao PDR, Malaysia, Myanmar, Philippines, Singapore, Thailand, Vietnam, Indonesia and India). The goal of the workshop was to explore avenues for developing a strong team of collaborating networks on Bioinformaticians in the ASEAN-India region. Apart from lectures by eminent Indian scientists working in the area of Genomics, Proteomics and Drug Design, the workshop also had a special session of presentations from the Indian Bioinformatics Industry showcasing the latest developments in technology. In addition, there were discussions on the ASEAN-India Bioinformatics Master Plan. Policy issues pertaining to manpower training, educational curriculum reform, sharing of computational hardware and software resources, strategic research collaborations and scientific exchanges between ASEAN countries and India were taken up.

New Focus on Biodesign

Department of Biotechnology organized a meeting between an expert team from Stanford University and around 35 participants from various Indian institutions such as IITs, medical colleges, life sciences institutions, technical universities and industry. The purpose of meeting was to (a) introduce the concept of biodesign into education and training as well as (b) promote innovation and product development and (c) create medical technology innovation in India in partnership with Stanford University. The meeting helped in identifying ideas for product design and developing prototype through public-private partnership, the focus being on indigenous production of medical devices, implants and bio-instruments.

Dr. M. K. Bhan, Secretary, Department of Biotechnology addressing the Stanford-India Biodesign meeting

The Stanford team consisted of i) Prof. Harry B. Greenberg, Dean of Research & Training, Stanford University School of Medicine, Stanford, CA; ii) Prof. Paul Gordon Yock, Director, Department of Bioengineering and Program in Biodesign, Stanford University Medical Center, Stanford, CA; iii) Prof. Philip Anthony Pizzo, Dean, Stanford University, School of Medicine, Stanford, CA; and iv) Prof. Rajiv Narendra Doshi, Department of Medicine, Stanford University, School of Medicine, Stanford, CA. Prof. Doshi presented the "Preliminary Proposal on Stanford-India Biodesign (SIB) Program" while the faculty of participating institutions presented an overview of their institutional programs, infrastructure and facilities.

Detailed discussions were held on various aspects such as team building, location, infrastructure, facilities, human ▶▶

resource development, training component and time line of the program, etc. The meeting concluded that there is a definite need for this initiative with details of the program needing further elaboration.

5th International Conference on Bioinformatics held at New Delhi

The Fifth International Conference on Bioinformatics (InCoB 2006) was organized from 18th-20th December 2006 by the Department of Biotechnology, Govt. of India, Indian Institute of Technology, Delhi and Jawaharlal Nehru University, New Delhi. This was conducted under the aegis of Asia Pacific Bioinformatics Network (APBionet). The conference was inaugurated by Honorable Minister for Science and Technology and Earth Sciences, Mr. Kapil Sibal.

Over 40 scientific presentations were made including the plenary talks and about 350 posters were presented on seven different Bioinformatics topics including computational biology, structural bioinformatics, datamining and databases, genomics and proteomics, protein folding and structure prediction, systems biology and molecular simulations. Plenary speakers, experts in their respective fields, were drawn form US, UK, France, Canada, Israel and Japan. About 1000 participants including 700 students attended the conference. The conference underscored the need for capacity building and undertaking hard core research in the area of Bioinformatics.

DBT-ICRISAT Centre of Excellence in Genomics gets going

The DBT has recently established a Centre of Excellence (COE) for high-throughput allele determination for molecular breeding of crops at International Crops Research Institution for Semi-Arid Tropics (ICRISAT), in Patancheru, Andhra Pradesh. The centre will strengthen the existing molecular

Dr. M.K. Bhan, Secretary, DBT and Dr. William G. Dar, DG, ICRISAT exchanging MoA for Centre of Excellence in Genomics

breeding facilities at ICRISAT by providing high-throughput, low-cost allele determination platforms to help in the molecular-marker assisted selection and breeding programs in the country. The centre will also organize training programs for scientists and students from Indian institutes in the use of high-throughput methods in breeding and research.

A Memorandum of Agreement (MOA) was exchanged between Dr. M. K. Bhan, Secretary, DBT and Dr. William Dar, Director General of ICRISAT on 13th December, 2006 at ICRISAT headquarters at Patancheru. Dr. Bhan stated that with this partnership the center will provide quick returns in terms of improved agricultural productivity through its cutting-edge molecular breeding techniques. William Dar, Director General of ICRISAT, felt that improved agricultural productivity will help alleviate the poverty of small farmers in dryland areas in India and other developing countries.

Joining hands with Canada

The Department of Biotechnology (DBT) signed two Memoranda of Understanding (MoUs) on December 5, 2006 with the Department of Agriculture and Agri-Food of Canada (AAFC) and National Research Council (NRC), Canada. Shri Kapil Sibal, Honorable Minister for Science & Technology and Earth Sciences graced the occasion.

The Hon'ble Minister for Science & Technology and Earth Sciences, Shri Kapil Sibal, at the Indo Canadian MoU function.

The major objectives of collaboration are to provide researchers and institutions with opportunities to exchange scientific information and facilitate the exchange of scientists. It will also foster scientific cooperation and promote cooperative projects, including industrial programs, between the two countries.

The MoU with Agriculture and Agri-Food, Canada was signed by Mr. Leonard Edwards, Deputy Minister, Agriculture & Agri-food Canada and Dr M.K. Bhan, Secretary, Department of Biotechnology on behalf of their respective countries.

The identified priorities for cooperation include a) agriculture and food processing and storage, b) bio-pesticides and bio-fertilizers, c) functional and nutraceutical foods and impact on human nutrition, d) agricultural biotechnology,

e) biomass utilization, f) sustainable alternative energy and environmental technologies, and g) water quality.

The MoU with National Research Council, Canada was signed by Vice President Dr. Roman Szumski, National Research Council, Canada and Dr. S. Natesh, Sr. Adviser, Department of Biotechnology. The identified priorities for initial collaboration between DBT and NRC are a) Harnessing plants for improving human and animal health, and b) Understanding and exploiting genomics of plants of common interest to the benefit of both the countries.

To set the ball rolling, a workshop on 'Plants for Health' will be organized by NRC Plant Biotechnology Institute, Saskatoon during March 2007.

International Conference on Stem Cell Research

Stem cell research is now at the forefront of scientific and medical innovation and is a rapidly expanding area of investigation. In the country, stem cell programs have been initiated with the aim of promoting both basic and translational research in view of its potential applications. The key components of the strategy of the Department of Biotechnology, Ministry of Science and Technology, Government of India for promoting stem cell research are: creation of center of excellence (CoE); virtual network of centers; generation of adequate human embryonic stem cell (hESC) lines; human resource development through training, short & long term overseas fellowships, seminar, workshops, conferences, etc.

With the support of the Department of Biotechnology, the Stem Cell Research Forum of India (SCRFI) organized an e in international conference from January 29 to February 1, 2007 at Bangalore. The conference brought together stem cell biologists and clinicians from within and outside the country to share knowledge, discuss recent findings and exchange theories for further advancement in this area. Some prominent lectures delivered in the conference were: a) "Therapeutic applications of human stem cells prospects and challenges";

Inauguration of DBT supported International Conference on Stem Cell Research in Bangalore

b) "Adult precursor cells: Progenitor cells an stem cells"; c) "Immunomodulatory effects of mesenchymal stem cells" and d) "The unique difficulties of translating basic biology to clinical use in stem cell repair of the heart". 350 participants including 25 foreign speakers covered areas such as embryonic stem cells, adult stem cells, including mesenchymal & hematopoitic stem cells; commercialization and banking; transnational research; guidelines and regulations. About fifty five posters by young researchers on various aspects of stem cells were also exhibited.■

Have an interesting thought? Share it with Biotech News!

Biotech News invites crisp write-ups (not exceeding 250 words) outlining your thoughts on education, innovation, commercialization and other related issues in life sciences and biotechnology. Every writeup selected for publication will get the author an honorarium of *Rs.1000/-.*

So what are you waiting for? Pick up your pen and get cracking!!

Email your write-up to biotechnews@dbt.nic.in

Call for Proposals

Knowledge Based Nanoscience and Nanotechnology for Application in Biology

The Department of Biotechnology invites proposals for basic research and development of new production processes and devices using nanoscience and nanotechnology derived knowledge-based multifunctional materials for use in agriculture, medicine, food processing industry, environment management and their toxicological studies.

DBT has set forth a vast domain of nanoscience and nanotechnology keeping in view present national priorities and future needs of the country. Some of these include a) basic research on nanoscience, nanotechnology and nanomaterial with future scope of application in biology, medicine, drugs, food, nutrition and alleviation of poverty, b) Nanoscience and nanotechnology for improving soldiers' and emergency relief workers' lives, health, food and nutrition, c) Biochip development, d) Diagnostics and therapeutic tools, e) Micro-nano technologies, f) Applications in health, agriculture, food, environment and industry nano-biotechnologies, g) Applications in areas such as health, chemistry, energy and environment. h)Nano-biotechnology related to genomics, proteomics, and i) Toxicological studies of materials developed

Last date for submitting concept papers is 30th March, 2007.

For more details and procedure for applying visit the department's website:*www.dbtindia.nic.in*

Small Business Innovation Research Initiative

The Department of Biotechnology invites proposals for establishment of product related pre-proof-of- concept, product related research or product development and evaluation in Biotechnology under the Small Business Innovation Research Initiative (SBIRI) Scheme.

The SBIRI aims to a) Strengthen those existing private industrial units whose product development is based on in-house innovative R & D, b) Create opportunities for starting new technology-based or knowledge-based businesses by science entrepreneurs, c) Stimulate technological innovation and product commercialization, d) Use private industries as a source of innovation and enhancing greater public-private partnerships, and e)Increase product development and commercialization in public-private sector derived from Government funded R & D projects.

The scheme, operational in two phases, will provide early stage funding to able scientists in private industries for high risk, innovative and/or commercialized product proposals. It covers all areas of biotechnology related to health care, agriculture, industrial products and processes and environmental biotechnology and bio-medical devices and instruments.

Visit DBT's website www.dbtindia.gov.in for structure of funding and other details of the scheme. Biotech Consortium India Limited (BCIL) is acting as the Special Purpose Vehicle for this scheme of the department and the last date to submit the proposal to BCIL is 31st March, 2007.

DBT Centers of Excellence in Biotechnology

The Department of Biotechnology (DBT) invites applications for support of centers, known as "DBT Centers of Excellence in Biotechnology'. These center grants will provide funding to augment and strengthen institutional research capacity in specific areas of biotechnology. The overall aim of this program is to facilitate pursuit of novel ideas and technologies. The specific goal is to enhance the innovative ability of institutions with well developed research programs in specific areas of biotechnology through flexible support to: i) Expand scientist density and develop faculty research capability, ii) Enhance research infrastructure and iii) Pursue ambitious goals by facilitating longer term funding. Some of the suggested centers of excellence could be (a) Center for Basic Biology, (b) Center for Science, Engineering and Technology and (c) Translation Centers.

For further details, visit www.dbtindia.govh.in/www.dbtindia.nic.in. Last date for receipt of letter of intent: 28th February, 2007.

Forthcoming Events

1) Eleventh Annual National Convention of ADNAT: A 3 day symposium on "Advances in Structural Biology and Structure Prediction", Venue: Hyderabad, February 23-25, 2007, Center for Cellular and Molecular Biology, Uppal Road, Hyderabad. Convener: Dr. Ranjan Sankaranarayan, Email: *sankar@ccmb.res.in*

2) National Conference on "Technological Advances and Emerging Societal Implications", Venue: Rourkela (Orissa), March 24-25, 2007, Department of Humanities and Social Sciences, National Institute of Technology, Rourkela (Orissa). Convener: Dr. (Ms.) Bhaswati Patnaik, Email:*bpatnaik@nitrkl.ac.in*

3) Biosafety Workshop on "Introduction to Risk Assessment for the Deliberate Release of GMOs: Assisting Decision-making in a Biosafety Framework", Venue: ICGEB Biosafety Outstation Ca' Tron di Roncade, Italy, May 14-18, 2007, International Centre for Genetic Engineering and Biotechnology, Trieste, Italy in collaboration with the Institute Agronomico l' Oltremare. Florence, Italy. Contact for details, Email: *courses@icgeb.org*

4) Practical Course on "Bioinformatics: Computer Methods in Molecular Biology", Venue: Trieste, Italy, June 25-29, 2007, International Center for Genetic Engineering and Biotechnology, Trieste, Italy. Closing date of applications: 15 February, 2007. Contact for participation details, Email: *courses@icgeb.org*

BioTech NEWS

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