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Maiden Flight of Indigenous Wankel Engine-powered Unmanned Air Vehicle: A DRDO/CSIR Partnership Accomplishment

It was a bright and sunny morning on 31 March 2009 at a World War II abandoned runway at Veerapura, a small village 8 km from Kolar, when the historic first ever flight of an indigenous engine powering a *NISHANT* Unmanned Air Vehicle (UAV) took place. The engine, a Wankel rotary type is the outcome of a developmental project which originated from Defence Research Development Organisation (DRDO) through Vehicles Research & Development Establishment (VRDE), Ahmednagar, and was jointly designed and developed by National Aerospace Laboratories (NAL), Bangalore, VRDE, and Aeronautical Development Establishment (ADE), Bangalore. *NISHANT,* which is catapult launched, has a Wankel engine fitted with a propeller and has been developed at ADE.

NISHANT, fitted with the indigenous Wankel engine, on the Hydro-Pneumatic Launcher

The flight took off at 1157 hrs in the morning and the vehicle climbed to an altitude of 1.8 km effortlessly before cruising for a duration of 35 min. The air vehicle was recovered safely at the intended place at the dried-up Muduvadi lake, after a total flight duration of 40 min. The event was witnessed by key personnel: Shri P.S. Krishnan, Director, ADE; Dr C.L. Dhamejani, Director, VRDE and Dr A.R. Upadhya, Director, NAL; Regional Director, RCMA and the Regional Director, AQA and other senior officers.

Wankel engine fitted with a propeller on the NAL Test Bed

The Wankel engine is the first of its kind that has been totally designed and developed in the country. Very few countries in the world have the capability to develop and master this technology. The critical core engine, including the special cylinder composite nickel-silicon carbide anti-wear coating and the special aluminium castings, was designed and developed by NAL. VRDE was responsible for engine peripherals such as ignition and fuel systems and ADE, for the flight testing. The Wankel engine, fitted with a propeller, had been earlier comprehensively ground tested as per a rigorous schedule laid down by the certifying agency, in a specially set-up test bed in NAL. The provisional flight clearance for the first indigenous prototype engine was given by the certifying agency, RCMA at a short ceremony held at the launch pad. The engine was cleared for flight after rigorous ground endurance test runs.

The Wankel rotary engine weighs 30 kg and has a power of 55 hp. For air-borne applications, the correct choice of an engine is crucial. The Wankel rotary engine has been preferred to a reciprocating engine because of its higher power to weight ratio in a single rotor category, and also due to its much lower balancing difficulties. Essentially, the Wankel engine comprises a triangular rotor moving in an elliptical path inside a 2-lobed trochoid. Consequently, the Wankel engine is quite difficult to design mechanically, particularly in providing effective seals between the three apices of the rotor and the trochoid inner surface and in providing a durable anti-wear coating on the trochoid inner surface. Around the world, the Wankel engine has had a long and chequered development history on account of these sealing and coating difficulties. However, NAL has been able to arrive at appropriate successful solutions. During the long and challenging development programme at NAL, every single failure encountered was successfully analyzed and solutions provided by the NAL's Failure Analysis Group.

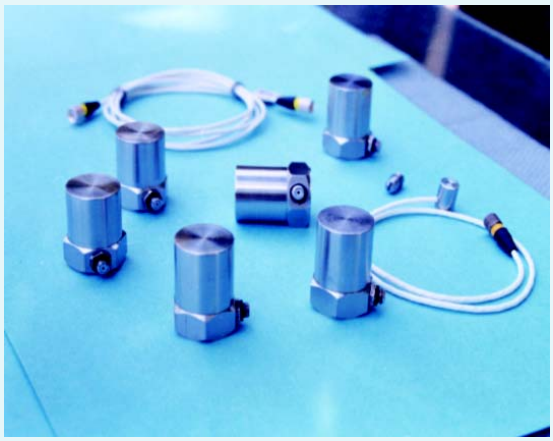
The engine performed very well in the flight, meeting all the requirements of the Air Vehicle. This indigenous engine is expected to replace the imported engine of *NISHANT*. This type of engine can also be used for powering smaller air vehicles and also in automotive, out-board motor and industrial applications.

The event signifies achievements in many categories. It is the first time that a Wankel engine has been developed within the country and a UAV flown with an indigenous engine. It is planned to use this developed technology for future applications for UAVs under development in ADE, Bangalore.

NISHANT is a reconnaissance UAV, which has completed its user trials with the Indian Army and a few of these air vehicles are to be handed over to the Indian Army shortly.

NPL Technology for Piezoelectric Accelerometer — Shear Mode licensed to M/s Powercon Engineers, Ahmedabad

The technology for a piezoelectric accelerometer, developed at National Physical Laboratory (NPL), New Delhi, has been licensed to M/s Powercon Engineers, Ahmedabad. The device has been designed for use in general purpose vibration measurement applications in industrial plants, test laboratories, aviation, automobiles, mines, engines and structures, etc. With a mass of 20± 0.5 g and reference sensitivity of 20 ± 10% pC/g the device enables reliable measurements of vibration in the frequency range 10-8,000 Hz and shocks up to 2000 g. In all stainless steel construction, the accelerometer has a hex base of 16.2 mm and a total height, 21 mm. The output is available through standard 10-32 UNF microdot connector. The accelerometer has a proven performance, comparable to that of most of the imported accelerometers.



Piezoelectric accelerometer-Shear mode developed at NPL

Memoranda of Understanding signed by CEERI

The Central Electronics Engineering Research Institute, (CEERI), Pilani, has signed a number of MoUs with industry and academia, recently. These include:

MoU with Semiconductor Laboratory (SCL), SAS Nagar, Punjab

Under the MoU, CEERI and SCL shall collaborate on the design, development and supply of piezoresistive MEMS pressure sensor chips.

CEERI will design, develop and realize prototype piezoresistive MEMS pressure sensor chips with diffused resistors in polysilicon/single crystal silicon. The sensor will be based on bulk micromachining technology using Si/SoI/SoS/SiC wafers. Detailed analysis, simulation, testing, characterization and optimisation will be carried out by CEERI on the MEMS chips. Prototype testing will be carried out for various pressure ranges in packaged condition. CEERI and SCL engineers will work together for the project, so that the MEMS absolute pressure sensor device meets all the requisite specifications.

CEERI will also design, analyze and fabricate MEMS dies and supply 1000 numbers each (in five ranges, viz. 30, 50, 70, 100 and 300 bar) in coordination with SCL engineers in packaged form on headers. CEERI and SCL shall use the available infrastructure and fabrication facilities for the MEMS pressure sensor chips. Calibration will be carried out after die mounting and wire bonding. Testing shall include temperature studies ranging from –40 to +120°C.

The MoU has the validity for a period of 18 months.

MoU with Jaipur National University

Under the MoU, M. Tech. students from Jaipur National University (JNU) will undergo training for two weeks at the Microelectronics Laboratory, CEERI, during every academic year. The training schedule will be decided by CEERI.

The MoU has the validity for a period of three years.

MoU with University of Delhi

Under the MoU, Delhi University and CEERI will undertake joint sponsored research and consultancy projects within the specified areas of cooperation. The concerned faculty of DU and scientists of CEERI will formulate project proposals. Both DU and CEERI have agreed to exchange staff through deputation on full-time/part-time basis for a limited period. Both institutes have agreed to hold joint workshops/conferences/ training courses in the areas of cooperation. The two institutes will share their facilities to promote academic and research interaction. Research Fellows/Project Assistants/Scientists of CEERI and research students of DU can register for Ph.D. programmes at DU under joint supervision.

MoU with SRM University, Chennai

SRM University and CEERI, Chennai Centre will undertake joint sponsored research projects in the areas of machine vision systems for societal applications, DSP/ Embedded system design and applications, etc. The two institutions have agreed to hold joint workshops/conferences/training courses. They will share their R&D facilities. CEERI Chennai Centre will extend facilities to UG/ PG students (up to eight students per year) of electronics, instrumentation and computer science departments of SRM University. Two staff members or Research Fellows/Research Associates of CEERI, working on approved joint projects at any given time may be registered for Ph. D. programmes at SRM University.

The MoU has the validity for a period of five years.

US-India Workshop on Metrology, Standards and Conformity Assessment and Their Use in Support of Technical Regulations

The National Physical Laboratory (NPL), New Delhi, in collaboration with National Institute of Standards and Technology (NIST), Gaithersburg, Maryland, USA, organized a workshop under the sponsorship of Indo-US Science and Technology Forum (IUSSTF) on 1-4 June 2009. The objectives of the workshop were to (i) familiarize participants with US and Indian systems in the areas of standards, conformity assessment and metrology and their applications to support technical regulations, (ii) examine the role that these system components play in enhancing global trade and spurring innovation and finally, (iii) explore opportunities for future collaboration. A team of 20 Indian delegates comprised not only from NPL but also from five other CSIR laboratories [IIP (Dehra Dun), CBRI (Roorkee), IICT (Hyderabad), CFTRI (Mysore) and SERC (Chennai)] and QCI (New Delhi), NABL (New Delhi), BIS (New Delhi), CII and FICCI. Dr A.K. Bandyopadhyay, Scientist G, and Head of Physico-Mechanical Standards, coordinated the event.

Dr Claire M. Saundry, Director, Office of International Affairs of NIST, welcomed the Indian participants and talked about the genesis of the workshop. She also spoke about NIST in her talk: "US: Promotion of Innovation and Industrial Competitiveness". Dr Michel Cheetham, representative of IUSSTF (USA), presented the history of formation of IUSSTF and its role in promoting R&D in cutting edge technology in US and India. Dr Vikram Kumar, Director, NPL, spoke on "NPLI present and future" and Dr M. O. Garg, Director, IIP, Dehra Dun, "The goal and priorities of IIP". The other speakers on the first day included: Mrs Madhulika Prakash (BIS, New Delhi), Dr A.K. Minocha (CBRI, Roorkee), Dr R. Nageswara Rao (IICT, Hyderabad), Mr Girdhar Jessaram Gyani (QCI, New Delhi), Mr Anil Relia (NABL, New Delhi), Dr M.N. Manjunath (CFTRI, Mysore), Dr K. Ravi Sankar (SERC, Chennai), Mrs Ranjana Khanna (FICCI, Washington), and Mr Ramani R. Iyer (CII, New Delhi). In addition, there were lectures by Dr Lorel Wisnewski of NIST (USA) and Dr M.O. Garg of IIP (India) on "Approaches to Innovation". The day ended with an open forum discussion.

The second day was devoted to "Standards Systems and

Their Approaches to Quality and Accreditation". It started with an overview of Documentary Standards Systems, mainly the "Role of Government in Documentary Standards Systems" and "US/Indian Industries in Documentary Standards". Speakers in the pre-lunch session included: Dr Elise Owens, ANSI; Mrs Madhulika Prakash, BIS, India; Dr Belinda Collins, NIST; Dr Sudarsan Rachuri, NIST and Mr Ramani R. Iyer, CII. The post-lunch session started with the talk on "Laboratory Accreditation-Priorities & Participation in International Programs" by Dr Sally Bruce, National Voluntary Laboratory Accreditation Program (NVLAP), USA and Mr Anil Relia, NABL who talked about "Status of the Accreditation Program in US and India". In their presentation on "Approaches to Quality Assurance", Dr Harry Hertz, Director, Baldrige National Quality Program, NIST, and Mr Girdhar Jessaram Gyani, Secretary General, Quality Council of India, discussed the key issue of quality assurance in both the countries. The last part of the session was devoted to the "Quality Initiatives in Food Safety". Dr Daniel Geffin, FDA, US, talked about the "FDA's regulatory role in ensuring the food safety" while Dr M.N. Manjunath, CFTRI (Mysore), India, talked about the "Food safety and analytical quality control". Participants felt that IUSSTF may be requested to support this activity so that another joint workshop could be organized after two years to critically assess the status of the US and India's standards and conformity assessment.

On the third day, pre-lunch session was dedicated to the laboratory visit. Indian delegates were provided free choice to visit various laboratories of NIST. It was a very fruitful exercise to interact with the experts and get exposed to the latest developments in the field of Nano Technology, Chemical Metrology, Building Materials Standards and Fire Safety Norms, etc. Post-lunch, session started with the presentations on Initiative in the legal metrology. Dr Carol Hockert, NIST, talked about the activities of Weight and Measures Division and Dr R. Mathurbootham, Director, Legal Metrology of India presented the Indian perspective. In the Physical Metrology sector, Dr William Ott of NIST and Dr A.K. Bandyopadhyay of NPLI discussed the progress of Physico Mechanical standards of both the National

This Apple tree genetically transferred from the original famous Apple tree under which Newton made the epoch making discoveries

Group photo of Indian delegates with Drs Claire M. Saundry and Maria Uhle, Office of International Affairs of NIST (USA), under the famous Newton Apple Tree

Metrology Institutes (NMI). Dr Jim Olthoff of NIST and Drs P. Banerjee and V.N. Ojha talked about the country status with regard to Metrology initiative in Electronics and Electrical Engineering. In the last session of the third day, the topic of discussion was the initiative in Materials Science and Engineering. Dr Mike Fasolka of NIST and Dr A.K. Srivastava of NPLI discussed the priorities of research in US and India. The third day ended with a note of mutual cooperation between the participating institutions.

Proceedings of the fourth day focused on "Metrology Initiatives, International Priorities and Industry Needs". The session started with initiative in Structural and Building research, Dr Shyam Sunder of NIST talked about the "Zero Energy Building", followed by Dr A.K. Minocha of CBRI. Thereafter, two parallel sessions were convened – one continued with the lectures on "Building Research" and the other covered the Chemical Metrology. In "Building Research" session, Dr Lorel Wisniewski of NIST and Dr K. Ravishankar of SERC (India) talked about their prospective and priority of research. In the session on Chemical Metrology, Dr Din Bims of US DOE talked about "Renewable and Sustainable Energy Sectors and US initiatives". Dr M.O. Garg, IIP, discussed the Biofuels. Dr P. K. Gupta of NPLI talked about the Indian Priorities in Chemical Metrology. Dr Willie May of NIST spoke on Standard Reference Materials. The last lecture was delivered by Dr G.V. Iyengar, Tufts University, Boston (USA) on "Food safety concerns with reference to capacity development needs". Dr Willie May of NIST summed up the proceeding of the Chemical Metrology.

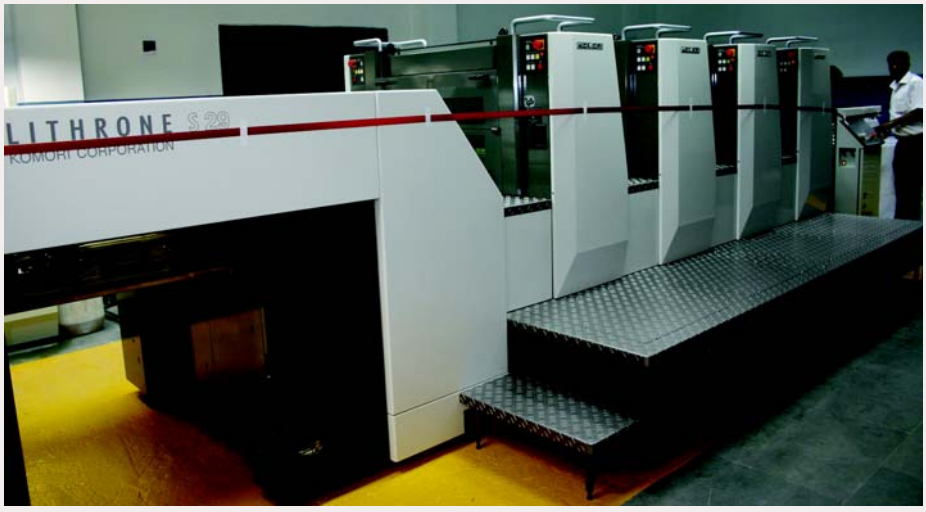
The post lunch session mainly focused on planning for the future collaboration on institutional basis. Members felt that the role of metrology and standards has not been widely discussed and published in public domain. As a

NISCAIR procures 4-colour sheet-fed offset printing machine

Well known for its S&T information products, resources and services, the National Institute of Science Communication and Information Resources (NISCAIR), New Delhi, has a full-fledged state of the Graphic Art & Print Production Division (GAPPD). This division not only meets the graphic art, print production requirements of NISCAIR publications but also undertakes a large number of assignments from various R&D/ S&T organizations/institutions.

Keeping in view the fast pace of technological advancements, GAPPD continuously strives to keep its expertise and infrastructure as up-to-date/modern as possible to deliver high quality print production results.

Recently GAPPD of NISCAIR has procured a 4-colour sheet-fed offset printing machine (LS429 maximum speed of 16000 IPH) from Komori, Japan. The new facility will help improve print quality, make operation easier, shorter make ready to higher production efficiency in a significant manner. It will help in formatting photographs, histological photograph in high quality. Surely this facility will not only help production of high quality publications of NISCAIR/CSIR but also of several other R&D organizations/departments.



result, understanding of the technical regulations always has a gap between the users and the producer. This kind of workshop reduces the burden on the regulated community and leveraging the benefits. The workshop, it was felt, would help delegates from both the countries in identifying potential areas of scientific cooperation under a broad line of metrology, standards and conformity assessments. It was resolved that a matrix would be formulated with the main objective to create a network of scientists, technologists and entrepreneurs who can work together to promote joint R&D projects to foster mutually beneficial innovation.

In the end, Dr Vikram Kumar, Director, NPL, thanked IUSSTF Indian counterpart Dr A. Mitra and his colleagues, for their support to host this workshop. He thanked Drs Claire M. Saundry and Maria Uhle for their contributions, and also all the participants for making the event a great success.

Deciphering Biological Function for Genome Variation

Jagadish Chandra Bose Award Lecture by Prof. Samir K. Brahmachari, Director General, CSIR

I will quote Sir J.C. Bose in whose honour this medal is given; and incidentally, this year also happens to be the 150th anniversary of his talk in the 1927 Indian Science Congress. It is amazing that he talked about the mechanism of life eighty years ahead of the Human Genome Sequencing when he stated, "In opposition to current views, I was convinced that the mechanism of life of the plant is essentially similar to the animal." And it is this understanding that led to the great convergence of general physiology, medicine, agriculture, and psychology. He introduced the concept of spontaneous movements, power of conductivity, and the inherent rhythm in life. If we look back, we see that he talked about the visible signal of death, which we have today named "apoptosis." He even talked about the storage of Solar Energy when he said, " …it may not be such an impractical proposition to devise a chlorophyll apparatus for trapping sunlight." And all of you know, Craig Venter's group is working on creating synthetic life forms with the dream to capture carbon dioxide to convert it into sugar. This is happening now.

J. C. Bose talked about how the 'nervous' impulse of the plants affects the molecular predisposition. He had beautifully described the molecules as, "…a row of standing books. A certain intensity of blow applied, say to the book on the extreme right, causes it to fall to the left, hitting its neighbour and making the other books topple over on succession."

The courage needed to take a contrary stand with respect to the beliefs of those prevalent in 30's must be appreciated. This was possible because of the general rebellion or non-acceptance of western thought and emphasis on novel innovative ideas. I believe that it was Aushutosh Mukherjee who propagated that extensively. And it was this belief with which Prof. Ramachandran, earlier at Madras and subsequently at the Molecular Biophysics Unit, IISc, was able to put forward new ideas; and how Sasisekharan thought of alternative structures of DNA.

In 2005, Thomas Friedman wrote, "In 1492 Christopher Columbus set sail for India, going west. He had the Nina, the Pinta and the Santa Maria. He never did find India, but he called the people he met "Indians" and came home and reported that he had circumnavigated the world and confirmed that the world was indeed round."

And then, 512 years later Tom Friedman came by the Lufthansa flight to India…and discovered a new India. He also realized that "the world was flat! And therein lies a tale of technology and geo-economics that is fundamentally reshaping our lives — much, much more quickly than many people realize. It all

happened while we were sleeping, or rather while we were focused on 9/11, the dot-com bust and Enron — which even prompted some to wonder whether globalization was over. Actually, just the opposite was true, which is why it's time to wake up and prepare ourselves for this flat world, because others already are, and there is no time to waste." This 'flat world' was made possible in the post Internet era, where the human genome sequence made available in the public domain made New Biology completely accessible.

Because of what has happened, thanks to the world-wide web/ Internet, is our ability to place the entire human genome sequence in the public domain. This, I believe, has changed Biology for ever.

Realizing this power, the Human Genome Organization (HUGO) was formed in 1988. In 1989, the Human Genome Project was launched formally. I got elected to HUGO in 1990. India had foreign exchange and resource crunch in the 1990s.

In 1996 when Europe and USA entered the genome sequencing phase, I strongly felt that India must participate. And that brought me from Bangalore to Delhi in 1997.

It was Dr R.A. Mashelkar at CSIR who could see the possibility of genomics being done in India. I came to Delhi with a passion to put India on the Genomics map. So we formed the first Functional Genomics Unit in 1998. We were the first in the world to coin the word "Functional Genomics." Subsequently, people thought that Functional Genomics means that you have to work on model organisms like rat, *Drosophila*, and *C. elegans*.

China established Genome center in 1998 and spent sixty million dollars to do the primary sequencing. We soon realized that with limited finances we could not compete in sequencing. We assumed that the primary data would become available by 2005. So we decided to collect the secondary data on population and patients. At that point of time, nobody thought that single-nucleotide polymorphisms or SNPs would be important.

In 2000 we got the first Working Draft of the Human Genome. In 2002, the world realized that the sequence of one genome would not suffice and that we needed hundreds and hundreds of the variations and representations of the variety across the world. Study of the genetic variation would tell us why we differ.

The HapMap Project, to develop a public resource to find genes associated with human disease and response to drugs had begun. India was asked to present 30 samples for the HapMap Project at a cost of several millions of dollars. We realized that unlike China or Japan, India cannot be represented by a mere 30 samples. So we decided not to participate but to have our own Indian Genome Variation Project starting in 2002. In 2003, HUGO declared the final Human Genome sequencing result in the public domain; two years ahead of time. In 2005, came the first result of HapMap and in 2007, the final draft of HapMap. In 2008, we announced the Indian Genome Variation data.

The Human Genome Sequence is the outcome of the imagination and dream of a few scientists. When technology did not exist, they imagined, created a demand and developed the technologies. Those who started, did not close the chapters. There came new scientists, new ideas and new project leaders, who finally completed the project and finished the complete sequencing. Today, we have a near-final draft of 3.25 billion nucleotide sequences of the human genome. The challenge of the new millennium is to unravel the function and the meaning of the sequences. It is an encrypted data set, which has to be deciphered.

What we have discovered today when we have three completely sequenced human genomes: that of Craig Venter, James Watson and Huming Yang (!) or YH (Han genome) of China is contrary to the belief that was held in the beginning. We have discovered that we differ substantially from one another.

For the bacteria and the prokaryotes, genetic information comes in a continuous fashion without any repetitive sequences. In eukaryotic or higher organisms, including humans, the information content is larger and is interrupted with sequences —whose function we do not understand. In the beginning of the human genome project, nobody focused on that. The focus was only on the coding sequence. The hope was to identify all the hundred thousand genes. The hope was to annotate all these genes and to identify disease genes. It all looked so simple!

In 1992 Bill Haseltine formed the Genomic Science Inc. At that time it was realized that the proteins could be used for various purposes. These could be used as therapeutic agents or even as reagents, etc. It turned out that various proteins could be used for research activities such as to find drug targets. But there were complexities involved and many surprises too.

By 2008 most of the coding genes had been mapped. The single function of most of the annotated genes number about 24,000. The interesting discovery was that the same gene can produce multiple proteins. It was discovered that a large number of splice variants offer protein diversity. Further diversity is offered by large number of protein post-transcriptional modifications making system analysis at protein level much more complex. This has led to 46,000 proteins being identified. In each of these proteins there are amino acid changes. This creates more diversity and thereby creates enormous complexities. It eventually leads to about half a million variations of proteins between you and I. So your proteins and mine are not similar! This was absolutely unexpected and contrary to what was the thought when genome studies began. Additionally, gene association studies show that disease-loci are mapping into regions of unknown function. Many whole genome associations for complex diseases map disease loci to non-coding regions !! The most unexpected discovery is that there are short RNA sequences which are transcribed but whose function escaped our understanding. These are called miRNA. These are novel functional noncoding RNA classes – miRNAs.

I am sure that there are many more discoveries awaiting us. I am equally sure that the next decade will see the emergence of technologies that will allow us to sequence a human genome for just over a thousand dollars. From three hundred million dollars for the first genome the expenses will come down to just a thousand dollars! This is the future direction. Every possible animal, insect genome sequences will be available. Whole genome expression profile of all possible tissues under various developmental conditions will be available. Present approaches of disease specific association studies will be obsolete.

By June next year, the first step in this direction will already have been taken. It will be possible to sequence a genome for ten thousand dollars by June 2010. It will be possible to sequence every possible animal or insect. Every one of us can get our genome sequence done. Whole genome expression profile will be done and the present method of discovery will change completely. Towards this the Archon Genomics X-Prize has been announced a ten million dollar award for whoever can do sequencing at 98 percent accuracy; 100 human genes in 10 days at ten thousand dollars per genome sequence.

What is interesting is that Indians from India are not participating in this competition; whereas a Scientist of Indian origin, sitting abroad in England, is a leader in this Project. So, are we not in a position to take up challenges? In this context I must add that when we tried to recruit people in 1998, there was no publication in the world, on genome studies, that included an Indian post-doc student. We could not get (trained) people. So, the entire process had to be built up *ab initio*. It was like putting together the *Lagaan* team for the Indian genome project.

I got an actual insight of the X Prize competition when the galaxy of scientists in the committee inducted me in the Advisory Board and into this process of discovery. This competition is changing technology. Can we use this trick to our advantage?

I think we can. We asked, "What do you think people will do if sequencing becomes possible at the cost of only one thousand dollars?" With the technology push and the demand for ideas; the entire situation is exploding! I believe we should be able to create some of this new knowledge. Everybody in the world thinks differently; we should be able to harness this difference to our advantage. We have adopted this approach for our Open Source Drug Discovery Project.

Let us take another area where this approach has great potential. Already we have genetic information about a thousand bacteria. We should be able to design new bacteria. This is the synthetic biology approach. I am very glad to say that we have not fallen behind in this field. In fact, we have invested in what is the world's second project on synthetic biology. The first project is headed by Jay Keasling of the University of

Berkeley. The second one is the CSIR-Berkeley Initiative on synthetic biology of cancer drugs. It has been initiated only recently.

At this point, I must emphasize that biology of higher organisms is to be understood very differently from that of the lower organisms. It has to be done in a holistic fashion and there has to be integration of the sciences. We cannot just create a knock-out human. We have to use the naturally aborted foetus to figure out why these genes are important. It is interesting to see in organisms with complex nervous systems that neither gene number, neuron number or cell size correlate, in any meaningful way, with respect to the measure of structural and behavioral complexity.

The present computational methods will be all obsolete for the database I have in mind. Yet, imagine a million people sequenced; a hundred thousand phenotypes; two thousand relational database and having 60 million variation in the other direction—this is the kind of database that crystallographers, astrophysicists or even monsoon predictors cannot have for cluster-analysis and co-relation etc. So there is a great opportunity of having a new generation of database; and a new architectural structure. It is with this in mind that the CSIR-IISc Centre for Neurosciences has been established. Of course it will take time. Understanding the complexities of the regulatory network and how variations of the genome cause disease; understanding the complexities of the cellular interactions; understanding the complexities of behaviour; and eventually, understanding the molecular basis of mind—I believe it will be a hundred years by the time we reach the last bit.

I will show you areas where we had to be different when it came to our dream of putting India on the genomic map. The dream was born at the Molecular Biophysics Unit (IISc) in 1987, much before I came to Delhi. The first Genome analysis workshop was conducted even before HUGO was formed. I still recall Dr Vijayan coming up and asking me if genome has anything to do with structure and function." I said, "Yes."

The 13th Human Genome Meeting was held in September 2008, at Hyderabad. This was the first time that HGM had come to India and I was chairing. Nature Publishing Group, whose publications include *Nature*, *Nature Genetics*, and *Nature Review Genetics*, sponsored the poster competition at HGM2008. There were five Prizes to be given to the best of the six hundred presentations that took place. Of these six hundred, we had two hundred papers from 47 different countries. Four hundred were from India. One prize went to Genome Institute, Singapore; another went to Institut Pasteur, France, and the other three came to India, to the CSIR laboratory called Institute of Genomics and Integrative Biology. Incidentally, in none of these three papers was I the co-author. I had come to Delhi for this purpose…and I was proud that my job was over!

Coming back to the HapMap project. Indian data was missing when the HapMap was done. This was, of course a deliberate choice because we did not want to be a part of the extravagant expenses. We wanted to do it differently.

We had realized that India is far more diverse than most of the other countries in the world. A mere 30 samples couldn't represent it neither statistically nor culturally. We had a linguistic map of India and in a truly co-coordinated national network project we generated genetic information on over 4000 genetic markers from over 1000 biomedically important and pharmacogenetically relevant genes in reference populations. We developed a genetic map of the Indian population; the first nation to have a genetic map of its diverse people.

The Chinese and Japanese HapMap goes well with it because the Indian populations bridge the Caucasians and Oriental Asian HapMap populations. Additionally, there are populations which are unique to India mostly derived from Austro-Asiatic and Dravidian speaking populations. Before we began the work, we codified everything so that nobody could question our findings if we discovered anything unusual.

You may ask, "What is the achievement of this paper with 158 authors and 24 PIs? What is the outcome of this work?" Simply put, without going into the complexities, it shows that if 'this' is the Japanese and Chinese HapMap data, and 'this' is the African and 'this' is the Caucasian; India (including the African population that India has) is spread across. India actually has a diversity that covers the entire humanity. It is fascinating!

This was the first time that data

on the genetic landscape of India was published. India became the first country to carry out such extensive work. I understand that Europe and US have only initiated it now.

Our studies have revealed many other facts. We found that people belonging only to a small region of India are naturally protected. Rest of India is HIV-susceptible because we do not have the natural or genetic protection against HIV-AIDS. Malaria is another example. There is a genetic risk of getting malaria mostly mapping to the eastern region of India. Therefore, one can vaccinate only 200 million people and take care of them.

Salbutamol is a commonly prescribed medicine for asthma. Variants in the ADRB2 gene can result in varying responses of the receptor to the drug. So good responders can be treated with this drug and for poor responders it is better to give other drugs. Our study provided data on this.

But the genome is only a static representation of the metabolic and regulatory capability of a cell whereas the phenotype is the dynamic, current state of the cell. So one should not make the mistake of assuming that the genetic makeup is the only information we have.

I think 2008 was a landmark for Indian science. There are five most important things in the history of Indian science that happened last year. Other than IGVdb, DST's INSPIRE is a huge project; the large number of S&T institutions that are being built this year; and the *Chandrayaan 1*, and the 1-2-3. These provide a clear demonstration that the apartheid of the past 34 years is over. The Indian Genome Variation is an example of how Indians can work together even in Life Sciences.

It was in 2008, that Sydney Brenner, the greatest living Molecular Biologist on Earth at this point of time, and one of the greatest proponents of the models system, said, "I also believe that we can now do a proper study of man, instead of (but certainly in addition to) mice and flies. Existing technologies now allow us to ask cogent questions about ourselves. I think this is the challenge for the future." (*Nature Reviews Molecular Cell Biology*, January 2008). It is interesting that we thought of it in 1998 while establishing Functional Genomics Unit at IGIB (earlier CBT) of CSIR, Delhi.

But I must caution that after reading Sydney Brenner in 2008, if somebody wants to take the decision in India to work on humans; today we are already ten years too late. To succeed, somebody has to take the risk early. I know that universities, even the prestigious Delhi University, have very limited facilities. To lead, we need to take strategic decisions. We have some advantages that the others do not have. For example, the large number of families with a large number of children per family, which China does not have. The failure of family planning is actually a boon for genetic studies and we should take advantage of it.

I want to show you the possibilities of looking at fundamental discoveries. Conservation and variation sustain Biological processes. In many ways you can create variation and eventually if you look at enzyme activity you will find that quantity of protein produced, activity of the protein, stability of the protein, interaction of the protein and regulation of the protein are the key factors that decide life processes. The conserved coding region determines the protein structure and function. Factors affecting genotype at the protein level bring change in activity, quantity and function. The time factor is also important. If the protein is not produced at the right time then one might have the disease. Of course, if the protein is produced in the wrong location, then too the disease may occur.

So how does genomic variation manifest in the above-mentioned changes? How do we study that? One can do high throughput cell biology, etc. Sydney Brenner, at his recent talk at IISc, put it very beautifully when he said that Biology for many today is, "… low-input of the brain, high-throughput, with zero output." We decided to do it the other way…with high input of the brain, moderate throughput and we expect a little higher output. That's exactly what we are doing.

Biology can be simplified as the interaction of complementary molecules. Entire Biology can be simplified as interactions of complementary charge and shape.

But a protein does not know it is interacting with DNA nor does it know it is interacting with another protein. An inert crystal cannot communicate. It just follows the laws of physics and the laws of chemistry. Similarly, there is no one-to-one correlation between the genetic variations to the disease for

complex disorders.

This is the first time that we drew a map and showed that this is very complex interaction. You can have a protein sequence variation or a protein structure variation. You can have a situation where the amino acid sequence does not change but there is variation in post-translational modification. There may be a problem with protein-folding. Or even a problem with protein structure. Protein activity may change. Many factors affect disease phenotype at the Protein level. For example:

- Change in Activity/Function of Protein
- Change in Quantity of Protein
- Change in Timing of Protein Production
- Change in Location of Protein Production

There may be more number of copies of the same gene, something that you have and which I do not have. An example is the alcohol dehydrogenase gene—whereby the ability to consume and metabolize alcohol varies from individual to individual.

We looked at the variation across the entire genome from the information which is available in the public domain. For example, with just two changes in the amino acids, you can change the entire receptor function.

Imagine you have these two changed amino acids and you discover that all those billion people actually have a different receptor. In the Human Genome out of the 39,396 genes there are: Protein Coding Genes: 21,785 (2,68,026 protein coding exons); Splice Variants: 46,705 proteins. Human Genome variation records 14.7 million SVSNPs of which coding regions have Synonymous SNPs: 61,367; Non-synonymous SNPs: 89,214. There are 53738 SNPs typed in 22 Indian populations. Does this mean that across different populations in India, people have different amino acids in the proteins? The answer is, Yes. This was not known earlier because nobody had done this study earlier.

I will give you another example. Here is the beta 2-adrenergic receptor or β2AR. 46th position SNP has been found to be significantly associated with bronchodilation in Indian Population. Variants in the β2AR gene can result in varying responses of the receptor to the drug. If both your chromosomes code for arginine in this gene, then you are a poor responder. And if both your chromosomes code for glycine there is a 73% chance you will be good responder to the salbutamol drug. Thus, responder status to salbutamol treatment and genotype at nucleotide position 46 in β2AR of asthmatic patients are significantly associated in the Indian population.

Synonymous SNPs do not produce altered coding sequences and therefore are not expected to change the function of the protein in which they occur. A silent change can actually change the substrate specificity and thereby the fundamentals. For example, a synonymous SNP in multidrug resistance 1 (MDR1) gene, part of a haplotype previously linked to altered function of the MDR1 gene product P-gp, nonetheless results in P-gp with altered drug and inhibitor inhibition. It is proposed that the presence of a rare codon, marked by the synonymous polymorphism, affects the timing of co-translational folding and insertion of P-gp into the membrane, thereby altering the structure of substrate and inhibitor interaction sites.

Functional polymorphisms with variable allele frequencies in population can destroy a Post-translational Modification Site and can create a new Post-translational Modification Site.

The question is: Without doing all this sequencing can I find where the variation will cause disease? My student worked on it and demonstrated that for monogenic disease, a mutation in highly conserved regions causes the disease. A large number of human genes—about ten thousand seven hundred and fifty seven genes were checked with one lakh nineteen thousand protein coding exons.

Highly conserved and invariant exons (EIS > 80) harbor higher percentage of disease associated variants, while variable exons (EIS <70) harbor higher percentage of benign SNPs. One can sequence the highly conserved exons and thereby reduce the cost substantially.

All over the world people are worrying about individualized risk of getting diabetes (or not getting diabetes) and that affects an individual's decision to take or not to take sweets or cheese and other high fat products in their diet. Nearly 80 million dollars have been spent on this experiment—much of it was funded by the Wellcome Trust. This level of funding is not available to entire Departments of the GOI. Not even to the Department of Biotechnology to

fund all their activities of Genomic research!

The idea is: Can we now use a comparative approach and find out what is important? Then there is the new discovery about how small RNA can control and silence DNA and thereby affect protein quantity. It is like a whistle that causes a process to 'hold on'; while another whistle causes it to stop! But it does not stop the transcriptional machinery. We were the first to show that miRNA is involved in host-pathogen interactions such as in HIV; both computationally and in eventual experiments.

These miRNA sequences are highly conserved in evolution. It would not be so, unless these have a very important function. miRNAs are not directly involved in protein synthesis. These control gene expression by interacting with the mRNA molecules. So, they do not code for specific proteins, but are important in gene expression. We built a simple model. If the transcript is produced and the intron is spliced out to make miRNA; and the spliced product is the miRNA; then when this protein is produced, simultaneously miRNA can control and shut off others. So you want to have one window open and the other window, closed. That means before I start one set of protein function I must shut off the rest of the protein's function and thereby I go with a single signal. This is like a new Jacob and Monad model trying to say that here is a new regulatory approach—a non-protein one.

When the gene expression goes up and the first gene is expressed, it carries some introns with miRNA. This miRNA can go and bind to all the target transcripts and thereby block their translation. As the same gene expression goes down, the process gets reversed. Therefore, for all the target genes; although transcription has taken place; translation did not take place. When we ran through the whole genome and tried to figure out miRNA—where they occur—we discovered that they are critical regulators of crucial biological processes.

So, we built a model for action of Intronic microRNAs in Oncogenesis with tumour suppressor gene making the tumour suppressor protein. The protein can come and block both the onco genes. However the lock is not so tight, some little transcription can take place…thereby the oncogene process will go on. Therefore the intronic miRNA can go and block the oncogene 1 and 2 transcripts. It is thus a double lock. Even if there is a leaky transcription, the same process applies–the protein whose job was to protect against transcription; but by chance, due to variation, if there is a little transcription, then the intronic part of the miRNA will go and inhibit translation. This is the hypothesis.

The question is, will it work out true? So we need to go through the whole genome; study many transcripts, and do huge supercomputing analyses before we do any experiments. Eventually we find out that one protein coding gene which fulfills all the criteria that was fitting the model. Now we open the box and ask "Is it true?" and it just comes out to be "hsa-mir-26". We find that wherever oncogenes are…wherever cancer strikes …all these protein expressions go up. Therefore this is the one that is critically controlled. So, without doing an experiment we are able to get the data. This was the first time that we found evidence by exclusively basing on the data taken from the literature. We built up the whole process. Today we have all the gene expression data with all protein profile data. We can build up hypothesis, execute and determine exclusively depending on the data taken from the literature. All this came out of novel thinking.

For example, we can actually demonstrate how MCM-7 and the CIM can together control the whole regulatory circuit. In the process one can think of a complete circuitry where feedback loop is taking place and thereby you can see the protein getting produced. The protein producing miRNA goes back and because this is important for that; we can actually build (based on RNA) a circuitry. In this, the transcription factor is a new model on-off switch and the clean-away switch is micro RNA. We assigned a new function to microRNA: for tunable switch rather than a transcription factor.

What is exciting is that if it goes and targets one transcription factor gene, then it can shut off all the processes. So it is very fundamental. During cell division – when one gene has to be up-regulated and all the other genes have to be shut down, a cascade of things happens. There is a model by which we can do this. Synchronized gene expression with source and regulator is a possibility.

So you can see, holistic view is what makes the difference. I'll show

quickly a similar holistic view involving mathematical modeling, using which, we quickly discovered, using less than quarter million dollars, two genes for which twenty million dollars was spent by the MIT group. This was a twenty million dollar experiment in which they found non-coding sequence – for which they didn't know the function. Nobody knew. We used this high throughput data, the available biological information, to do moderate throughput experiment.

We took a decision to take all chromosomal locations in which geneticists have found a linkage and put them in a pathway. From the pathway, we isolated the signal transduction pathway. Then we built a mathematical model using Boolean algebra. Based on the Boolean algebra stipulations, we looked at and checked the parameters. Of course calcium was a surprise. When we looked at calcium, we found one calcium/K^+ channel MHC I in chromosome 22 region. Then we studied hundreds of patients *vs* non-patients. We found in 44 families association of a specific haplotype with high statistical significance. We found the haplotype. Based on the haplotype, and based on the exon predictions, we started sequencing the regions we expected to yield results. When we sequenced, we started seeing the protein mutations. Then we measured the mutations, and went back to see where those mutations were falling.

And this is how you simplify the model. You no longer look at a complex disease as being complex but convert the entire thing into simpler steps. We have been looking for Schizophrenia and Bipolar disorder genes and pathways through analogy. Voltage gradient is nothing but ion transport; insulation is myelination; conductance is axon synapses and fuse is nothing but calcium-mediated apoptosis. Then we go through the literature and pick up all these genes and build up all literature that just talks about interaction of any of these genes with any other gene. Now from relational database, you start building networks and use calcium as a node. You now start seeing new networks. Then you put all this together. Then you start predicting how calcium-mediated and various apoptosis process and synaptic plasticity, is what could be responsible. You pick up those genes and sequence them. My young colleague Dr Abhay Sharma, eventually found a gene and mutation, which is associated with a very large number of Schizophrenia and Bipolar disorders. What we showed is, at the end, only the tip, of the tip of the iceberg. But it proved that one could make discoveries with far less experimental expenditure and by doing things differently.

The human system has to be looked at in a completely new way. It is the most efficient bioreactor. It only uses 86 calories per hour. It is a chemical engineer's paradise. Therefore the whole perception has to be different. We have to look at disease as nothing but an efficient bioreactor which has gone wrong in some of the functions. We must not now look at a gene or protein in isolation. We must look at it holistically. This is the way of the future.

Two scientists got the Nobel Prize after spending their entire lives studying two proteins to teach us about haemoglobinopathy, so that we understand it in molecular terms. There are 50,000 proteins. So we need 50,000 scientists like Kendrew and Perutz to understand the entire genome. Is this possible? We therefore have to innovate! We have to think differently. We must look at Kendrew's and Perutz's work and ask the questions: "What is the Unfinished Agenda?" What is it that their work did not tell us? Is everything known about the disease? We must ask these fundamental questions about how alpha and beta globin (genes) produce the exact amount although they are located on two different chromosomes. This is a beautiful project. Another project could ask: Can we activate the fetal globin gene (perhaps only a small amount) for thalassemia patient—that is what innovation in translational research is!

In 1994, I went to Kolkata to get samples from thalassemia patients; looking for unusual mutation. I told myself these children would not have been born that way had we made some PCR products for them. I remember the projects of the Technology Development Mission: we developed all those thalessemia detection primers for Bangalore Genei. I went back to Kolkata five years later, I saw a photograph of those 16 children who were born to thalassemia carrier parents and I thought this was better than my 16 papers on nucleic acid in JBC and JMB. The happiness of those sixteen mothers who had those children!

Can we not solve these

problems if everybody puts their brains together? We have Open Source resources. We have taken this initiative as CSIR-led initiative for affordable health for the developing world. Our first project involves Tuberculosis drug discovery as an Open Source initiative. Those who are interested may go to www.osdd.net for more details.

I have pursued all my science with curiosity. I used to think, after becoming FNA in 1995, that at age 62 I'll retire from the Indian Institute of Science: and then, five more years of science—from 1995 to 2019; that is 24 years. But Dr Mashelkar called me before that. You know, scientific discoveries and scientific knowledge have been achieved only by those who have gone in pursuit of it without any practical purpose whatsoever, as stated by Max Planck.

Today, I understand that it is important that some of the science must get translated and you should start worrying about it when you cross 45. I must say that I learnt at MBU to believe that world class science can be done in India. When I was young I remember seeing Prof. Vijayan taking the challenge of doing Protein Crystallography in this country. I salute the courage he demonstrated. I remember as a post-doc whenever I wrote HH1 and HH2 on the X-ray machine, we used to jokingly refer to these as High Hope 1 and High Hope 2 saying that one day we will solve the protein structure in India. The fact remains that it is an achievement India can be proud of.

In summation, I quote, not a Westerner but our own Dhirubhai Ambani, *"Our dreams have to be bigger. Our ambitions higher. Our commitment deeper. And our efforts greater."* This is also my dream for CSIR and for India.

IIP Golden Jubilee Year–Curtain Raiser

The Indian Institute of Petroleum (IIP), Dehra Dun, began its Golden Jubilee Year celebrations from 27 April 2009. The institute was established by the act of the Parliament in the year 1960. It started functioning from its office in Central Road Research Institute, New Delhi. Shifted to a *kothi* in Dalanwala, finally moving to its newly constructed campus in 1962.

The Chief Guest at the 'Golden Jubilee Curtain Raiser' function was Padma Vibhushan Prof. M. M. Sharma, ex- Director of University Department of Chemical Technology, Mumbai.

Speaking on the occasion, Prof. Sharma said that the need of the hour is to use all streams of the refineries to value addition. We should not go for the technologies which are based on irregular supply of raw material. He informed that many bio-diesel plants in Germany are at the verge of closer because traditional diesel from the fossil is the cheapest. In India, we have very large population living below the poverty line and so we should look for technologies which will help the masses, he concluded.

Prof. Sharma also laid the foundation stone of the new state of the art laboratory, the Golden Jubilee Laboratory.

Earlier, Dr M. O. Garg, Director, IIP, welcomed the distinguished guests and felicitated ex-employees of IIP. An ex-employee of IIP, Dr K. S. Jauhri spoke on 'Fifty years of IIP's down the memory lane'. Dr Garg highlighted the events planned during the Golden Jubilee Year. He informed that IIP is planning to host six symposia/seminars. A book on *Glorious Fifty Years of IIP* will be published. Dr Arunabha Datta gave the introduction of the Chief Guest.

The programme was compered by Dr S. K. Sharma and Hindi Officer Dr D. C. Chamola recited a poem on the Golden Jubilee of the institute.

Prof. M. M. Sharma releasing the Golden Jubilee publication *Innovation & Technology of IIP*. Others seen (*from left*) are: Dr A. Datta, Dr M. O. Garg and Dr K. S. Jauhri

Silver Jubilee Celebrations at IHBT

The Institute of Himalayan Bioresource Technology (IHBT), Palampur, celebrated its 25th year of establishment on 15 June 2009, to commemorate the R&D contributions of the institute in promoting economy for industrial and societal benefits.

Addressing the distinguished gathering through teleconferencing mode, Shri Prithviraj Chavan, Minister for Science & Technology and Vice President, CSIR, stressed the importance of the fragile ecosystems of the Himalaya, and related issues like climate change, conservation of ecosystem and biodiversity, access to the biodiversity, management of natural resources, joint forestry management, tribal rights *vis-à-vis* equity sharing of resources. He opined that the endeavours of IHBT in development of biofertilizers, bio-pesticides, new cropping systems, and conservation of plant biodiversity will play significant role in sustainable utilization of bioresources and value addition to the livelihood options in the fragile ecosystem.

Prof. Samir K. Brahmachari, Director General, CSIR, also addressing through teleconferencing mode on the occasion, revealed that CSIR is going to establish a High Altitude Research Centre. The Centre will be involved in societal programmes, climate research and installation of permanent weather monitoring system, bioresource conservation for high altitude plants, bioprospection of novel enzymes working at low temperature, and creating a science museum, perfafrost facilities and analytical facilities for quality evaluation of produce and products in the region.

Prof. V.L. Chopra, former Member, Planning Commission, Government of India, in his presidential address, was highly appreciative of the contributions of the institute. He mentioned that IHBT has made significant progress from an institute dealing with crop husbandry of tea to one with international recognition, in a short span of 25 years. He emphasized that there is need to formulate strategy for management and regeneration, of natural and bioresources, and in meeting the expectations of the livelihood options. He opined that there is need to strategically aligne the goals of IHBT for generating high quality knowledge on one hand and its flow into developmental activities to sustainable management of bioresources and restoration of our ecosystems in the larger interest of the region, and nation as a whole, on the other.

Prof. Jai Rup Singh, Vice Chancellor, Central University, Bhatinda, Punjab, who was the Chief Guest, appreciated the world class infrastructure and manpower at IHBT, commited to molecular genetics, cytology, natural products, floriculture, tea and crops of commercial value. He hoped that the Central University, Punjab, will have MoU with IHBT for R&D and academic collaboration.

Presenting the Annual Report of the institute, the Director of IHBT, Dr P.S. Ahuja highlighted the stupendous 25 years journey from CSIR Complex to IHBT as one of the finest S&T outfits in Himalaya. With its world class infrastructure combined with highly competent manpower, the institute is focused at the cutting edge areas of Biotechnology, Natural Product Research, Nanobiology, Climate Change and Adaptations, Proteomics, Genomics & Metobolomics, and Biodiversity Conservation. Significantly, the institute is attracting strategic alliances and collaborations worldwide. Historically the institute is responsible for revival of the dilapidated tea industry in the region, generation of data for fixing CODEX norms and identification of core germplasm collections through molecular characterization for tea. Technical information on aroma profile and quality parameters provided to the H.P. State Government has helped in the award of Geographical Indications for Kangra tea.

The survey, inventorization, mapping and research on high altitude medicinal and aromatic plants have laid the basis for strategic bioprospection of microbes, enzymes, molecules and genes.

Pioneering work carried out in Plant Virology has helped in the establishment of an accredited laboratory for detection of viral infection in economically important plants. Highly sensitive viral diagnostic kits of commonly prevalent viruses have been

Shri Prithviraj Chavan, Minister for S& T and Vice President, CSIR, addressing the distinguished gathering during the Silver Jubilee Celebrations of IHBT through teleconferencing mode (*above*).

Seen on the dais during the celebration function *(above left) (from left)* are: Shri Anil Sood, Prof. V.L. Chopra, Dr Ram A. Vishwakarma, Prof. Jai Rup Singh, Prof. Anupam Varma, and Dr P.S. Ahuja

A view of the audience *(below)*

developed which enable detection of viruses at a very early stage and are extremely useful for quarantines.

The institute is also a Centre of Excellence in bamboo and over 700 acre has been brought under bamboo in different parts of the country with the planting material supplied by the institute. A highly significant achievement of the institute has been development of large-scale planting material of *Gingko bioloba* which will be utilized by the country for producing gingko-based products.

IHBT has developed cultural practices and generated quality planting material for several ornamental, medicinal, aromatic, spice (saffron) and plantation crops of commercial value. New cultivars have been released for the benefit of farmers and industry. The institute has filed patents and transferred several technologies to the industry which include production of steviosides, aescein, vinyl guaiacol, natural colours and dyes, novel RNA isolation kit, mini laminar flow, mini distillation unit, tea withering machine, tea concentrate and tea wines. The institute has also transferred technical know-how for setting-up of tissue culture units to private industry and government institutes. Two significant initiatives of the CSIR in positioning the Technology & Innovation Management Centre (TIM) and Technopreneur Promotion program (TePP) at IHBT have provided regional entrepreneurs and innovators to articulate their regional needs around technological priorities and to promote innovations at the grassroots level through governmental support. The institute has been awarded ISO 9001:2000 for quality management and NABL accreditation for pesticide residue analysis, microbial load determination and for chemical analysis of aromatics and BCIL accreditation for Virus indexing of tissue culture plants and for DNA fingerprinting.

Prof. Anupam Varma, former Vice-President INSA, opined that IHBT has done remarkable efforts to revive the century old dilapidated tea industry in Himachal Pradesh. He mentioned that development of biofertilizers; bio-pesticides will pave way to organic tea production. Development of diagnostic-kits for viral management is another significant achievement of this institute.

Dr Ram A. Vishwakarma, Director, I.I.I.M., Jammu, delivered the Siliver Jubilee Foundation Day Lecture on 'Post translational Modifications and New Opportunities for Drug Discovery' in which, he mentioned that chemical biology offers tremendous opportunities for new generation of drugs and therapeutic approaches. He highlighted importance of protein kinases as future drug targets in treating deadly diseases like cancer.

The Annual Report of IHBT in Hindi and English, separately, and a technical brochure on chrysanthemum in Hindi were released by the Chief Guest, Prof. J.R. Singh. The celebration ended with presentation of the vote of thanks.

Earth Day Celebrations at NAL & C-MMACS and IIP

A dais view of Earth Day Celebrations at NAL

The National Aerospace Laboratories (NAL), and Centre for Mathematical Modelling And Computer Simulation, (C-MMACS), Bangalore, jointly celebrated the 39th anniversary of the Earth Day (22 April 2009) by inviting school students and arranging talks by experts. About 300 students from Kendriya Vidyalaya, NAL, nearby central schools and children of NAL and C-MMACS staff visited NAL and were introduced to NAL, watched the *SARAS* flight video and the excellent video of C-MMACS. Dr Goswami of C-MMACS welcomed the children and announced the topics of three different categories for the painting competition held on the occasion, i.e. for Category 1 (Class V and below) : 'Environment Around You'; Category 2 (Class VI-IX): 'The Global Warming', and Category 3 (Class X-XII): "Violent Earth".

Children participating in the painting competition held at NAL during Earth Day Celebrations

The afternoon session had talks by Dr E.V.S. Prakasa Rao, Scientist -in-charge, CIMAP Regional centre, Bangalore; Dr Vinod Gaur, C-MMACS, Bangalore and Dr K.S. Rajam, Head, SED, NAL, Bangalore. Dr Rao's talk enthralled the children with the humorous cartoons loaded with message about the environment, degradation time for various materials, striking the right chord in the children's mind about saving our Earth from pollution. He began his talk with an introduction about the genesis of Earth Day and the need to celebrate it. Definition of 'Biovillage' indicates concern for all living organisms in the village, including human beings as well as natural resources such as soil, land, water and biodiversity. Dr Gaur took the children on top of the world with his excellent slides of the universe in his talk entitled 'The blue planet'. Dr Gaur elaborated the effect of global warming and how we can prevent it. Dr Rajam's talk on solar energy dealt with the advantages of using solar energy. It enticed the children to save energy as "A watt saved is a watt generated' with a little technical aspects thrown in for the brighter ones. The application of the NALSUN technology developed at NAL was also highlighted.

Dr A.R. Upadhya, Director, NAL, spoke about how the responsibility of future clean environment rested on the children's shoulders. He urged them to become leaders to protect the environment and propagate the message to keep the environment clean especially the staff quarters. Dr Upadhya mentioned that each one of us must not be mere spectator but contribute our mite to a clean environment. The programme ended with vote of thanks proposed by Mrs Gomathy Sankaran, Group Head, HRD.

The occasion was also celebrated at the Indian Institute of Petroleum (IIP), Dehra Dun, in similar lines. Here also, over 300 students from various schools, e.g. St. Joseph Academy, Convent of Jesus & Marry, SGRR Nehrugram, Kendriya Vidyalaya IIP, Marshall's, Bright Lands, took part in the painting competition held in three categories as in the case of NAL & C-MMACS.

In the second part of the function, the Chief Guest Dr Rai Avdhesh Kumar Srivastava, Ex. Chairman, Commission for Scientific and Technical Terminology, Ministry of Human Resource Development, gave a talk in Hindi *"Jaroori Hai Prithvi Ko Bachane Ki Muhim'*. (There is a need for revolution to save the earth), pointing out that the places which were desert once are experiencing snow and the places which were covered with snow once are seeing the melting of glaciers and are deprived of snow.

Dr M. O. Garg, Director IIP, in his introductory remarks said that we have not inherited this earth from our forefathers but have borrowed it for our children from them and we should look after it well and should hand over it to our children safely.

Dr Dinesh Chamola, Sr. Hindi Officer, compered and Dr S. K. Sharma, Chairman of the Celebration Committee, proposed the vote of thanks.

Dr Prantik Mandal and Dr V.M. Tiwari get National Mineral Award

Dr Prantik Mandal, Scientist EII and Dr V.M. Tiwari, Scientist E.I of the National Geophysical Research Institute (NGRI), Hyderabad, have been awarded the National Mineral Award for the year 2007.

Dr Prantik Mandal has received this award in the field of Disaster Management. In the field of seismic hazard assessment of Kachchh, Gujarat, his studies provided the first estimates of sediment thickness, ground motion attenuation relation and the site amplification maps that will be extremely useful for the earthquake disaster mitigation in this region. His work in the field of triggered earthquakes in Koyna-Warna region has led to the understanding of earthquake nucleation phenomena, which provides a satisfactory explanation for the continued occurrences of reservoir-triggered earthquakes in the region for last 47 years. These studies resulted in a US patent for a method of short-term forecasting of moderate size reservoir-triggered earth-quakes.

Dr Mandal is a recipient of the Young Scientist Award by ISCA and CSIR in the year 1995 and 2000, respectively and the prestigious Raman Fellowship in 2004 from CSIR. He has so far published 53 research papers in SCI journals and presented 72 papers in national and

international conferences.

Dr V.M. Tiwari received the National Mineral Award-2007 (Geophysics) for his significant scientific contributions to the study of structure, behaviour and geodynamics of different parts of the Indian lithosphere through gravity and magnetic studies.

Dr Tiwari has received Young Scientist Award from Indian National Science Academy, CSIR, Council of Science and Technology UP, Best Thesis Award from the Association of Exploration Geophysicists and the Krishnan Medal from the Indian Geophysical Union. He has published 25 peer reviewed research papers and submitted 15 technical reports to industry and sponsoring agencies.

Dr Tiwari's present area of research is Lithospheric Configuration and Deformation of Converging Plate Margins and Water Mass Balance from new generation Satellite Data.

Shri K.C. Velappan receives POSTER AWARD for Liquid Biofuels in the 17th European Biomass Conference

Shri K.C. Velappan Scientist, Central Leather Research Institute (CLRI), Chennai's paper titled 'Gas-Liquid process, Thermodynamic characteristics (19 blends), Efficiency Environmental Impacts, SEM Particulate Matter Analysis and On-Road Bus Trail of Proven NOx-less Biodiesel', presented in the 17th European Biomass Conference was commended by the jury of experts as the most outstanding scientific visual presentation on Liquid Biofuels and was given the POSTER AWARD during the conference on 3 July 2009.

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