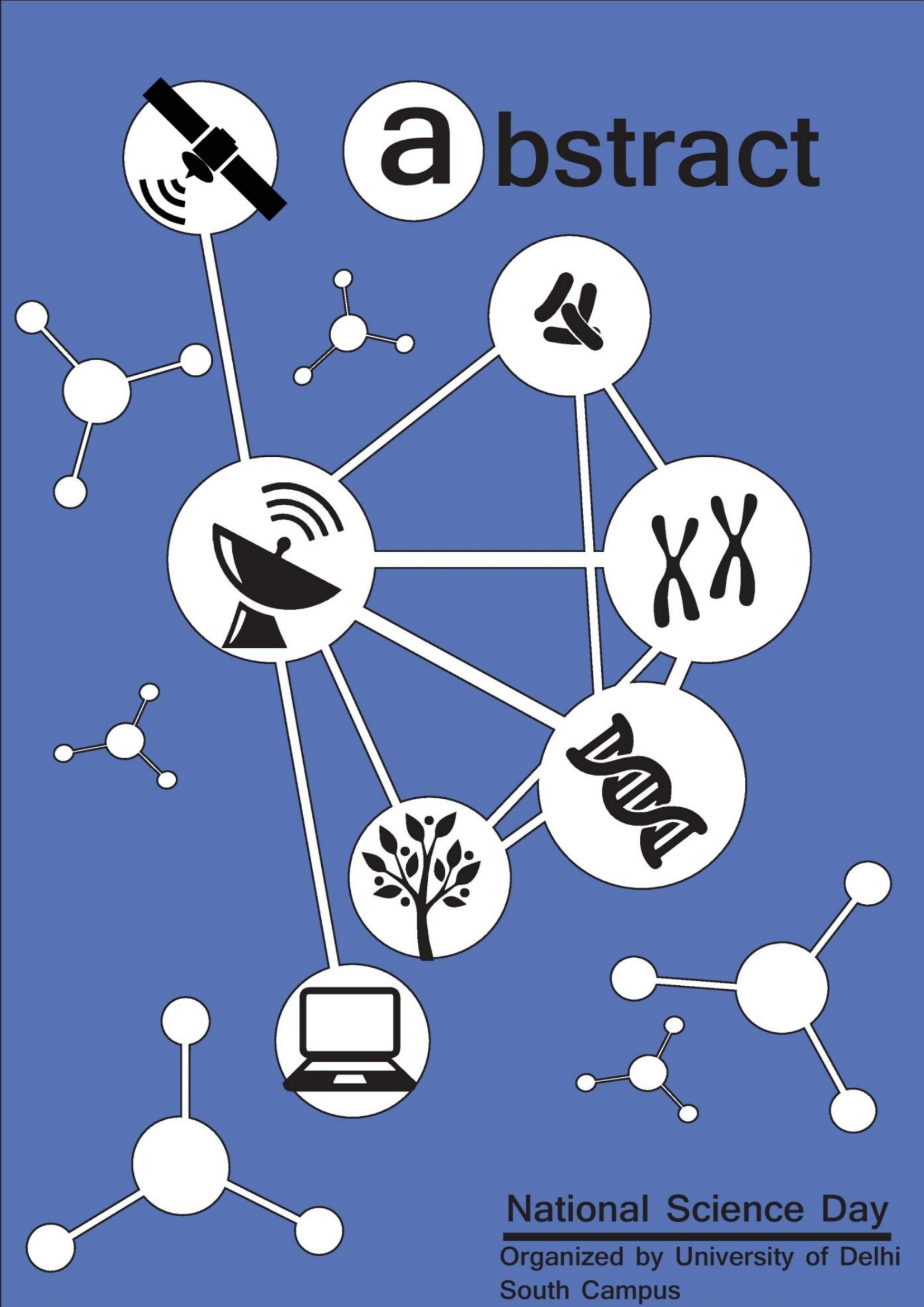
abstract
National Science Day
Organized by University of Delhi
South Campus

Cover Page designed by Rohan Pal, M.Sc. (P), Dept. of Microbiology.

This Year Theme: **"Interdisciplinary Nature of Modern Science"**

My cover-page signifies the interdisciplinary nature of modern sciences. Today the task of solving puzzles in any field of basic sciences requires a cooperative approach between all arms of science. Also the University of Delhi South Campus houses the faculty of inter-disciplinary and applied sciences and is eminent for its inter-disciplinary approach towards scientific research.

My cover page is designed in the form of a molecule where each atom of the molecule represents different technologies or field of science and the bonds between them show their interconnected nature.

Also my cover page gives rough idea about how the different department of University of Delhi south Campus can together towards achieving a common goal of forwarding the boundaries of science.

***This Cover Page has been selected as the "Best Cover Page Design" for NSD-2016.**

National Science Day Symposium 2016

(29th February, 2016)

Organized Jointly by

University of Delhi South Campus

&

INSA-TWAS India Chapter

The Preamble

The most anticipated annual event of South Campus - "National Science Day Symposium (NSDS)" – is here, sixth time in a row, in all its glory and extravaganza to enrich our academic pursuit outside the confines of class-rooms, hallowed offices and laboratories and beyond the boundaries of departments. On February 29, 2016, the student community of life sciences departments brings to life NSDS 2016. The annual scientific cum cultural festival to commemorate the National Science Day on February 28 has now become a part and parcel of the serene campus. This event of the students, by the students, for the students, promises to be a soulful enrichment that will last long in our memories as we go about performing our mundane daily routine.

The success of an event is measured by its ability to adapt to the changing needs of the time and yet deliver the punch necessary. NSDS 2016 lives up to the expectations. While the last five years celebrated the event over two days, NSDS 2016 took up the challenge to deliver the same intensity in half the amount of time. The extremely tight semester schedules, the lack of time all around and the paucity of funds needed NSDS to respond to a change of plan and it did so with elan. This year's event has been all planned in a days' time and promises not to cut down either on academic joy or cultural activities. NSDS 2016 will potentially be tight and breezy but promises to be short, sweet and eventful with plenty of memories to cherish.

NSDS has given a new meaning to National Science Day celebrations on campus. It has infused life into scientific activities on the campus. It has brightened the already shining student force on the campus. It has created a common platform for the diverse life sciences research on campus, allowing students and teachers to share their discoveries and deliberate on scientific issues. It has allowed us to share the ecstasy and agony that invariably accompany research at the highest level. It has given us a reason and it has forced everyone to step out of the confines of a small world we fondly called "laboratory". It has allowed students to wander into other departments, to interact scientifically and to widen their horizon of scientific quest and knowledge. The fruits of such an exercise are sure to explode in terms of more collaborations, camaraderie, scientific relationship and tolerance, sense of justice and compassion and better understanding of biology in general. NSDS will surely help forge many a bonds, create memories to cherish, induce healthy competition and above all an element of fun that will go a long way

in every student growing up into a respectable and responsible citizen of the country.

NSDS has ushered in glorious key note lectures in the past. Luminaries like Dr. G.P. Talwar, Dr. Manju Sharma, Dr. K. Vijayaraghavan and Dr. S.K. Sarin have enthralled us in the last few years with their wisdom, vision and high quality oration. The tradition lives on and doubles up this year – with not one but two key note lectures. The one in the morning will be delivered by Prof. Anil K. Gupta, IIM Ahmedabad, on creativity and innovation. The one in the afternoon will be delivered by Prof. M.S. Raghunathan, IIT Bombay on mathematical past, present and future of India. I am sure what excites the reader is the diversity of the key note lectures and their diversion from biology or medical science witnessed in the previous years. While biology entertains us round the year, a pleasant shift from the familiar might be a welcome break and an opportunity for different perspectives to prosper. Amid the change of subject of key note lectures, the constant is the fact that like the previous year, the plenary lectures are being hosted and organized by INSA-TWAS India Chapter. The INSA-TWAS association has surely added a distinction to NSDS 2016.

Another aspect of dynamism and an experimental change that NSDS 2016 will witness is that the faculty talks from the campus have been kept on hold this year. Instead, students from all life sciences departments will present their work and generate excitement in both fellow students and teachers. This is an eagerly awaited event since the oral presentations are assessed and prizes awarded. NSDS is not all about talks though and a repertoire of other events adds to its aura and is present in full flavor this year as well. Poster presentations by students will represent the landscape of life science research in the campus. Team events like quiz competitions, which are immensely popular, will surely command full house. The novelty of NSDSs also lies in the "idea" presentations, which is a fiercely competed team event as well, with each team coming out with a novel concept in science. These presentations will add color to the event and provide insight into the fertile brains of students. Awards in each of these events promote healthy competition and helps sustain high quality.

NSDS over the five years has been marked by innovations and new entrees. This year is no exception. In a moment of inspiration, students came up with the idea that such an interdisciplinary platform should also be used to felicitate our faculties who have been beacon of shining light over the years in the campus and who have met with the inevitable, we term "retirement" or "super-annuation".

They deserve a fitting and rousing farewell and loads of good wishes. It is of striking coincidence that Prof. Deepak Pental officially ends his long and illustrious career on 29th Feb itself. The other star, Prof. R.K. Saxena, ended his fabulous journey on 31st December, 2015. Both these practitioners of life sciences will be felicitated with fondness.

Cultural programme at the end of the day will add color, vibrancy and dynamism to the NSDS. It will provide an avenue for talents to flourish and a snapshot of our cultural strength. NSDS 2016 thus leaves no stone unturned to make this a memorable event.

It needs no mention that an event of such magnitude needs help and support from all quarters. The event would not have survived without the generous financial, infrastructural and moral support from the administration. The Director of South Campus Prof. Umesh Rai deserves special accolades for his unconditional support. The finance and academic sections of South Campus have been magnanimous in their support as well. The dynamic Dean of FIAS, Dr. Pradeep Burma, has always lent a helping hand with a smile for bonus. All heads of the departments and every single teacher have been instrumental to NSDS success. Financial support has also been provided by students themselves and faculties in terms of contributions. Several corporate establishments came forward with generous support as well and their help is appreciated. We are sure we will receive help from all other staff of South Campus including security on those days of the event. There are faculties who have helped behind the curtain with generosity, who will never be forgotten. Over and above, the entire dream that NSDS is owes to our fabulous students who work day and night to make this wholesome event an outright success!!!

Prof. Suman Kundu
Faculty Coordinator, Department of Biochemistry

Prof. J.P. Khurana
Faculty Coordinator, Department of Plant Molecular Biology

Dr. Yogender Pal Khasa
Faculty Coordinator, Department of Microbiology

Dr. Surajit Sarkar
Faculty Coordinator, Department of Genetics

Dr. Manish Kumar
Faculty Coordinator, Department of Biophysics

Chief Patrons

Vice-Chancellor, University of Delhi.

Director, University of Delhi South Campus.

Patrons

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Prof. M.V. Rajam, HOD, Department of Genetics

Prof. J.P. Khurana, HOD, Dept. of Plant Molecular Biology

Prof. T. Satyanarayana, HOD, Department of Microbiology

Faculty Coordinators

Prof. J.P. Khurana, Department of Plant Molecular Biology

Prof. Suman Kundu, Department of Biochemistry

Dr. Yogender Pal Khasa, Department of Microbiology

Dr. Surajit Sarkar, Department of Genetics

Dr. Manish Kumar, Department of Biophysics

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Microbiology

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Genetics

Naveen Sharma
Plant Molecular Biology

Abhishikha Srivastava
Biophysics

Schedule

09:00 A.M-10:00 A.M.: Registration & Tea

10:00A.M- 11:00 A.M.: INSA-TWAS Key Note Lecture
Prof. Anil K Gupta, IIM Ahmedabad:
"Is Autopoietic Model of Creativity and Innovation Self-limiting?"

11:00 A.M.-11:20 A.M.: High Tea

11:20 A.M- 11:35 A.M.: Student Talk, Mr. R. Vinoth,
Dept. of Biochemistry

11:40 A.M- 12:00 P.M.: Student Talk, Mr. Kavish Kr. Jain,
Dept. of Microbiology

12:05 P.M- 12:20 P.M.: Student Talk, Ms. Abhishikha Srivastava,
Dept. of Biophysics

12:25 P.M- 12:40 P.M.: Student Talk, Mrs. Rosetta M Devi
Dept. of Plant Mol. Biology

12:45 P.M- 01:00 P.M.: Student Talk, Ms. Anamika Upadhyay,
Dept. of Genetics

01:00 P.M. - 01:45 P.M.: Lunch and Exhibition

1:15 P.M. Onwards: Poster Presentation

02:00 P.M. - 03:00 P.M.: Idea Presentation

03:00 P.M. - 04:00 P.M.: INSA-TWAS Science Popular Talk
Prof. M.S. Raghunathan, IIT-Bombay, Mumbai:
"Making Mathematics in India"

04:00 P.M. - 04:15 P.M.: Tea

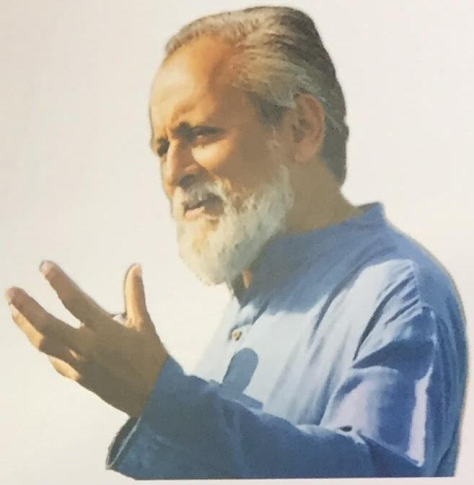
04:00 P.M. - 05:00 P.M.: Quiz Competition

05:00 P.M. - 05:30 P.M.:
Felicitation of Prof. Deepak Pental and Prof. RK Saxena

05:30 P.M. - 07:00 P.M.: Cultural Program

07:00 P.M. - 07:30 P.M.: Valedictory Session and Prize Distribution Ceremony

INSA-TWAS Key Note Lecture



National Science Day Symposium

2016

February 29, 2016
10:00 AM

Venue:
S.P. Jain Centre

University of Delhi South Campus
New Delhi-110021

February 29, 2016
4:30 PM

Venue:
JNU Convention Centre

Is Autopoietic Model of Creativity and Innovation Self-limiting?

Professor Anil K. Gupta

Centre for Management in Agriculture, Indian Institute of Management, Ahmedabad

Founder Honey Bee Network

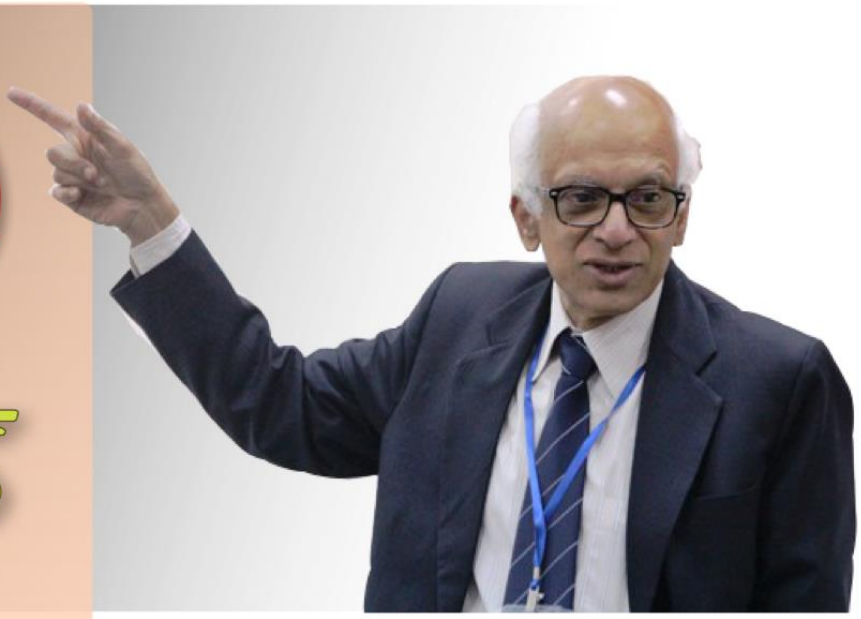
Gandhian utopia of self-governing 'village republic' served one important purpose. It fertilised imagination, it deepened democratic agenda and also by implication warned against too much of interference in local knowledge and governance system. But it will be a grave neglect on our part if viable bridges were not built been local knowledge systems and the formal scientific systems of inquiry for mutual enrichment. Based on our shodhyatras and other explorations across the country to learn from creativity and innovation at grassroots through Honey Bee Network over last 26 years, we have realised that knowledge rich-economically poor people cannot go very far if linkages with formal science and technology system and other institutions are not built. It will require major policy reforms including recasting the employment guarantee programs, and district innovation fund, start-up policy targeted at rural innovation based entrepreneurs etc.

Scientific institutions may need to include validation and value addition in local knowledge system as part of their mandate, of course within their disciplinary bounds. National Innovation Clubs aimed at searching, spreading, celebrating innovations and sensing the unmet needs will need to be linked with financial and local development institutions, and stationery incubators will need to be supplemented with online sanctuary of innovations, and final year projects of engineering and other technology students will need to be linked with unmet needs of society.

Organized by:

The World Academy of Sciences - India Chapter,
& Indian National Science Academy New Delhi

INSA-TWAS Popular Science Talk



National Science Day Symposium 2016

Making Mathematics in India

Professor M.S. Raghunathan

Distinguished Guest Professor and Head

National Mathematics Centre, Department of Mathematics, IIT, Mumbai

India has had a long engagement with mathematics and some very important developments in mathematics came from the subcontinent. However exaggerated claims about ancient India's contributions tend to discredit even our genuine landmark achievements. After a somewhat long gap, creating new mathematics was resumed in India in the late nineteenth century, but the moderns drew upon European mathematics rather than our own tradition for inspiration and guidance. Indian mathematicians have over the last 150 years "made" a lot of excellent mathematics, but we still have a long way to go to sit at the high table of the leading mathematical powers of the world.

February 29, 2016

3:00 pm

Venue:
S.P. Jain Centre

University of Delhi South Campus
New Delhi-110021

Organized by:

The World Academy of Sciences - India Chapter,
& Indian National Science Academy New Delhi

Platform Presentations

OP 1

Liposome Mediated Delivery of Antimalarial drugs for the Treatment of Malaria

Vinoth Rajendran and Prahlad C. Ghosh*

Department of Biochemistry, University of Delhi South Campus, New Delhi, India.
E-mail: pcghose@gmail.com*

Chemotherapy is the only treatment option for malaria due to lack of efficient vaccine candidates. Evolution of clinical resistant malarial parasites to existing antimalarial drugs has led to search for new antimalarials and combination chemotherapies. The anticoccidial drug monensin is a lysosomotropic agent, has strong antimalarial activity on multiple life cycle stages. We have developed a liposome-based drug delivery of monensin and evaluated its antimalarial activity in lipid formulations of soya phosphatidylcholine (SPC) cholesterol (Chol) containing either stearylamine (SA) or phosphatidic acid (PA) and different densities of Distearoyl phosphatidylethanolamine-methoxy-polyethylene glycol 2000 (DSPE-mPEG-2000). Liposomes exhibited spherical shape, with size ranging from 90 to 120nm, as measured by dynamic light scattering and high resolution electron microscopy. The developed liposomal formulations of monensin were found to be more effective than a comparable dose of free monensin in *Plasmodium falciparum* (3D7) cultures and established mice models of *Plasmodium berghei* strains NK65 and ANKA. Monensin in long-circulating liposomes of stearylamine with 5mol% DSPE-mPEG-2000 in combination with potent antimalarials resulted in enhanced killing of parasites, prevented parasite recrudescence, and improved survival. Chloroquine in long circulating liposomal formulations decreased the parasitic burden in chloroquine-resistant malaria. Our liposomal formulations containing stearylamine with DSPE-mPEG-2000 may provide a novel strategy to deliver potent hydrophobic antimalarials in combination with antimalarials, to overcome drug resistance in *P. falciparum* and prevent malaria relapse.

OP 2

Enhanced cellulase production from thermophilic fungus *Thermoascus aurantiacus* RCKK and its applications

Kavish Kumar Jain[1], Sandeep Kumar[1,] Kailash N Bhardwaj[2], Ramesh Chander Kuhad[1, 3,] *

[1]Lignocellulose Biotechnology Laboratory, Department of Microbiology, UDSC.
[2]Uttarakhand State Council of Science and Technology [UCOST], Uttarakhand.
[3]Vice Chancellor, Central University of Haryana, Mahendergarh, Haryana-123029

Thermophilic fungi are potential source of thermostable enzymes and other value added products. Thermostable cellulases offer several advantages like higher rates of substrate hydrolysis, lower risk of contamination and increased flexibility with respect to process design. The production of cellulases and xylanase from a thermophilic fungus identified as *Thermoascus aurantiacus* RCKK (Acc. No. JN676149) has been optimized up to tray level under SSF and a more than 2.5 fold than unoptimised increase was obtained. The crude enzymes were stable up to 70°C for more than 4 h. The CMCase enzyme of 35 kDa was purified to homogeneity and found to be thermostable ($t_{1/2}$ at 60°C -400 min, 70°C- 238 min, 80°C- 128 min) and pH stable (stable in pH range from 3-7). The efficiency for cellulose hydrolysis of enzyme produced from *T. aurantiacus* RCKK was evaluated on diverse cellulosic substrates i.e. crystalline substrate avicel, wheat straw, office paper waste and algal pulp. The crude Cellulase produced from *T. aurantiacus* RCKK was also tested for its pulp biorefining capability.

In addition to hydrolases, *T. aurantiacus* RCKK was found to produce antioxidants as fermentation byproducts with significant %DPPH• (2, 2-diphenyl-1-picrylhydrazyl) scavenging, ferric reducing antioxidant property (FRAP) and *in vivo* antioxidant capacity against H_2O_2 treated Saccharomyces cerevisiae (28% survival) and H_2O_2 treated CHOK cell lines (up to 80%). Further, in order to increase production level of cellulases and eventually economize the process, heterologous expression of Endoglucasnase and β-glucosidase gene from *T. aurantiacus* RCKK in *Pichia pastoris* was carried out. Capability of *T. aurantiacus* RCKK to produce thermostable cellulases and antioxidants in a single process holds potential to exploit crop byproducts for providing various commodities.

OP 3

Exploring and understanding β-lactamases for their fast characterization and development of novel drug targets

Abhishikha Srivastava[1*], Neelja Singhal[2], Manisha Goel[1], Jugsharan Singh Virdi[2] and Manish Kumar[1]

[1]Department of Biophysics, University of Delhi South Campus, New Delhi, India

[2]Department of Microbiology, University of Delhi South Campus, New Delhi, India

*Email: abhisri@south.du.ac.in

β-Lactam drugs constitute an important and major class of drugs used against infectious microbes. The increase of microbial resistance against the available drugs is a worldwide problem. The microbial β-lactamase enzyme(s) hydrolyze the β-lactam bond in β-lactam drugs rendering them ineffective. The persistent exposure of bacteria to a swarm of β-lactams induces continuous and dynamic mutations in β-lactamases, thereby expanding their activity even against the newly developed β-lactam drugs. Propagation of drug resistance cannot be checked until the fine details of mechanism of evolution and expansion of drug resistance is understood *via* the protein sequential, structural and functional relationship.

Research in the last decade has produced vast data related to β-lactamase-mediated resistance. Unfortunately, the accumulated data is dispersed in diverse and heterogeneous sources of information which might be inaccessible to microbial researchers, attempting to extract the maximum functional and evolutionary information for gaining insights into biological processes, and understanding the mechanism by which β-lactamase carry out their regulatory function. To facilitate quick characterization, we have built a comprehensive catalogue of such data in the form of a database, CBMAR (Comprehensive β-Lactamase Molecular Annotation Resource). The CBMAR is based on Ambler classification scheme and provides information about molecular and mechanistic details of β-lactamases. We have also developed a prediction system which differentiates β-lactamase from non-β-lactamase proteins and classify the predicted β-lactamase to one of the four Ambler's classes. To facilitate quick identification of family of a β-lactamases, we have also catalogued the family specific fingerprints (unique for each family) in the form of a characterization system named, "LactFp".

The exact origin of β-lactamase as well as effect of different mutations on the spectrum of drug hydrolysis are not adequately understood. In future, we plan to explore the role of functional divergence and positive selection pressure to determine the extent to which positive and natural selection had played its role in the diversified evolution of β-lactamases.

OP 4

Identification and characterization of miRNAs from rice and orthologous miRNAs from garden pea

Roseeta Devi Mutum and Saurabh Raghuvanshi

Department of Plant Molecular Biology, University of Delhi, South Campus.

MicroRNAs (miRNAs) are well known for their role in gene regulation *via* target degradation or translational inhibition. Despite the fact that a large amount of work has been done in the field of miRNA identification in plants, there remains unexplored pool of miRNAs. Rice, being a staple food, for which genome sequence is available, we chose N22 (Nagina 22), an *indica* rice variety for novel miRNA identification. N22 is a heat- and drought-tolerant upland rice variety. sRNA libraries preparation with *in-silico* data analyses followed by manual screening and expression profiling were the performed to identify miRNAs. The target genes of the miRNAs were identified by preparing 'Degradome' libraries from N22 tissues.

On the other hand, we initiated a novel approach of miRNA identification from a plant genome whose reference sequence is unavailable. Target enrichment technique was modified to enrich miRNA coding genomic loci from garden pea, *Pisum sativum* var. Arkel.

Although the number of miRNAs reported in a species may not be complete yet, the characterization of known miRNAs are still limited. This is because the expressions of miRNAs are generally spatio-temporal and condition specific in nature. Dynamic expression pattern of a known conserved miRNA (miR408) was observed in contrasting *indica* rice varieties. A drought-tolerant (N22) and sensitive (PB1) varieties showed differential expression pattern under dehydration and drought conditions in young as well as adult tissues.

OP 5

Zinc biosorption mediated by exopolysaccharide in plant growth promoting *Pseudomonas fluorescens* Psd

Anamika Upadhyay[1], Mandira Kochar[2], Manchikatla Venkat Rajam[1] and Sheela Srivastava[1]

[1]Department of Genetics, University of Delhi South Campus, New Delhi-110021, India
[2]TERI Deakin Nanobiotechnology Centre, The Energy and Resources Institute (TERI), India Habitat Centre, New Delhi- 110003, India

Zinc is an essential trace element required for the growth and development of all organisms including bacteria, but may exert toxic effects at higher concentrations. Extracellular biosorption is the mechanism of zinc resistance in the plant growth promoting (PGP) bacterium, *Pseudomonas fluorescens* strain Psd. Our study aims to identify the key players involved in Zn^{2+} biosorption and their effect on the plant-growth promoting potential of the strain. The increased Zn^{2+} accumulation by the strain was accompanied by an increase in the various PGP parameters like siderophore, phenazine production and phosphate-solubilization. IAA production, however, was found to decrease with increasing Zn^{2+} concentrations. Higher Zn^{2+} accumulation also led to increase in total exopolysaccharide content and biofilm formation. Compositional analysis of the exopolysaccharides secreted was performed using FT-IR spectroscopy. Expression analysis was carried out for genes responsible for biosynthesis of two of the important exopolysaccharides, alginate (*alg8*) and psl (*pslA)*. Quantitative RT-PCR analysis revealed an increase in expression of *alg8* with increased Zn^{2+} accumulation by the strain, whereas *pslA* expression levels remained unchanged. The role of alginates in Zn^{2+} biosorption was further confirmed by generation of an *alg8* negative mutant and elucidation of biosorption and PGP traits of the same.

Our study explores the property of plant-growth promoting rhizobacteria to secrete exopolysaccharides under metal-rich/contaminated environments, which aids in bacterial survival as well as its attachment to the root surface ensuring better plant-rhizobacterial association.

Poster Presentations

P 1

Production, purification and characterization of carbonic anhydrase from a thermo-alkali-philic bacterium *Aeribacillus pallidus* TSHB1

Himadri Bose and T. Satyanarayana

Department of Microbiology, University of Delhi South Campus, New Delhi - 110021

Anthropogenic carbon emissions have increased at an alarming rate since the advent of industrial revolution that has led to global warming. Carbon capture, utilization and storage (CCUS) is an effective solution to this problem. Current carbon capture techniques are associated with risk of leakage and high cost. There exists in nature a biological CO_2 sequestration process which relies on the enzyme carbonic anhydrases (CAs), which catalyzes hydration of CO_2 to bicarbonate, thereby, CO_2 can be stored in the form of mineral carbonates (biomineralization). This biomineralization process requires mild alkaline condition. CAs are Zn^{2+} metalloenzymes which are present ubiquitously in all the life forms. In this context, the use of thermo-alkali-stable CAs from extremophilic microbes to capture and storage of CO_2 from industrial effluents can provide an onsite solution to sequester CO_2 directly from flue gas, thereby making the process economical, greener and safer. The present investigation reports production, partial purification and characterization of carbonic anhydrase from thermo-alkali-philic bacterium *Aeribacillus pallidus* TSHB isolated from hot springs of Pipariya (Choti and Badi Anhoni), M.P. The enzyme production has been optimized by One-Variable-at a Time (OVAT) and statistical approaches. Carbonic anhydrase was partially purified by anion exchange and affinity chromatography and characterized.

Keywords: Carbonic anhydrase, global warming, CCUS, flue gas, biomineralization, thermo-alkali-phile, purification.

P 2

Liposomal Delivery of Antimalarial Drugs Under *in vitro* and *in vivo* Conditions

Aakriti Singal, Hina Bharti, Neha, and Prahlad C. Ghosh*
(pcghose@gmail.com)

Malaria is a parasitic infectious disease caused by a protozoan of the genus Plasmodium. It is one of the major global health problems, mainly in subtropical countries. Despite various advances in modern science, combating malaria is a challenging task due to the emergence of drug resistance towards the commonly used antimalarial drugs. Thus, the need of the hour is to search for novel drugs or combination based therapy using the available drugs or to develop suitable delivery vehicle for antimalarials. Liposomes have been widely used as delivery vehicle against various diseases. In the present study, we have evaluated the therapeutic efficacy of liposomal monensin (Carboxylic ionophore) in combination with curcumin (Liposomal/Free Form) by checking the growth inhibition of Plasmodium falciparum (3D7) in culture using [3H] hypoxanthine labelled incorporation assay as well as in Plasmodium berghei NK65 infected mice. Moreover, we have also demonstrated the antimalarial potential of Stearylamine (SA) bearing cationic liposomes alone and as well as in combination with Artemisinin (ART) and monensin. The drug interaction studies have shown that combination of liposomal monensin with free curcumin (Oral) presents enhanced growth suppression of the parasite both in culture as well as in mice model. Similarly, we have also observed that administration of stearylamine loaded cationic liposomes leads to reduction in blood parasite load in treated animals (10mg/kg dose of SA) as compared to control. Combination of liposomal SA with free artemisinin and free monensin displays additive effect as compared to either of these drugs used alone in culture condition. Overall, our results clearly indicate, that liposomal formulations of various drugs utilised in the study demonstrate profound antimalarial efficacy as compared to their free form. The developed formulations may find suitable effective means in the chemotherapy of human malaria.

P 3

High-level expression of recombinant streptokinase in *Pichia pastoris* fed-batch culture

Adivitiya and Khasa Y.P.*

Department of Microbiology, University of Delhi South Campus, New Delhi-110021, India
* Corresponding author e-mail: yogi110@gmail.com

Cardiovascular diseases are the leading cause of mortality worldwide. Thrombolytic drugs are commonly used to bypass the need for surgical intervention in blood clot dissolution. Streptokinase is the most widely used thrombolytic agent in the developing countries due to its cost-effectiveness. Many upstream bottlenecks such as protein toxicity and plasmid instability affect its over-expression in *E. coli*. Therefore, a high-level production of bioactive recombinant streptokinase in *Pichia pastoris* is envisaged in this work. The 1242 bp streptokinase (skc) gene from *Streptococcus equisimilis* H46A was cloned under the control of the alcohol-inducible AOX1 promoter and the *Saccharomyces cerevisiae* α-mating factor signal sequence with and without a C-terminus 6xHis tag for its extracellular expression. Optimization of host-vector combinations helped in the production of 582 mg/L of rSK and 538 mg/L of rSK-His upon induction at OD_{600} of 20. High cell density fermentation in 1 L complex medium increased the volumetric product concentration of rSK-His to 4.25 g/L, which was 7.9 folds higher than the shake-flask results. A specific product yield ($Y_{P/X}$) of 49.75 mg/g DCW was obtained with a volumetric productivity of 57.43 mg/L/h. Purified rSK-His had a specific activity of 64,903 IU/mg with 1.48 fold purification while that of rSK was 55,240 IU/mg with 1.22 fold purification. The purified protein was predicted to have 15.43% α-helix and 26.43% β-sheet using far-UV CD spectra while tryptophan emission maxima at around 347 nm was obtained using fluorescence spectroscopy.

P 4

Human Dopamine Receptors Interaction Network (DRIN): A systems biology perspective on schizophrenia disease biology

Avijit Podder and N. Latha*
Bioinformatics Infrastructure Facility, Sri Venkateswara College (University of Delhi),
*Email: lata@bic-svc.ac.in

Dopamine receptors (DR) are one of the major neurotransmitter receptors present in human brain. Malfunctioning of these receptors is well established to trigger many neurological and psychiatric disorders. In this context, a network based approach is more suited to capture the combined effect of multiple genes, accompanied by their interactions with external effectors (such as drug molecules) to enable a global understanding of the disease. To capture comprehensive interactions of candidate proteins associated with human dopamine receptors into human interactome, we performed a protein-protein interaction network (PPIN) analysis and constructed a human Dopamine Receptors Interaction Network (DRIN) [1]. Furthermore, based upon the co-expression statistics of the disease genes, we constructed a common interacting co-expression network of disease genes in schizophrenia. We examined fundamental network topologies to sequester essential common candidates for schizophrenia. In a comprehensive search against all the available drugs for schizophrenia, we appreciated that our topmost probable candidates can serve as novel drug targets for the disease [2]. Besides, we explored the topology of dopamine receptors as molecular network, revealing their characteristics and the role of central network elements. More to the point, a sub-network analysis was done to determine major functional cluster in human DRIN that governs key neurological pathways. Conclusively, our study pinpointed distinctive topological and functional properties of human dopamine receptors that have helped in identifying potential therapeutic drug targets in schizophrenia disease network.

P 5

Production, purification and characterization of Ca^{2+}- independent α-amylase from alkalitolerant *Streptomyces* sp. DB-1

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Amylases are enzymes, which act on starch to produce hydrolytic products including dextrin and sugars. Amylases have diverse biotechnological applications in textile, food and pharmaceutical industries. They contribute approximately 25% to world enzyme market. The world market of amylases was about US$ 2.7 billion at 2012, which is expected to increase by 4% annually. Extracellular production of amylases is most widely distributed among actinobacterial group especially *Streptomyces* spp. Amylases from some *Streptomyces* spp. can hydrolyze raw starch granules releasing a high quantity of simpler sugars (glucose, maltose, maltotriose and maltotetraose). These sugars can directly be used in fermentation industries. This investigation deals with the production, purification and characterization of Ca^{2+}- independent α-amylase from alkalitolerant *Streptomyces* sp. DB-1. The optimization of medium components and cultural variables has been done by OVAT and statistical approaches, which led to 5.1-fold enhancement in amylase production. The purified amylase is of 48 kDa on SDS-PAGE.

Keywords: α-amylase, *Streptomyces* sp., alkalitolerant, production and purification.

P 6

Study of *wee1* homolog in *Dictyostelium discoideum*

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Wee1 is a ser/thr kinase identified firstly in fission yeast *Schizosaccharomyces pombe* as a regulator of cell size by inhibiting Cdk1 function preventing premature entry into mitosis. Cdk1 inhibition is through phosphorylation which is relieved by the action of Cdc25 phosphatase. Loss of Wee1 function produces smaller than normal daughter cells because cell division occurs prematurely and overexpression of wee1 causes cell cycle arrest, a phenotype similar to loss of function cdc25 mutants. Besides its function in cell cycle regulation, it also functions in chromatin remodelling which is reported from studies of Wee1 and its homologues. *Dictyostelium discoideum*, our model organism of interest, offers a unique growth and development phases which allow us to find any other function of Wee1 homolog in both these phases. Interestingly multiple homologs of *S. pombe* Wee1 namely, WeeA (DDB_G0277539), WeeB (DDB_G0291133), WeeC (DDB_G0291842) are encoded in the genome of this organism similar to higher eukaryotes like in humans for which the functions are unknown. Also, cell cycle phase is one of the factor determining cell fate determination in this organism prompted us to investigate the function of Wee1 homologs. Genetic and biochemical methods will be used to analyse their functions separately. w*eeC* is expressed in *D. discoideum* Ax2 cells. For studying their functions, knock-out constructs for each of the three wee homologs have been made. For overexpression, GFP-WeeC fusion expression is confirmed in Ax2 transformed cells and phenotypic characterisation is underway. Preliminary localisation studies using WeeC-YFP in Ax2 cells showed that the fusion protein is in nuclear as well as cytoplasmic. WeeC has been successfully expressed in bacteria as N-terminal GST fusion protein in order to carry out in-vitro biochemical studies and also raise antibody. Results of the studies undertaken will be presented.

P 7

Engineering Heme Stability in Human Hemoglobin: Potential toward Development of Hemoglobin Based Blood Substitutes

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Certain lifesaving medical conditions like surgery, trauma and infected blood necessitate blood transfusions. The transfusion process is associated with several risks and side effects. Limited shelf life of human blood and storage problems add to the outcry. Over the last few years, studies have focused on developing "recombinant hemoglobin based oxygen carriers" (rHBOCs) which can be used as an alternative to blood during transfusion therapy. Recombinant human hemoglobin is produced in heterologous expression system in order to fulfil the need of artificial blood substitute. However, such hemoglobins suffer quite a few disadvantages like dissociation into dimers, poor stability, easy clearance from circulation, high blood pressure, poor expression yields, improper ligand affinities and fast heme dissociation. Of there, a major problem that prevents wider use of HBOCs is the relative ease with which recombinant Hb dissociates "heme" prosthetic group from its protein matrix. The released heme results in serious renal cytotoxicity which needs to be minimized. Our laboratory is currently involved in solving this problem. We successfully engineered heme stability into the prototype myoglobin by introducing covalent linkage using knowledge from the naturally occurring cyanobacterial globin (with unprecedented heme stability). Currently, we are interested in translating heme stability in human hemoglobin. The present study involves the expression and purification of tetrameric recombinant human hemoglobin (rHb). Using *insilico* approach, we have determined the potential residues in rHb that can be mutated to "His" in order to engineer heme affinity. In future, we will generate site-directed mutants of rHb and characterize the mutants using various biochemical and biophysical techniques. We will also perform heme loss assay to determine the heme retention ability in comparison to wild type rHb, engineered myoglobin and cyanobacterial hemoglobin.

P 8

Modulation of human metastasis suppressor Nm23H1 by Hepatitis C Virus (HCV)

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Hepatitis C Virus (HCV) infects more than 170million people around the world. Most of patients cannot clear the virus with the help of currently available treatment resulting in persistent infection, increasing the risk of long-term liver disease and hepatocellular carcinoma (HCC). HCC is the most common of liver cancers and HCV is a leading cause of HCC around the world including developed nations like U.S. and Japan. An important characteristic of HCV-related HCC is incidence of metastasis, which makes the cancer treatment extremely difficult. HCV has a small genome of only 9.6kb and encodes for only ten known proteins; structural proteins viz. Core, E1, E2 and p7, and non-structural proteins viz. NS2, NS3, NS4a, NS4b, NS5a and NS5b. Studying the physiological effects imposed by expression these proteins in human cell lines, the protein/s responsible for metastatic effect can be identified. In our studies, we found that HCV E1 and HCV core protein expression caused physiological changes in cells that increased their motility, hence imparting them higher metastatic potential. Nm23H1 is a human metastasis suppressor protein discovered in 1989 by Steeg *et al.* Its expression and functions have been reported to be directly or indirectly deregulated by several oncogenic viruses. Nm23H1 has been reported to be directly interacting with some of the oncogenic viral proteins as well. The current study is an attempt to identify and investigate a relationship between metastasis regulating proteins of HCV and host Nm23H1 expression levels and functions using human cancer cell lines as model system.

Keywords: HCV, Hepatocellular Carcinoma (HCC), Nm23H1, metastasis.

P 9

Identification of a novel homozygous mutation Arg459Pro in SYNJ1 in an Indian family using next generation sequencing

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A novel homozygous missense mutation (c.773G>A; p.Arg258Gln) in Synaptojanin1 (*SYNJ1*, 21q22.2) has been recently reported in two Italian and one Iranian consanguineous families with autosomal recessive juvenile Parkinsonism (ARJP). Contribution of this synaptic gene which encodes a phosphoinositide phosphatase to Parkinsonism phenotypes in other populations remains unknown. An ARJP family with two affected sibs characterized by frequent tremor with bradykinesia and rigidity, and intense dyskinesia and dystonia following Syndopa administration was recruited in this study. The family found to be negative for mutations in *PARKIN, PINK1* and *DJ1* was analysed by whole exome sequencing (WES) using Agilent Sure Select V5+UTR kit. Using the standard bioinformatics pipeline, we identified a novel homozygous mutation (c.1376C>G, p.Arg459Pro, exon 11) in *SYNJ1* segregating in the family. This mutation was not observed in ~285 additional PD samples (32 Familial, 81 early onset and 172 late onset) screened by PCR-Sanger sequencing. It was also absent in dbSNP148, 1000g, EXAC and EVS databases and in >200 ethnically matched non-PD exomes available in the laboratory. The Arginine residue is highly conserved across species and predicted to be damaging by almost all the *in silico* tools. It is in the Sac1 domain of the protein similar to the previously reported p.Arg258Gln mutation which has been demonstrated to impair phosphatase activity *in vitro*. Of note, finding a second novel mutation in *SYNJ1* in an Indian consanguineous family with ARJP lends further support to the possible role of Synaptojanin1 protein dysfunction in PD pathogenesis and also across different ethnicities.

P 10

Structural, functional and inhibiton studies of *Leishmania major* 4' Phosphopantetheinyl transferase to combat Leishmaniasis

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Leishmaniases impose devastating impacts on much of the world's population. The increasing prevalence of drug resistant parasites and the growing number of immuno-compromised individuals, particularly patients infected by HIV, are exacerbating the problem to the point that the need for novel, inexpensive drugs is greater now than ever. The presence of Type II fatty acid synthesis (FAS) pathway in *Leishmania major* as suggested by genome sequencing has provided a wealth of potential novel drug targets. Since this pathway is both essential and fundamentally different from the cytosolic Type I pathway of the human host, Type II FAS has tremendous potential for the development of parasite-specific inhibitors.

The first enzyme involved in the fatty acid biosynthesis pathway of *Leishmania major* is 4' phosphopantetheinyl transferase (LmPPT) which helps in the transfer of 4'-phosphopantetheine arm of Coenzyme A to Acyl carrier protein. Extensive study of PPTs from other pathogens like *M.tuberculosis*, *P.aeroginosa* has underscored its importance in the survival and pathogenecity of the organism. Since, *L.major* genome encodes a single PPT; it can act as a potential drug target.

The present study involves homology modeling of LmPPT followed by its validation using Ramachandran plot and Electrostatic energy calculations using Autodock. Biophysical and biochemical characterization of LmPPT is being carried out using CD, fluorescence and Native-PAGE analysis. Along with its characterization, our study focuses on virtual screening, scoring and ranking of small molecule chemical libraries from the National Cancer Institute USA, against LmPPT. Best hit molecules are being tested against *Leishmania donovani* promastigotes cultures. We aim to test these molecules against LmPPT using *in vitro* enzymatic assays and taking forward these inhibitors to animal models of Leishmaniasis.

P 11

Drosophila globin1: a novel suppressor of human Tau mediated neurodegeneration and cellular toxicity

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Neurodegenerative diseases such as Alzheimer's disease (AD), Frontemporal Dementia with Parkinsonism Linked to chromosome 17 (FTDP-17), Pick's disease, Cortico Basal Degeneration(CBD) etc. represent a group of disorders which are characterized by abnormal hyperphosphorylation of Microtubule Associated Protein (MAP), Tau. The abnormal hyperphosphorylation induces Tau protein to aggregate into predominant insoluble toxic species to form Paired Helical Fillaments (PHFs) and Neurofibrillary Tangles (NFTs), which epitomizes the brain lesion hallmark of such disorders.The present study was focused to identify genetic modifier(s) of human neurodegenerative tauopathies in *Drosophila* disease models, which in turn could be utilized as potential drug target. Genetic crosses were performed to identify potential genetic modifier of tau associated neurotoxicixity using two disease models of human tauopathy i.e., *htau-WT* (longest isoform, 0N4R) and *htau-V337M* (0N4R, Val337 to Met).Our preliminary screening results suggest that tissue specific reduced expression of *glob1*dominantly suppresses human Tau mediated neurodegeneration in *Drosophila*. Moreover, cellular abundance, hyperphosphorlation and localization of misfolded Tau and other associated proteins were also reduced in such cases. We propose that downregulation of *glob1* gene could have a major impact on the pathogenesis of human neurodegenerative tauopathy.

Keywords: *Drosophila*,Tauopathy, *globin1*

P 12

Leishmania donovani Histone Acetyltransferase HAT2 Acetylates Histone H4 at K10 Position and Modulates S-phase Progression

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Leishmaniases are a group of tropical diseases manifested in 3 forms: Cutaneous, Sub-cutaneous and Visceral Leishmaniases, Visceral Leishmaniases (caused by *Leishmania donovani*) being the prevalent form of the disease in Indian-subcontinent. Due to emerging drug resistance it has become important to identify more sites for therapeutic intervention and therefore, understanding prasaite's cellular biology is very important. Histone modifications affect various aspects of cellular biology such as DNA replication, transcription and DNA repair, and thus, understanding the functional relevance of histone post translational modifications in *Leishmania* is vital in the fight against leishmaniases. Our lab has been studying histone acetylation events in *Leishmania donovani*. Histone acetylation (occurring primarily on tails of H3 and H4) is regulated by co-ordinated functioning of Histone Acetyltransferases (HATs) and Histone Deacetyltransferases (HDACs). By using kinetoplast morphology and segregation pattern as marker of different stages of cell cycle we found HAT2 (tagged with eGFP) to be nuclear throughout the cell cycle in indirect immunofluorescence studies. HAT2 heterozygous knockout (HAT2-hKO) was created by knocking out one of the two HAT2 alleles using homologous recombination, and levels of H4K10 acetylation in HAT2-hKO pomastigotes was drastically reduced in comparision with wld type clls. Growth analysis revealed that HAT2-hKO population showed reduced cell growth rates al;though the percent of live cells in the population was comparable in HAT2-hKO and wild type. Cell cycle synchronization followed by Flow Cytometry Analysis revealed slower progression of HAT2-hKO cells through S-phase as compared to the wild type, indicating a possible significant role of HAT2 mediated acetylation in DNA replication. Our results indicate HAT2 has an important role to play in modulating S-phase events of cell cycle. The mechanisms by which it mediates its effect will be examined further.

P 13

Heterologous expressionof lipase YLIP9 from *Yarrowia lipolytica* MSR80: effect of host-vector combinations, fusion tags and codon usage.

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A gene encoding a thermostable, methanol-stable and enantioselective lipase YLIP9 of *Yarrowia lipolytica* MSR80 was cloned and expressed in pEZZ10-HB101 vector-host system. pEZZ18 vector has a 14 kDa ZZ-tag and the purified protein of 60 kDa was obtained. In this system, constitutive extracellular expression of ZZ-YLIP9 was observed, after 48 h incubation at 37 ºC/300 rpm, with expression level of 0.25 ± 0.15 U/ml. As the titres were low, this gene was sub-cloned and expressed in vectors with different tags- pET22b (C-terminal His-tag), pET51b (N-terminal Strep and C-terminal His-tag), pET22b-SUMO (N-terminal His, 10 kDa SUMO-tag and C-terminal His-tag) and pGEX-4t1 (N-terminal 26 kDa GST-tag) with protein of 45, 45, 55 and 70 kDa, respectively. Periplasmic expression in pET22b and pET22b-SUMO and intracellular expression in pET51b and pGEX-4t1 was observed 3h after IPTG induction. In pET22b the expressed protein was inactive, while expression of 3.25 ± 0.13, 3.5 ± 0.09 and 1.75 ± 0.21U/ml was obtained with pET51b, pET22b-SUMO and pGEX-4t1, respectively. Around 14-fold enhancement was observed with pET22b-SUMO. However, the expression was not substantial so the usage of codons in *E.coli* was compared to that of *Y. lipolytica* using the codon usage database (http://www.kazusa.or.jp/codon/). About 80 % of the codons were changed and the gene was synthesized, re-sequenced followed by its sub cloning and expression in pET22b, pET51b, pET22b-SUMO and pEZZ18 vector-*E. coli* host systems. As compared to earlier observation this time the protein that was expressed in pET22b was active with an expression level of 2.98 ± 0.18 U/ml and a further 2-3 fold enhancement was observed for pET51b and pET22b-SUMO, whereas, a significant 40-fold enhancement was observed in pEZZ18-HB101 system. Hence, host-vector combinations, tags and codon usage have a significant effect on protein expression.

P 14

Artificial microRNA-mediated silencing of ecdysone receptor gene affects growth and development of *Helicoverpa armigera*

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Food production is seriously affected by various biotic stresses such as insect pests, nematode parasites, pathogens and weeds. Hence, it is necessary to increase the crop production to feed the ever growing population. Among the different biotic stresses, insect pests affect the crop productivity to a great extent. *Helicoverpa armigera*, popularly known as cotton bollworm is one of the serious agricultural pests which affect more than 360 plant species including 50 crop plants. This pest is a great threat to the farmers due to its host range, high mobility and fecundity, and the ability to adapt and develop resistance against all common groups of insecticides. Bt technology paved the way for this problem to a great extent, but reports came up with insects gaining resistance against Bt toxins. Therefore, there is an urgent need for an effective and long lasting pest control strategies. The present study focuses on the use of artificial microRNA (amiRNA) to target ecdysone receptor (*EcR*) gene of *H. armigera*. The insect steroid hormone ecdysone and its receptor play important roles during development and metamorphosis and regulate adult physiology and life span, making it a potential target for pest control. Insect feeding bioassays with amiRNA-*HaEcR* caused significant reduction in target gene transcript level and affected the growth and development of the insect when compared to control. These results suggest that the use of amiRNA technology may serve as a potential alternative to the current pest management practices.

P 15

Heterologous expression and characterization of a novel S-enantioselective lipase TALipB from *Trichosporon asahii* MSR54: Kinetics, conformational stability and homology modeling

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A novel lipase encoding gene, *TALipB* from *Trichosporon asahii* MSR54 was heterologously expressed in *Escherichia coli* using three vectors, pET22b, pET28a & pEZZ18. Purification was done using respective affinity chromatography as N-hexahistidine fused HLipB, N and C-hexahistidine fused HLipBH and ZZ-fused ZZLipB. Study showed that the enzyme was mid to long chain selective on *p*-NP esters and S-enantioselective irrespective of tags. Among these, HLipB had lowest activation energy (3.5 $Kcalmol^{-1}$) and highest catalytic efficiency (254 $mM^{-1}min^{-1}$) on p-NP caproate followed by HLipBH and ZZLipB. However, ZZLipB demonstrated best pH stability (pH: 6-10), thermostability ($t_{1/2}$:70 ºC for 50 min) and stability towards denaturants (GdmCl 500 mM and acrylamide 100 mM). Far-UV CD and fluorescence study showed that N-terminal ZZ-tag conferred stability by altering both secondary and tertiary structure. All the three proteins were thiol activated and structural changes during activation revealed that ZZLipB required higher concentration of BME to attain the similar velocity which indicated the involvement of additional disulfide bonds in its conformational stability. *In silico* analysis revealed that the enzyme had low identity with the available database. However *Candida antarctica* lipase B was identified as closest structural homolog using PHYRE[2]. MULTALIN with CALB predicted the active site residues (Ser137-Asp228-His261) which were confirmed by superimposition and site directed mutagenesis.

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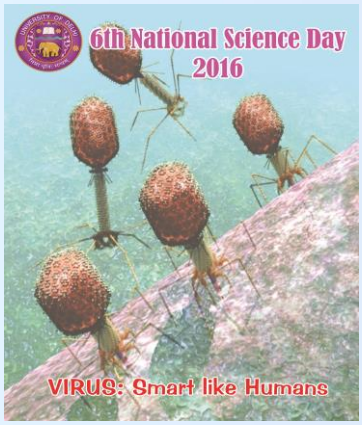

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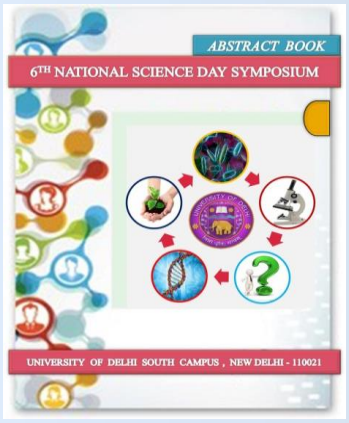

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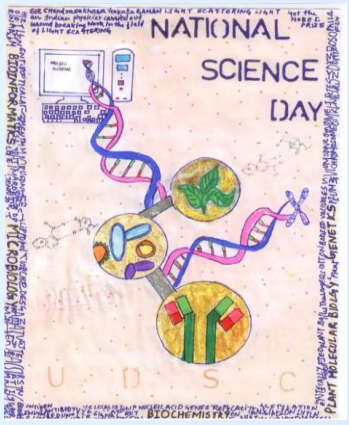

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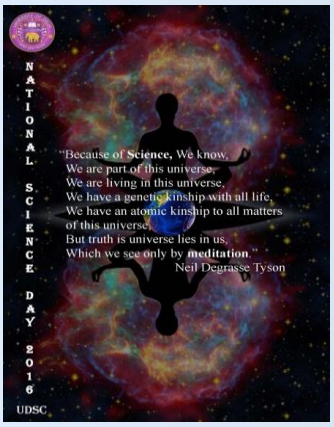

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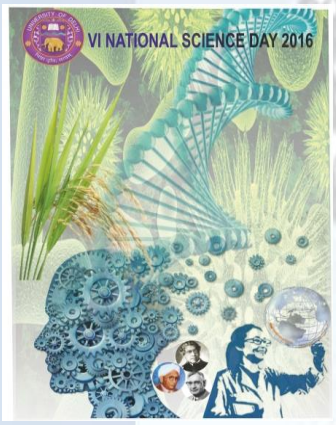

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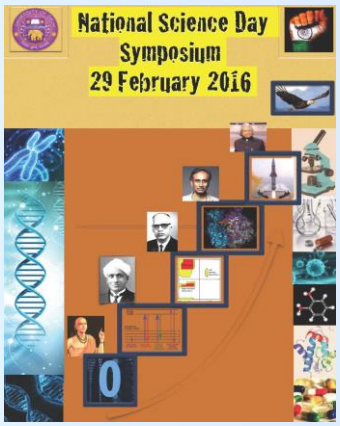

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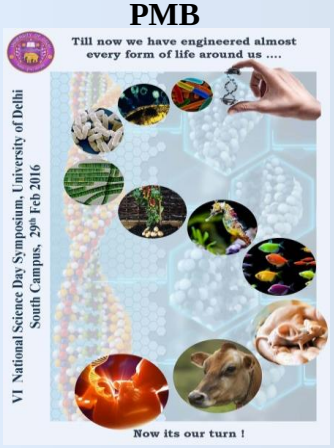

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