Proceedings

7th National Science Day 2017

Science and Technology for Specially Abled Persons

February 27-28, 2017

"I am the master of failure.....
If I never fail how will I ever learn."

Organized by

University of Delhi South Campus, New Delhi

Cover page was designed

by

Mr. Ajay Singh (PhD Student)

Department of Electronics Science

As we all kwon **Sir Chandrasekhara Venkata Raman** discovered the Raman Effect on 28 February in the 1928. For his great success in the field of science in India, C. V. Raman was awarded and honoured with the Nobel Prize in Physics in the year 1930. In India National Science Day is being celebrated to commemorate the invention of the Raman Effect with great enthusiasm on 28th of February every year. University of Delhi South Campus is also celebrating National Science Day on the same day since 2011.

On the Occasion of the National Science Day, Organizing committee of NSD-2017 gave me the opportunity to participating to design the cover page of the NSD-2017 proceeding. In this regard, I have designed this cover page with a question **"what is Science?"** Is it a real discovery or invention? Which is to be achieved without afraid of failure as said by our great Physicist **Sir Chandrasekhara Venkata Raman "I** *am the master of failure.....If I never fail how will I ever learn."*

***This Cover Page has been selected as the "Best Cover Page Design" for NSD-2017.**

National Science Day Symposium 2017

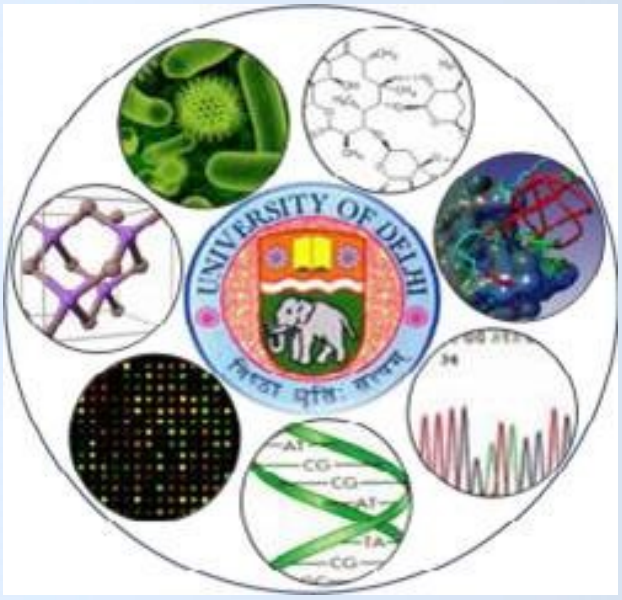
(27th and 28th February, 2017)

Organized Jointly by

University of Delhi South Campus

&

INSA-TWAS India Chapter



Preamble

Research scholars of the Faculty of Interdisciplinary and Applied Sciences, University of Delhi (South Campus) have been organizing National Science Day Symposium for the last 6 years to commemorate National Science Day of the country (Feb 28) in memory of the seminal discovery of "Raman Effect" by C.V. Raman. This is an event for the students, by the students, of the students with support and participation by every faculty. This has slowly turned out to be the flagship programme of the life sciences department of the campus and is growing in stature by the day. In its short life span, it has already assumed significance of great proportions and is a crucial part of development of students on the campus, their scientific acumen and dynamism. It has boasted of some of the top notch scientific talks in the city and show-cased its own scientific merits and standards. This event over the years has nurtured science, technology and innovation and has been a part of building the nation.

This event is being organized in 2017 on Feb 27th and Feb 28th, moving back to the 2-day format unlike the 1-day format followed in 2016, speaking volumes of the importance of the event. A pioneer in medical research, **Prof. Balram Bhargava** from All India Institute of Medical Sciences (AIIMS) will be delivering an hour long talk that is expected to motivate and inspire students to take up science as a career option in the long run with commitment to the betterment of the Society. Prof. Bhargava is a renowned cardiologist, innovator and medical educationist. He has been bestowed the Padma Shri for his exemplary work and service to the nation in the field of medicine. He is fellow of all major academies worldwide and is highly decorated. He is a leader in the field of biomedical innovations and is primarily responsible for the Stem Cell Facility in AIIMS. His presence will lighten up the event.

The event will also see scientific talks by one faculty of each life sciences department of the campus, which in itself is an enviable cast of orators. One student from each department will also share the platform with the faculties thus bringing in enthusiasm and vigour. This year for the first time Department of Electronic Sciences will also be part of the coveted event, with one faculty delivering a scientific talk and few students presenting posters. The symposium, since its inception has been instrumental in facilitating exchange of ideas and thoughts between the life sciences departments and now will cross over to integrate electronic sciences as well. In the past INSA has also collaborated with us to bring science and technology to the masses.

In a moment of inspiration in 2016, 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. This year Prof. T. S. Satyanarayana from Microbiology Department, whose seminal contributions in the area of microbiology and enzymology has inspired scores of students, will be felicitated with fondness. We look forward to the glorious presence of this practitioner of life sciences research.

In addition, the two days will also see poster presentations, quiz contest and idea (concept) presentation. All these events are very popular and highly competitive drawing heavy participation. The two days will be capped by a cultural programme that will be presented solely by the students of the campus to allow a creative outburst. With "Champions Trophy" also to be won by the department with maximum prize winning performances, this is the event that keeps the heart racing.

We welcome you all to this mega event. It is yours, so go for it !!!

Student Organizers

NSD 2017

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Prof. Suman Kundu, Department of Biochemistry

Dr. Yogender Pal Khasa, Department of Microbiology

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Electronic Science

Schedule

Day 1 (February 27, 2017)

VENUE- S.P. Jain Auditorium

09:00 A.M. - 09:30 A.M.	Registration & Reception Tea
09:30 A.M. - 10:00 A.M.	Welcome address by Prof. J.P. Khurana, Director, University of Delhi South Campus
10:00 A.M. - 11:00 A.M.	Key Note Lecture by Prof. Balram Bhargava, AIIMS, New Delhi "Ghandhian Innovation in Healthcare"
11:00 A.M. - 11:30 A.M.	High Tea
11:30 A.M. - 12:00 P.M.	Prof. J. S. Virdi (Department of Microbiology)
12:05 P.M. - 12:25 P.M.	Ms. Bhawna Israni (Department of Genetics)
12:30 P.M. - 12:50 P.M.	Mr. Pradeep Singh (Department of Biochemistry)
12:50 P.M. - 01:50 P.M.	Lunch
02:00 P.M. - 03:00 P.M.	Poster Presentation
03:00 P.M. - 03:30 P.M.	Dr. Girdhar K. Pandey (Department of PMB)
03:35 P.M. - 04:05 P.M.	Prof. Suman Kundu (Department of Biochemistry)
04:05 P.M. – 04:40 P.M.	Felicitating Prof. T. Satyanarayana
04:40 P.M. - 05:00 P.M.	Tea
05:00 P.M. - 06:00 P.M.	Quiz Day 1
6:00 P.M.	Concluding Remarks for Day 1

Day 2 (February 28, 2017)

VENUE- Biotech Building Auditorium

09:30 A.M. - 10:00 A.M.	Tea
10:00 A.M. - 10:30 A.M	Prof. Enakshi K. Sharma (Department of Electronic Science)
10:35 A.M. - 11:05 A.M.	Prof. Pradeep Kumar Burma (Department of Genetics)
11:10 A.M. - 11:40A.M.	Prof. Subhendu Ghosh (Department of Biophysics)
11:40 A.M. - 11:55 A.M.	High Tea
11:55 A.M. - 12:15 P.M.	Mr. Rajan Shrivastava (Department of Biophysics)
12:20 P.M. - 12:40 P.M.	Mr. Nambram Somendro Singh (Department of Microbiology)

VENUE- S.P. Jain Auditorium

12:50 P.M. - 01:50 P.M.	Lunch
02:00 P.M. - 04:00 P.M.	Idea Presentation
04:00P.M. – 04:30 P.M.	Tea
04:30 P.M. – 05:30 P.M.	Quiz Finals
05:30 P.M. – 07:30 P.M.	Cultural Program
07:30 P.M. - 07:50 P.M.	Valedictory Function & Prize Distribution
07:50 P.M. onwards	Special Dinner

INSA-TWAS

Key Note Lecture

By

Prof. Balram Bhargava

AIIMS, New Delhi

On

"Ghandhian Innovation in Healthcare"

Platform Presentations

Faculty Talk (I)

Genomic insights into clinical and environmental strains of *Yersinia enterocolitica* isolated from India

Prof. J.S. Virdi

Department of Microbiology, University of Delhi South Campus,

New Delhi - 110 021, Email: virdi_dusc@rediffmail.com

Yersinia enterocolitica is an important food- and water-borne zoonotic enteropathogen. In India, the first outbreak of gastroenteritis due to this bacterium was reported in 1996. In our laboratory, the organism was isolated from wastewater, pork, pigs (reservoir) and the stools of the diarrheic human patients. All strains were authenticated by WHO Reference Laboratory at Pasteur Institute.

The Indian strains belonged to several serotypes. However genotyping using REP- and ERIC-PCR showed that the strains belonged to only two clonal groups indicating limited genetic heterogeneity. Similar results were inferred from genotyping based on *rrn* and *gyrB* loci. Sequencing of beta-lactamase genes (*blaA*, *blaB*) also discerned two clonal groups. These studies also showed that the serotype 6,30-6,31 strains isolated from wastewater were genotypically different from the serotype 6,30-6,31 strains isolated from stools of diarrheic humans.

The detection of a large number of virulence-associated genes (*inv*, *ail*, *virF*, *ystA*, *ystB*, *ystC*, *myfA*, *fepA*, *fepD*, *fes*, *hreP*, *ymoA*, *tccC*, *sat*) in the Indian strains showed that Indian strains belonged to low virulence group. Multilocus variable number tandem repeat analysis (MLVA), multilocus enzyme electrophoresis (MLEE) and multilocus restriction typing (MLRT) and their analysis by minimum spanning tree and e-BURST suggested that the clinical strains probably originated from environmental strains by host adaptation and genetic change. Interestingly some functional parameters did not reflect the two clonal groups. Suppression subtractive hybridization (SSH) between clinical and environmental strains and proteomic analysis indicated that several iron-acquisition and storage genes were present in clinical strains but not in environmental strains. These are currently under study. Knowledge and expertise on beta-lactamase and other antibiotic resistance genes gained during this study is being used to develop a rapid test for detection of antibiotic resistance.

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Faculty Talk (II)

How a Ca^{2+} regulated kinase modulate oxidative stress responses in Arabidopsis? Role of CIPK-VDAC module

Dr. Girdhar K. Pandey

Department of Plant Molecular Biology, University of Delhi South Campus, Benito Juarez Road, Dhaula Kuan, New Delhi-110021

Calcium has been widely recognized as a key secondary messenger in mediating various plant adaptive responses. Calcineurin B-like interacting protein kinases (CIPKs) are involved in diverse signaling pathways in plants by decoding calcium signals into various phosphorylation events downstream. VDAC, voltage-dependent anion channel, was identified as a novel interactor of one of the CIPKs. This CIPK physically interacts and phosphorylates C-terminus of VDAC in *in vitro* conditions, and Ser191 at the C-terminal of VDAC is one of the sites of phosphorylation. Co-localization and FRET experiments proved their physical interaction in the mitochondria. Analysis of loss-of-function mutants of both the genes exhibited a methyl viologen (MV) induced oxidative stress tolerant phenotype. Our analysis proved that *cipk* and *vdac* mutants accumulate less reactive oxygen species in roots under MV stress, which conclusively supports the results obtained by phenotypic analysis. Although this CIPK was previously characterized for its role in K^+ nutrition signaling, our study suggests a novel role of this CIPK along with its interacting partner VDAC in regulating methyl viologen-mediated oxidative stress in Arabidopsis.

Faculty Talk (III)

Towards New Drugs for High Blood Pressure and Cardiac Hypertrophy: An Heartening Initiative

Prof. Suman Kundu

**Department of Biochemistry, University of Delhi South Campus,
New Delhi- 110021, Email Id: suman.kundu@south.du.ac.in**

Hypertension, a risk factor for several cardiovascular diseases and stroke, is a silent killer that has spread its wings across the globe. Treatment of this deadly cardiovascular disease relies on lifestyle changes and therapeutics that mainly target the renin-angiotensin-aldosterone system. As such, there are several drugs available commercially that have been developed and re-designed against this conventional pathway to combat hypertension, without the discovery of any new drugs in the last several years. However, there are difficulties in that these drugs affect kidney, often cause abrupt hemodynamic changes and more than one drug is often required to control blood pressure adequately. More often than not, the origin of hypertension remains enigmatic and a universal mode of regulating blood pressure irrespective of its origin is warranted. The need for new drugs, especially against unconventional targets, thus remains and offers immense scope and challenges. One such target is the catecholamine biosynthetic pathway, whereby the levels of dopamine and norepinephrine/epinephrine regulate blood pressure by tuning the receptors that regulate vasodilation and vasoregulation, respectively. Dopamine beta hydroxylase (DBH) is a key player in this pathway, which can be inhibited to obtain the desired effect since this enzyme catalyzes the conversion of dopamine into norepinephrine. Hyperactivity of the enzyme due to specific mutations or otherwise, results in higher levels of norepinephrine, which promote elevated blood pressure through vasoconstriction of blood vessels. In addition, in case of essential hypertension, where the origin of elevated blood pressure is unassigned, this enzyme may serve as a handle to counter blood pressure by promoting vasodilation. Inhibitors against this therapeutic enzyme have been designed in the past based on ligand structure. They have been unsuccessful as drugs due to their adverse effects like their ability to cross blood brain barrier thus inhibiting brain DBH. As a solution to such problems, we have proposed enzyme structure-based design of inhibitors against DBH. An *in silico* three-dimensional model for DBH was built and validated. Multiple small molecule

libraries were screened against the DBH model and few top hits identified. These were subsequently screened *in vitro* using appropriate biochemical assays including reversed-phase HPLC and IC_{50}s determined. The interaction of the molecules with DBH, which were successful in inhibiting the enzyme, was validated using a repertoire of biophysical and structural methods like CD, fluorescence and ITC. The affinities of the best compounds (lead) were determined and their cytotoxicity and hemolytic abilities were evaluated *ex vivo*. The specificities of the lead molecules for their target were verified by performing assays against other enzymes of the pathway to rule out off-targets. The interaction of the leads against the drug metabolizing enzyme cytochrome P450 was evaluated. The ones that passed these set of screens were evaluated *in vivo* in hypertensive rat models. The structure-based drug discovery initiative successfully identified novel molecules that can significantly control hypertension with the potential to be developed into anti-hypertensive drugs. Currently, we are evaluating plant extracts from traditional cardiotonic plants against DBH, with encouraging results that can lead the way to natural products against hypertension.

Faculty Talk (IV)

Fibre Optic Biosensors

Prof. Enakshi K. Sharma

Department of Electronics Science, University of Delhi South Campus, New Delhi-110021, E mail Id: enakshi54@yahoo.co .in

In the past few years there has been a lot of interest in the use of optical fibres in biosensor technology for label free detection of metabolites in blood. Optical fibre sensors are preferred because of electrical isolation, compact and light weight, wide dynamic range and they are amenable to multiplexing and remote sensing. Depending on how the molecular recognition event is quantified the following three classes of fibre sensors have been developed based on Surface Plasmon Resonance (SPR), Long Period Fibre gratings (LPG) and Localized Surface Plasmon Resonance (LSPR). As an example the detection of triacylglycerides level in an aqueous solution by SPR based fibre optic sensor is presented. Lipase enzyme is the biomolecule used to detect the presence of the analyte triacylglyceride in a solution. In the SPR based sensor lipase enzyme is immobilised on a silver coated unclad portion of a multimoded plastic coated optical fibre by gel entrapment method. The shift in resonance wavelength of the SPR transmission spectra is directly proportional to the concentration of triacylglycerides in the solution. The fabricated sensor can measure the entire physiological range of triacylglycerides (40 mg/dl - 500 mg/dl) and shows optimum response when operated at 37° C at pH 7.0 of the solution with a response time 1 minute, sensitivity 3.17 nm/mM and limit of detection 0.1 mM (1mM is equivalent to 88.54 mg/dl) A similar LSPR based fibre optic sensor can be fabricated by covalently immobilizing lipase enzyme on silver nanoparticles (AgNPs) coated on the unclad portion of a multimoded plastic coated optical fibre. The absorbance spectra measured in transmission shows that the shift in the peak of the absorbance spectra is a function of triacylglycerides concentration. The sensor shows a response time of 40 sec at pH 7.4 and temperature 37 ºC, and has a higher sensitivity of 28.5 nm/mM and limit of detection of 0.016 mM due to larger surface area of the immobilised lipase on the nano-particles.

Faculty Talk (V)

Developing Insect Resistant Cotton Transgenics – Our Experience

Prof. Pradeep Kumar Burma
(*on behalf of everyone who worked on this problem*)

Department of Genetics, University of Delhi South Campus, New Delhi-110021.

In this talk I will share the lab's experience on developing insect resistant transgenic cotton plants. After the protocol for regeneration and transformation of cotton (using the cultivar Coker 310 FR) was established in the lab development of Bt. cotton (expressing the *cry1Ac* gene) started in earnest somewhere in the year 2000. It took us about 15 years, and the hard work of several Ph.D scholars and post- doctoral fellows before we could successfully develop insect resistant lines that can now be used to transfer the character to high yielding pure lines and hybrids of cotton. We learnt several lessons along the way, trying to translate a known technology that looked relatively straightforward at the start. In initial years we constantly aimed at achieving high levels of expression of the Cry1Ac protein with the help of different strong constitutive promoters. In a few years we realized that it was difficult (though not impossible) to develop transgenic plants with high cytoplasmic levels of Cry1Ac protein as it affected the normal growth and development of the plant. We were able to overcome this problem by targeting the Cry1Ac protein to the chloroplast. Some leads have been obtained in our attempts to identify the reasons for this problem.

Of the thousand odd transgenic plants that have been developed over the years, a line (Tg2E-13) having high cytoplasmic levels of Cry1Ac protein and with normal phenotype is available. A line (TM2) has also been developed where the protein is targeted to the chloroplast. Insect bioassays carried out with the pest, Helicoverpa shows 100% mortality of larvae fed on these lines. Tg2E-13 has been transferred to other groups for transferring it to commercially grown cultivars.

Faculty Talk (VI)

How Repeated Input helps Learning a Pattern?

Prof. Subhendu Ghosh

**Department of Biophysics, University of Delhi South Campus,
New Delhi 110021.**

It is known that repeated viewing or listening of a pattern or phrase or composition helps learning. We present a neuro-physiological basis of how repeated listening or viewing helps this process. When some stimulus comes to the brain, e.g. auditory signal input to the ear, an electrical spike called action potential is generated, which travels through the specific nerve to the cortical region of the brain followed by a complex process called cognition or learning. It is known that the neural basis of learning and memory is synaptic plasticity. However, lately it has been realized that neuronal plasticity can take place beyond the synapse; Neurons can modulate themselves with experience, learning, external stimuli and give rise to Intrinsic Plasticity. The latter is accompanied by reduction in After-Hyper-Polarization (AHP), which leads to increase in excitability. We have modelled (mathematical) the threshold of Action Potential based on Hodgkin-Huxley's equations and showed computationally that the AHP of an action potential undergoes reduction due to repeated input giving rise to higher excitability or increased frequency of firing, thus making the process of learning easier.

Oral Presentations

OP 1

Development of Insect Resistant Cauliflower by RNAi-mediated Knock-down of Important Genes of *Plutella xylostella*

Bhawna Israni and Manchikatla Venkat Rajam

Department of Genetics, University of Delhi South Campus, New Delhi-110021.

Plutella xylostella (Diamondback moth) is a serious pest of Brassicaceae family members, including cauliflower (*Brassica oleracea*), and significantly affects the yield and quality of the produce. The pest is highly adaptive and has become increasingly difficult to control owing to the emergence of resistance to a broad range of chemical insecticides and bio-pesticides. RNAi is a widely used tool for various functional genomics studies and has found application in a host of areas. In the realm of insect pest management, RNAi has been successfully applied against several agriculturally important pests. In the present study, RNAi-based strategy has been used for the control of diamondback moth. Three candidate genes namely ecdysone receptor (*EcR*), insect intestinal mucin (*IIM*) and sericotropin (*STP*) were chosen, encompassing some of the most crucial biological functions in the pest. As a prelude to this investigation, *in vitro* insect feeding assays were carried out to ascertain the importance of the target genes in the functioning of the pest. Bacterially produced dsRNA was chosen as the molecule of choice for delivery into the insect system to silence the target genes. RNAi mediated knock-down of the target genes led to the impairment of molting process, reduction in reproductive potential, high insect mortality and an overall stunted growth. Expression analysis revealed a significant reduction in the target gene expression in treated insects with respect to controls. For continuous expression of insect-specific dsRNA, cauliflower transformations were carried out using *Agrobacterium tumefaciens* harboring RNAi constructs separately against the genes of interest. The transgenics so developed were evaluated for resistance to the pest. Down-regulation of the target transcripts was seen in the larvae fed with the leaves of cauliflower transgenics, with a significant developmental arrest and larval mortality. The study successfully reports the application of host-induced gene silencing (HIGS) for the control of *P. xylostella* as an alternate approach to tackle the pest menace.

OP 2

Identification of Novel Small Molecule Inhibitors against FoxM1 with Implications in Cancer Therapy

Pradeep Singh Cheema, Neha Jaiswal, Deeptashree Nandi, Sanjay Kumar Dey, Sumeet Baweja, Suman Kundu and Alo Nag

Department of Biochemistry, University of Delhi, South Campus,
New Delhi-110021.

'Cancer' prevails to be one of the most dreaded ailments characterized by its unrestrained cellular proliferation, frenzied regulatory machinery and the potential to invade any tissue. Recent years have witnessed tremendous efforts to decipher this multifaceted disease and the oncogenic transcription factor FoxM1 (Forkhead transcription factor M1) has been recognized as one of the major driving force in triggering and sustaining this malady. High levels of FoxM1 not only help in evading cell cycle check points, apoptosis, but also stimulate angiogenesis, tumor invasion and confer resistance to various anti-cancer therapies. This underscores the promising prospect of FoxM1 in the fight against cancer and makes it a molecule of significant clinical interest. Following these lines, there has been emergence of inhibitors, peptides, and RNAi approaches exploiting its supremacy in cancer development and progression, sadly none of them has made it to the clinics so far. Therefore, the present study is dedicated to identify FoxM1 specific small molecule inhibitors using structure based drug designing approach. Molecular Docking tool was utilized for virtual screening of NCI library diversity set compounds against X-ray crystal structure of DNA-binding domain of FoxM1. The candidate molecules causing substantial cytotoxicity were further tested for their ability to affect FoxM1-specific transcriptional activity, cellular proliferation, migration, invasion and apoptosis in cervical cancer cells. Overall, our investigation led to identification of potent inhibitors showing remarkable inhibition against FoxM1 and hence hold great promise for future explosion of novel anti-cancer treatment modalities.

OP 3

Detection and analysis of β-lactamase genes, their genetic environment and integrons of aquatic *Escherichia coli*

Nambram Somendro Singh and J S Virdi

Microbial Pathogenicity & AMR Diagnostics Lab.
Department of Microbiology, University of Delhi South Campus,
New Delhi - 110 021

Prevalence of antibiotic resistant *Escherichia coli* in aquatic environment is a major public health concern. Therefore, it is important to assess the genetic markers of resistance in aquatic *E. coli*. The present work was carried out to study β-lactamase genes, their genetic environment and the type of integrons, as these play role in the mechanism of resistance and dissemination of resistance. A total of sixty one well characterized *E. coli* strains isolated from the river Yamuna (Delhi, India) belonging to four well known phylogroups (A, B1, B2 and D) were used. bla_{TEM}, bla_{SHV}, and bla_{CTX-M} including their genetic environment, type of integrons and gene cassette arrays were characterized by PCR. bla_{TEM-1} was detected in all the 61(100%) strains, 10 (16%) strains were found to carry $bla_{CTX-M-15}$ gene. None of the *E. coli* strains harbored the bla_{SHV} gene. The bla_{TEM} genes in all *E. coli* carried *P3* type promoter, which is one of the most prevalent type of promoters; two strains were also found to have the insertion sequence IS*26* in the upstream region of bla_{TEM-1}. However these insertion sequences were present at different positions of the upstream region of bla_{TEM-1}. IS*Ecp1* insertion sequence was located in the 5' conserved region of $bla_{CTX-M-15}$ gene and the promoter sequence was present within this insertion sequence. Non-coding element ORF477 was also detected in the downstream region of the $bla_{CTX-M-15}$ genes. Class I integron was detected in 33(53 %) isolates, of which 9 strains had variable regions. The cassette array of class I integron possessed *aacA4*, *catb3*, *dfrA1*, *aadA1*, *dhfr1*, and *aadA2*. None of the strains harbored class 2 and 3 integrons. From this study we found that the promoter sequences of bla_{TEM-1} and $bla_{CTX-M-15}$ were conserved and the *E. coli* strains from the river Yamuna harboured the "international $bla_{CTX-M-15}$" genetic environment.

OP 4

Origin of Noise in Open Channel Current of S6 Peptide from KvAP Channel.

Rajan Shrivastava and Dr. Subhendu Ghosh

Department of Biophysics, University of Delhi South Campus,
New Delhi-110021.

Open channel current noise in synthetic peptide S6 of KvAP channel was investigated in a voltage clamp experiment on bilayer lipid membrane (BLM). It was observed that the power spectral density (PSD) of the component frequencies follows power law with different slopes in different frequency ranges. In order to know the origin of the slopes PSD analysis was done with signal filtering. It was found that the first slope in the noise profile follows 1/f pattern which exists at lower frequencies and has high amplitude current noise, while the second slope corresponds to $1/f^{2-3}$ pattern which exists at higher frequencies with low amplitude current noise. In addition, white noise was observed at very large frequencies. It was concluded that the plausible reason for the multiple power-law scaling is the existence of different modes of non-equilibrium ion transport through the S6 channel.

Poster Presentations

P 1

Characterization of amyloidosis properties of Cytoglobin

Ushma Anand, Ravi Kant and Suman Kundu

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Cytoglobin is ubiquitously expressed hexacoordinate hemoglobin that facilitates diffusion of oxygen through tissues and serves a protective function during oxidative stress. Recently, there has been a report suggesting that this novel globin might undergo amyloid formation (Ferreira et. al, 2015), which would probably perturb its protective function and imply a role in diseases. Our laboratory has also demonstrated recently the cytotoxicity associated with amyloid formation by another novel globin, neuroglobin (Uppal et. al, 2016). Investigating the amyloidogenic properties of cytoglobin can give potential insights into the mechanism which dictates the development of diseases due to amyloids formed by globins.

The universality and ubiquitousness of amyloidogenesis can be assessed once the condition in which it forms amyloids gets known. With this understanding, cytoglobin was expressed in a heterologous host,E. coli, and purified to homogeneity by Ni-NTA affinity purification and gel filtration chromatography. Apo-cytoglobin was made from holo-cytoglobin by Teale's method and 12 different conditions varying in temperature and pH were explored to identify the condition under which cytoglobin form amyloid fibrils. The reactions were initiated using 25μM and 50μM of apo and holo isoforms. Both apo and holo-cytoglobin formed soluble aggregates at pH 10 for reactions set at 60°C and 75°C within 30 days.

Enhanced fluorescence intensity in Thioflavin T assay and the difference spectrum with absorbance maximum at 540nm in Congo red assay, characteristic of amyloid, hinted at the formation of amyloid fibers. A negative ellipticity at 215-218 nm in CD spectroscopy along with the observation of branched fibers in TEM confirms the formation of β-sheet and amyloids, respectively.

This study is of prime significance not only to understand the mechanism by which cytoglobin forms amyloids but also to mimic the disease patho-physiology. Further investigation of some enhancers of amyloidoses and the key residue responsible for its formation can help develop a model on which studies regarding amyloids can be done.

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P 2

Unintended expression observed with tapetum specific promoters in transgenic tobacco.

Preeti Apurve Sharma, Neetu Verma and Pradeep Kumar Burma

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Promoters are key component in developing transgenic plants. In several instances when a transgene needs to be expressed in a tissue specific manner, its appropriate length ensuring the similar promoter activity at ectopic site becomes a paramount requirement. The spatial and temporal activity of a promoter can be analyzed by (i) cellular localization of the endogenous transcripts e.g., by *in-situ* hybridization, microarray, RNA seq and (ii) transgenic approach using a promoter-reporter construct. The first case reflects the activity of a promoter at its native genomic location while the second, reflects the activity of a promoter at an ectopic location. In the transgenic approach the activity of the promoter can be influenced by its site if integration, i.e. position effect. However, information about 'leaky expression' of a tissue specific promoter due to position effect is usually not highlighted in the published literature and based on the experience from work done in our laboratory, leaky expression of a tissue specific promoter becomes a major deterrant in developing transgenics where transgene expression needs to be spatio-temporally restricted and/or the reporter gene is lethal.

The presentation will summarize our observation on the 'unintended expression' patterns of two important tapetum specific promoters A9 from *Arabidopsis thaliana* and TA29 from *Nicotiana tabacum* in transgenic lines developed in tobacco. Using different lengths of promoters and the reporter gene, *β-glucuronidase* it was observed that a substantial percentage of the transgenic lines developed with A9 promoter construct showed leaky expression in callus, roots and stem whereas in case of TA29 promoter the leaky expression was restricted to roots and stem. More strikingly, it was observed that the leaky expression was spatially restricted to the meristematic regions. This indicated that the TA29 promoter carried cryptic meristem-specific elements that were activated when the promoter was integrated at certain genomic location. Presentation will also highlight the use of *barnase* gene (encoding a cytotoxic protein) as a sensitive reporter gene for analyzing leaky expression. The importance of this information to developers of transgenic events for commercial purposes will be discussed.

P 3

Structure based virtual screening for the identification of inhibitors against *Mycobacterium tuberculosis* BioA.

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7,8-Diaminopelargonic acid synthase (BioA), an enzyme of biotin biosynthesis pathway, is a well-known promising target for anti-tubercular drug development. In this study, structure based virtual screening was employed against the active site of BioA to identify new chemical entities for BioA inhibition and top ranking compounds were evaluated for their ability to inhibit BioA enzymatic activity. Seven compounds inhibited BioA enzymatic activity by greater than 60% at 100µg/ml with most potent compounds as A36, A35 and A65, displaying IC_{50} values of 10.48µg/ml, 33.36µg/ml and 39.17µg/ml, respectively. Compounds A65 and A35 inhibited *M. tuberculosis* growth with MIC_{90} of 20µg/ml and 80µg/ml, respectively whereas compound A36 exhibited relatively weak inhibition of *M. tuberculosis* growth (83% inhibition at 200µg/ml). Thus, compound A65 emerged as the most potent compound identified in our study that inhibited BioA enzymatic activity, growth of the pathogen and possesses drug-like properties. Further optimization of this lead compound would result in the improvement of its potency. Our study has also identified a few hit molecules against *M. tuberculosis* BioA that can act as promising candidates for further development of potent anti-tubercular therapeutic agents.

P 4

Gamma-Glutamyl Transpeptidase from *Bacillus atrophaeus* GS-16: Heterologous Expression, Characterization and Synthesis of γ-D-glutamyl-L-tryptophan

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Gene encoding γ-glutamyl transpeptidase from a mesophilic bacterium *Bacillus atrophaeus* GS-16 (*Ba*GGT) was cloned into pET51b(+) vector and expressed heterologously in *E.coli* BL21 (DE3). Expression studies were conducted at 16˚C, 200 rpm for 16 h after IPTG induction. *Ba*GGT was active as a heterooctamer in native form, consisting of four heterodimeric units combined together. One heterodimeric unit constituted two subunits with molecular masses of 45 kDa and 21 kDa, respectively. *Ba*GGT was purified to homogeneity by his-tag affinity purification procedure with a specific activity of 90 U/mg and 5.2 fold purity. The purified enzyme had a pH and temperature optima of 10.0 and 50˚C, respectively. It exhibited broad pH stability (6.0-12.0) and was thermostable ($t_{1/2}$ of 54 min at 50˚C). The enzyme was strongly inhibited in presence of NBS, azaserine and DON. Kinetic studies carried out using G*p*NA as a donor and glycylglycine as acceptor revealed that *Ba*GGT had a K_m of 0.15 mM and 0.37 mM and V_{max} of 23.09 μmole/mg/min and 121.95 μmole/mg/min for hydrolysis and transpeptidation reactions, respectively. The enzyme displayed broad substrate specificity for various amino acids. The potential of *Ba*GGT for the synthesis of an immunomodulatory peptide, γ-D-glutamyl-L-tryptophan was studied. The peptide has been reported to have success in reducing progression of renal and lung carcinoma, attenuation of radiation-induced oral mucocitis and treating various diseases such as tuberculosis and genital viral infections and is currently under Phase II clinical trials. Hence, demand of this peptide as a drug, in pharmaceutical sectors, is envisaged in future. Reactions conditions for the enzymatic synthesis of γ-D-glutamyl-L-tryptophan were optimized. After optimization of various parameters, product yield of 25 mM with a conversion rate of 50% was achieved within 6 h of incubation using 50 mM D-glutamine as donor and 50 mM L-tryptophan as acceptor and 0.3 U/mL of *Ba*GGT in the reaction, performed at pH 10.0 and 37˚C. The product was purified to homogeneity using Dowex 1 X 2 column and its purity was confirmed by HPLC and H^1 NMR.

P 5

Engineering methanol-stable lipase YLIP9 from *Yarrowia lipolytica* MSR80 for its application in biodiesel synthesis: *In silico* studies revealed enhanced hydrophobicity, improved lid flexibility and accessibility for long-chain fatty acyl esters

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Biodiesel is an environment friendly alternative for fuels containing methyl esters of long-chain fatty acids. Enzymatic synthesis of biodiesel using lipases has significant commercial potential, however stability of the enzyme in polar solvents such as methanol is a pre-requisite. We explored the diversity of lipases from *Yarrowia lipolytica* MSR80. Among 13 lipases, ZZ-YLIP9 exhibited unusual stability in polar solvents, however, YLIP9 showed short-chain specificity. Hence, attempts were made to alter substrate specificity of YLIP9 by comparative analysis with its closest homolog YLIP2, a long-chain specific lipase. Comparison of lid sequences of YLIP2 and YLIP9 revealed that the lid of YLIP9 was 3-times more hydrophilic than that of YLIP2 with significant differences at two positions, Glu116 and Ser119. Mutations at these two positions, E116L (YLIP9L1) and S119V (YLIP9L2), increased the hydrophobicity of the lid by ~1.5-fold. Of the two mutants, YLIP9L1 showed double catalytic rate than YLIP9 with no change in substrate specificity. Thereafter, six residues were selected in the binding pocket and were introduced into pET22b-*ylip9L1* vector to develop double mutants. Of all the mutants, YLIP9L1Bp3 (E116L/E256G) showed desired property of long-chain specificity with 11-fold higher catalytic efficiency and improved thermostability along with lowered activation energy while retaining its original methanol stability. Homology modelling and MD simulations were then performed to study the catalytic triad and lid flexibility of YLIP9 and YLIP9L1Bp3 and the effect of mutations on activation energy and thermostability. YLIP9L1Bp3 was evaluated for its potential as a prospective catalyst for biodiesel using palm oil and methanol.

P 6

Epithelial to mesenchymal transition of cancer cells associated with tumor metastasis is modulated by Epstein–Barr virus latent antigens EBNA3C and EBNA1

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Epstein-Barr Virus is a ubiquitous human herpesvirus associated with lymphoid and epithelial melegnancies. Epithelial–mesenchymal transition is an important mechanism in cancer invasiveness and metastasis. Previously we had observed that cancer cells expressing Epstein–Barr virus (EBV) latent viral antigens EBV nuclear antigen EBNA3C and/ or EBNA1 showed higher motility and migration potential and had a propensity for increased metastases when tested in nude mice model. In current study we observed that both EBNA3C and EBNA1 can modulate cellular pathways critical for epithelial to mesenchymal transition of cancer cells. Our data confirms that presence of EBNA3C or EBNA1 result in upregulation of transcriptional repressor Slug and Snail, upregulation of intermediate filament of mesenchymal origin vimentin, upregulation of transcription factor TCF8/ZEB1, downregulation as well as disruption of tight junction zona occludens protein ZO-1, downregulation of cell adhesion molecule E-cadherin, and nuclear translocation of β-catenin. These cell modifications are key markers for epithelial to mesenchymal transitions. We further show that the primary tumors as well as metastasized lesions derived from EBV antigen expressing cancer cells in nude mice model display EMT markers expression pattern suggesting their greater propensity to mesenchymal transition.

P 7

Expression and functions of Cellular Metastasis Suppressor Nm23-H1 are modulated by E1 protein of Hepatitis C Virus (HCV)

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Nm23-H1 is a human metastasis suppressor protein first reported by Steeg et al in 1989. Generally, its expression in cancer cells is found to be inversely proportional to metastatic potential of the tumor. Our group supports the opinion that it can be a better approach to try and control the spread of cancer, restricting it to the primary organ only from where it can be removed by a surgery in most of the cases. Stabilizing the expression and functions of metastasis associated proteins like Nm23-H1 can be of great help in this direction. It has been reported that expression and functions of Nm23-H1 can be directly/indirectly regulated by several oncogenic viruses. Some oncogenic viral proteins have also been reported to directly interact with Nm23-H1.

Hepatitis C Virus is one such oncogenic virus that infects >170million people around the world. More than 85% patients fail to clear the virus posing a challenge for the currently available drug therapy. Added pressure comes from the fact that there is no HCV vaccine available. HCV persistently infects these patients and imparts higher risk of long-term liver disease and hepatocellular carcinoma (HCC). HCC is the most common liver cancer 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 higher incidence of metastasis, making the treatment extremely difficult. HCV has a small genome of about 9.6kb that encodes for minimum ten 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 of these viral proteins in human cell lines can help in identifying the protein/s responsible for the higher metastatis. In our studies, we found that the independent expression of one of the (recombinant) structural proteins of the HCV viz. E1 (Envelope protein 1) caused physiological changes in cells that increased their motility and aggravated their metastatic potential. The current study is an attempt to identify and investigate a relationship between HCV E1 protein mediated metastasis and cellular Nm23-H1 using human cancer cell lines as model system.

Keywords: HCV, Hepatocellular Carcinoma (HCC), Nm23-H1, metastasis.

P 8

Biophysical Characterization of archaeal cyclophilin like chaperone protein

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Chaperones are proteins that help other proteins fold correctly, and are found in all domains of life i.e prokaryotes, eukaryotes and archaea. Various comparative genomic studies have suggested that the archaeal protein folding machinery appears to be highly similar to that found in eukaryotes. In case of protein folding;slow rotation of peptide prolyl-imide bond is often the rate limiting step. Formation of prolyl-imide bond during the folding of a protein requires assistance of other proteins, termed as peptide prolylcis-trans isomerases (PPIases). Cyclophilins constitute the class of peptide prolylisomerases with a wide range of biological function like protein folding, signaling and chaperoning. Most of the cyclophilins exhibit PPIase enzymatic activity and play active role in substrate protein folding which classifies them as a category of molecular chaperones.Till date there is not very much data available in literature on archaeal cyclophillins. We aim to compare the structural and biochemical features of the cyclophilin protein from within the three domains to elucidate the features affecting their stability and enzyme activity. In the present study, we carry out in-silico analysis of the cyclophilin proteins to predict their conserved residues, sites under positive selection and compare these proteins to their bacterial and eukaryotic counterparts to predict functional divergence. We also aim to clone and express these proteins in heterologous system and study their biophysical characteristics in detail using techniques like CD and florescence. Overall we aim to understand the features contributing to the folding, stability, and dynamics of the archaealcyclophilin proteins.

P 9

Analysing archaeal short type FKBPs from Mesophilic and Halophilic organisms

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Chaperons are the proteins which assist correct folding of other proteins. Cis–trans isomerization of peptidyl-prolyl bonds is one of the rate-limiting steps in protein folding. Peptidyl prolyl cis–trans isomerases (PPIase, EC 5.2.1.8) catalyze this step and thereby accelerate protein folding. Currently known PPIases are classified into three families: Cyclophilins, FK506-binding proteins (FKBPs) and Parvulins. The PPIases of FKBP class have been studied in eukaryotes and bacteria while very little is known about archaeal FKBPs. Archaea comprise of a class of organisms which often thrive in extreme conditions like high temperature, high salt concentration and low pH etc. Maintaining a functional protein repertoire can be challenging under such conditions, and it is therefore expected that archaeal chaperones and protein folding enzymes play an important role in their viability. In archaea, (unlike bacteria and eukaryotes), two types of archaeal FKBPs have been reported; one which is a long-type FKBP (26-30 kDa) and a short-type FKBP (16-18 kDa). Structures of short type FKBPs have been reported from *Methanothermococcus thermolithotropicus* and *Methanococcus jannaschii*, both of which are thermophilic organisms. However, no short types FKBPs from mesophilic or halophilic archaea have been characterized so far.

In my present study, I am focussing on cloning, expression, and purification of short-type FKBPs from *Methanosarcina mazei* (mesophile) and *Haloferax mediterranei* (halophile). My studies aim to biochemically characterize the short-type FKBPs from these organisms, contributing to understanding of their function, folding and stability along with comparative phylogenetic studies, motif prediction and homology modelling.

P 10

Human Metastasis Suppressor NM23-H1 mediated functions are modulated by Core protein of Hepatitis C Virus (HCV)

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Liver cancer is the fifth most common cancer in men and the eighth most common in women, with an estimated 711,000 new cases worldwide in 2007. Hepatocellular carcinoma (HCC) is the most common among primary liver cancers occurring worldwide, accounting for 70 –85% of cases. HCV (hepatitis C virus) has emerged as a major causative agent of liver disease, resulting in acute and chronic infections leading to fibrosis, cirrhosis and hepatocellular carcinoma infecting nearly 3% of the population worldwide. The incidence of metastasis is an important characteristic of HCV-related HCC, which makes the cancer treatment extremely difficult. The genome of HCV is about 9.6kb that encodes for the ten known viral 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 of these proteins in human cell lines, the protein/s responsible for metastatic effect can be identified. In our studies, we found that upon expressing two of the recombinant HCV proteins (Core and E1) physiological changes in cells were observed 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 regulated 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 HCV proteins and Nm23H1 mediated metastasis in infected cells using human cancer cell lines as model system.

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

P 11

Artemisinin Targets foxm1: Novel Insight into the Tumor Suppressive Mechanism of Artemisinin

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Cancer is a multifarious malady, with a high mortality rate, despite access to improved diagnostics, screening techniques and vaccines. A rising issue in cancer treatment is the failure of cancer cells to respond to the available chemotherapeutic agents with progressive advancement of the disease. FoxM1 is a proliferation associated transcription factor known to overexpress in most human cancers and its level directly correlates with disease progression and poor prognosis. More importantly, compelling evidences from knockdown studies have proven FoxM1 to be an attractive target for therapeutic intervention in cancer treatment.

Recent years have witnessed a paramount increase in use of non-toxic natural compounds with selective anti-tumor activities and minimal side effects *in vivo*. Artemisinin, derived from *Artemesia annua L.,* is one such product with highly promising anti-tumor activity. However, the molecular mechanism of such activity remains elusive. Here, we show for the first time that Artemisinin mediates its anti-cancer effects through FoxM1 in hepatocellular carcinoma cells. Artemisinin was shown to exhibit a dose and time dependent inhibitory effect on FoxM1 and its downstream targets, including Plk-1, Aurora B Kinase and Cyclin B that are implicated in driving its oncogenic functions. We also show the suppressive impact of Artemisinin on the clonogenic ability and wound healing property of liver cancer cells. Overall, this study shed light on mechanistic aspects of the anti-cancer activity of Artemisinin and identifies a potent inhibitor of FoxM1.

P 12

A quadruple gene mutant of *Mycobacterium tuberculosis* is highly attenuated in guinea pigs and imparts protection against tuberculosis.

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Tuberculosis remains one of the top ten causes of death worldwide. BCG, the only vaccine available against tuberculosis, imparts variable protection against adult pulmonary tuberculosis. Thus, a new vaccine against tuberculosis is urgently required. The development of attenuated *M. tuberculosis* strains as vaccine candidate primarily relies upon the assumption that the vaccine strain should be antigenically similar to the disease-causing pathogen. Based on the previous studies from our laboratory, we selected four important genes namely, *mptpA*, *mptpB*, *sapM* and *bioA* for the development of a novel attenuated *M. tuberculosis* quadruple gene mutant. MptpA and MptpB are involved in host-pathogen interactions and are important for the virulence of *M. tuberculosis*. SapM is a secretory acid phosphatase, which is involved in the arrest of phagosome maturation. BioA is required for *de novo* biosynthesis of biotin, which is an essential cofactor for enzymes involved in key metabolic pathways. In this study, we generated a quadruple gene mutant of *M. tuberculosis* (MtbΔ*mmsb*) by involving the above four genes. MtbΔ*mmsb* was found to be sufficiently attenuated in guinea pigs as the mutant was cleared from the lungs and spleen by 6 weeks and 1 week, respectively. Moreover, at 4 weeks post challenge, MtbΔ*mmsb* imparted protection similar to BCG in guinea pigs, which sustained even after 12 weeks post infection. Thus, this study highlights the importance of multiple gene knockout strains of *M. tuberculosis* as safe and efficacious vaccines against TB.

P 13

Thermo-alkaliphilic HSL-like lipase of *Bacillus halodurans* C-125: characteristics and applicability in synthesis of pNP fatty acyl esters

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Lipases (Triacylglycerol hydrolases, EC 3.1.1.3) catalyze both triacylglyceride hydrolysis as well as synthesis of esters via esterification, transesterification and interesterification reactions. Thermostability and tolerance to organic solvents are essential features for carrying out biosynthetic reactions in micro-aqueous environments. *Bacillus halodurans* C-125 genome (NC_002570.2) contained a single annotated gene for lipase (Gene locus BH2248), coding for a 385 amino acid protein with a molecular mass of 42 kDa. PDB-BLAST showed structural similarity with archaeal homologs from *Pyrobaculum calidifontis, Archaeoglobus fulgidus, Sulfolobus tokodaii* and *Alicyclobacillus acidocaldarius* belonging to Hormone Sensitive Lipase (HSL)-like family. The enzyme was heterologously expressed in *E.coli* BL21 (DE3). It was optimally active at pH 9.0 and stable over pH 8.0 to 10.0. The enzyme was exceptionally thermostable with a $t_{1/2}$ of 200 min and 35 min at 90 °C and 100 °C, respectively. At 45 °C, it retained 57.3 % activity even after 96 h of incubation. Biophysical studies revealed that following thermal denaturation, the enzyme could spontaneously refold to its active conformation on lowering the temperature. Hydrolysis of triglycerides and oils indicated the preference for unsaturated fatty acids. Chemical modulation of amino acids and site directed mutagenesis confirmed its catalytic triad as S184, D280 and H310. It was also found to be extremely stable in organic solvents making it an excellent candidate for biosynthetic reactions. The enzyme was used for synthesis of pNP-laurate with an optimised conversion of 95.94 ± 0.24 %. A simple procedure for purification of the product was developed with 89.91 ± 0.33 % product recovery and 97.01 ± 0.01 % fatty acid removal.

P 14

Investigating the Structural Impact of S311C Mutation in DRD2 Receptor by Molecular Dynamics & Docking Studies

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Abnormalities in normal brain function lead to several neurological and psychiatric disorders in human. Dopamine receptors (DR) are one of the major neurotransmitter receptors that mediate the action of dopamine in brain. Dopamine receptor D2 (DRD2) is a major therapeutic target for schizophrenia and Parkinson's disease. The third inter cellular loop (ICL3) in DRD2 is essential for coupling G proteins and several signaling scaffold proteins. We have examined the deleterious effect of serine to cysteine mutation at position 311 (S311C) in the ICL3 region that is genetically well associated with diseases like schizophrenia and alcoholism. The structures of both wild and mutant DRD2 were modeled. To assess the conformational dynamics induced upon ligand binding, all-atom explicit solvent molecular dynamics (MD) simulations in membrane environment were performed. To provide information on intra-molecular arrangement of the structures, a comprehensive residue interactions network was studied. We observed a marginal effect of the mutation in dopamine binding mechanism throughout the trajectories. However, we noticed a significant structural alteration of the mutant receptor which affects Gαi/o and NEB2 binding that can be causal for malfunctioning in cAMP-dependent signaling and Ca+ homeostasis. The present study will open future avenues to design and develop selective agonist/antagonist that can be employed in the treatment of DRD2 implicated neurological disorders.

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P 15

OsTLP, an F-box containing TUBBY protein in rice, is involved in light-regulated development and stress signalling pathway.

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The TUBBY genes were identified in mammals as a small group of 4-5 members based on a mutation in mice that caused obesity on maturation. In animals, they also regulate insulin pathway, retinal maintenance, neuronal development, etc. These class of proteins, harboring a C-terminal TUBBY domain, are bi-partite transcription factors that translocate to the nucleus from the plasma membrane on perceiving certain signals and have both DNA binding and transcriptional activation properties. In plants, these C-terminal TUBBY domain containing proteins are invariably coupled with a conserved N-terminal F-box domain and are thus called as TLPs (TUBBY LIKE PROTEINS). Both *Arabidopsis* and rice have nearly 14 *TLPs* that regulate diverse functions such as abiotic stress signaling, hormone signaling, plant-pathogen interactions and so on. Our lab identified a few F-box proteins in rice that are regulated under different light conditions including an *OsTLP*. This *OsTLP* has been further characterized and found to be up-regulated under blue light and is also under circadian control as its expression dips at midnight. It played role in light-regulated hypocotyl growth in *Arabidopsis*. The gene also showed up-regulation under salt and drought stress and in ovary tissues. The protein harbours a canonical F-box domain which interacted with OsSKPs showing that it is a component of a functional SCF-type E3 ligase. The protein was found to be localized to the plasma membrane that shifted to the nucleus under stress conditions. The over-expression lines in *Arabidopsis* showed better over-all growth and involvement of the gene in various abiotic stresses. The data thus far indicate involvement of the *OsTLP* in abiotic stress signalling and contribution towards overall growth and development.

P 16

Rice F-box protein, *OsFBK,* regulates circadian-clock controlled development and photoperiodic flowering pathway

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The F-box proteins (FBPs) are components of SCF ubiquitin-ligase complexes and are one of the largest multi-gene super-family in plants containing a conserved N-terminal F-box motif that binds to the SKPs, a component of the SCF, and a variable C-terminal protein interaction domain that selectively binds target proteins for turn-over by the 26S proteasome. There are over 900 FBPs in Arabidopsis and rice that are involved in all the facets of plant biology such as stress signalling, photomorphogenesis, hormone signaling, flower development, self incompatibility, biological rhythms and defence responses. Our lab identified a few F-box proteins in rice that are regulated under abiotic stresses, one of which was *OsFBK*. The gene was found to be up-regulated under drought, heat and salt stresses and also in Y-leaf and flag- leaf. The protein harbours a canonical F-box domain which interacted with OsSKPs demonstrating that it is a component of a functional SCF-type E3 ligase. The OsFBK protein showed formation of homodimers and heterodimers with its paralogs in yeast two-hybrid assays. Also screening of heat stress rice library showed interaction of OsFBK with some proteins known to play roles in heat tolerance. The protein was found to localize in the nucleus as well as cytosol. Over-expression lines in *Arabidopsis* showed role of this gene in heat response and other abiotic stresses. Also, the over-expression lines flowered earlier. The above results indicate involvement of *OsFBK* in abiotic stress signalling and photoperiodic flowering.

P 17

Functional Characterization of an *OsbZIP* gene in rice for its possible role in light signalling

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Plant growth, development and response to environmental stimuli are determined by programmed expression of its genes which are regulated by transcription factors. These transcription factors are usually members of multigene families. One of the largest and most diverse transcription factor families in eukaryotes is the basic leucine zipper (bZIP) transcription factor family. Over 120 bZIP transcription factor genes have been identified in different plants, out of which 89 have been identified from rice and 67 from *Arabidopsis*. Phylogenetic analysis of the bZIP transcription factors across plant species has predicted a majority of the rice bZIP transcription factors to be orthologs of *Arabidopsis* bZIP transcription factors. One of the most well characterized bZIP transcription factor in *Arabidopsis*, HY5, has been predicted to have three orthologs in rice. At least two of these *AtHY5* orthologs have been shown to functionally complement the *hy5* mutant in *Arabidopsis* with respect to its photomorphogenic development. Expression levels of one of these orthologs of *HY5* has been checked in different developmental stages as well as in different tissues of rice by real time PCR. Analysis of its expression in 2-10 day old light as well as dark grown seedlings has been done and these results indicate difference in expression patterns of both these orthologs in rice. Transgenic analysis in both rice as well as *Arabidopsis,* however, points towards their functional similarity.

P 18

Genome-Wide Survey and Expression Analysis of Genes Involved in RFOs synthesis during Development and Thermal Stress in Wheat

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The raffinose family oligosaccharides (RFOs) are synthesized by addition of alpha 1,6 galactosyl to sucrose. Increase in levels of RFOs has been associated with the thermal stress such as heat and cold stress. The availability of wheat survey sequence and transcriptome data open avenues to comprehend the genes involved in RFOs synthesis during thermal stress. By searching available survey sequence and flcDNA sequences from IWGSC, we identified genes involved in synthesis of RFOs eg. Galactinol Synthase (GolS; EC 2.4.1.82), Raffinose Synthase (RS; EC 2.4.1.82), Stachyose Synthase (STS; EC 2.4.1.67), and Sucrose Synthase (SUS; EC 2.4.1.13). Extensive sequence analysis has been done of these putative RFOs encoding genes to elucidate their structure, chromosomal location and Phylogenetic relationships. Their expression profiling by RNA Seq data analysis, revealed RFOs encoding genes showing specific and co-expression at different stages of wheat plant and in response to thermal stress. The expression analysis of differentially expressing genes were complimented by Real Time PCR analysis. This study implicates the role of RFOs during thermal stress in higher plants.

P 19

Unraveling the Genome Content of Short arm of Chromosome 2A of Wheat using BAC End Sequencing

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Wheat (*Triticum aestivum*) is an allohexaploid by genetic constitution. It has one of the largest genome of 1700 Mbp which is approximately 40-fold larger than rice. As part of International Consortium on Wheat Genome Sequencing, India is responsible for sequencing of chromosome 2A BAC ends of wheat. Work on sequencing in India started in 2011 with two BAC libraries obtained from Institute of Experimental Botany (Czech Republic) for chromosome 2A of wheat, *Triticum aestivum* cv. Chinese Spring. 55,648 BAC clones has been completed from both the ends generating approximately 1,11,296 BES sequences. In total, nearly 66.7 Mbp of wheat genomic sequence having an average read length of ~600bp per BAC end has been generated. These BES were mined for repeat sequences using REPEATMASKER revealing approximately 81.9% repetitive elements. Thereafter these sequences were subject to BLAST analyses with different Databases with appropriate E-value (range 1E-10 - 1E-100) and Bit Score (>150). Blast analysis lead to the conclusion that a sizeable number among the significant hits obtained represent the genic region but a vast majority of them represent repeat elements. Protein coding genes which are represented in blast hit are from the diverse biological processes ranging metabolic pathways to signaling pathways. In addition to the above analysis, the BES generated data will help in physical and genetic mapping of wheat genome.

P 20

Exploring the Biological Function of Rice Tetraspanin Family Proteins

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Tetraspanins (TET) represents a large family of evolutionary conserved integral membrane proteins with conserved structure (four transmembrane domains, two extracellular loops of unequal sizes, short cytoplasmic tails and highly conserved cysteines and 'GCCK' motif). TET proteins known to function as 'facilitators' of protein interaction and performs various biological functions in diverse organisms. Few studies in *Arabidopsis* have implicated TET in regulation of developmental process, such as embryo development, leaf morphogenesis, root development, floral organ development and reproductive process. Current study was designed to elucidate the role of rice tetraspanins in various tissues and under abiotic stresses. Rice genome exploration revealed the existence of 15 tetraspanin genes. We performed comprehensive sequence analysis, genomic organization and phylogenetic studies on these rice tetraspanin genes. Further, we prepared a comprehensive expression atlas of *TET* in several rice tissues collected at different stages of development and rice seedlings exposed to plethora of abiotic stresses and in response to exogenous applications of phytohormones. Several *TET* exhibited significant differential expression in various tissues and variable stress conditions. Transient subcellular localization of selected tetraspanins in tobacco epidermal cells found that OsTETs were localized to plasma membrane. We generated transgenic rice plants for overexpression and downregulation of *OsTET5* for its detailed functional characterization. Preliminary phenotypic analyses of these rice transgenic lines suggest role of *OsTET5* in drought tolerance. The present study has provided valuable insights into the possible biological function of TET in regulating development and response to abiotic stress.

P 21

Histone acetyltransferase HAT4 modulates navigation across G2/M and re-entry into G1 in Leishmania donovani

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Histones undergo various post-translational modifications, thus affecting different biological processes like DNA replication, repair, and transcription. Histone acetyltransferases mediate the acetylation of specific lysine (and arginine) residues, thus loosening DNA-histone contacts and making chromatin more accessible to the proteins that mediate the various DNA-related processes. In the present study genomic knockout was created to characterize the functional importance of histone acetyltransferase HAT4 in the protozoan parasite *Leishmania donovani*. We found that HAT4 was not essential to cell survival. However, HAT4-nulls exhibited decreased cell viability and cell cycle defects, with a prolonged G2/M phase. Survival of HAT4-null parasites in macrophages was also significantly lower. Results of DNA microarray analysis showed that HAT4 is not a major player in regulating global gene expression in *Leishmania*. However, *cdc20* was among the small group of genes whose expression was compromised in HAT4-nulls. Ectopic expression of LdCdc20 in HAT4-nulls alleviated the patterns of growth and cell cycle defects displayed by HAT4-nulls, with cells now moving through G2/M phase and re-entering G1 phase in timely manner. Ectopic expression of LdCdc20 in HAT4-nulls also improved survival of the parasites within macrophages, implying that G2/M defects were responsible for poor survival of HAT4-nulls within host cells also. These results are the first direct demonstration of a role for Cdc20 in regulating trypanosomatid G2/M events, and lay the foundation for further studies examining G2/M events in trypanosomatids, particularly in *Leishmania*.

P 22

Therapeutic Efficacy of Doxycycline Loaded Liposomes against *Plasmodium falciparum* in Culture and *P. berghei* Infection in Mice Model.

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Emergence of drug resistant *Plasmodium falciparum* malaria parasite is impeding the therapeutic efficacy of existing antimalarial drugs in clinical use. Therefore, there is an urgent need to develop an efficient drug delivery system to circumvent drug resistance and improve the efficacy of existing antimalarials. The antibacterial drug Doxycycline has been shown to exhibit antimalarial properties. Here, we developed a liposome-based drug delivery of doxycycline and evaluated its antimalarial activity in different lipid formulations against blood stages of *P. falciparum* (3D7) in culture and established *P. berghei* NK-65 infection in murine model. The developed liposomal formulations were found to exhibit superior efficacy than a comparable dose of free doxycycline. The enhancement of antimalarial activity was dependent on the liposomal lipid composition and preferential intracellular uptake by infected red blood cells (RBCs). The enhanced antiplasmodial activity of doxycycline with a 50% inhibitory concentration (IC_{50}) in stearylamine (SA) liposome (IC_{50} 0.36 μM) and SPC:Chol-liposome (IC_{50} 0.85 μM) was markedly superior to that of free doxycycline (IC_{50} 14 μM), with minimal toxicity to erythrocytes. In addition, Polyethylene glycol (DSPE-mPEG-2000) coated liposomes loaded with doxycycline resulted in enhanced killing of parasites in blood circulation with improved survival in mice relative to the free drug. This study clearly demonstrates that doxycycline delivery in liposomal system has chemotherapeutic potential against human malaria infections at lower dosages.

P 23

MTG3, a GTPase that regulates mitochondrial translation in *Saccharomyces cerevisiae*

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Mitochondria are vital organelles which produce almost all energy required for cellular functions. For the optimum functioning of mitochondrial protein synthesis machinery, several auxiliary factors like GTPases, RNA helicases and ribosomal subunits are required to support the formation of a stable ribosomal complex. Unprocessed pre-rRNA molecules translocate from cytoplasm to mitochondria and assemble to form a stable ribosome complex. Mutations in these factors lead to improper ribosome biogenesis which consequently slows down all translation in the organelle. Approximately 25% of mitochondrial proteome is involved in its own establishment, replication, and maintenance. Baker's yeast *Saccharomyces Cerevisiae* provides a useful model system for studying these mutations as it is capable of carrying out cellular metabolism without intact mitochondrial function, via fermentation. Our laboratory is focused on studying effects of mutations in *MTG3* which is one of the genes involved in mitochondrial ribosome biogenesis. MTG3p is a GTPase which belongs to YawG/YIqF family of circularly permuted GTPases. MTG3p associates with both the small and large ribosomal subunits in a salt-dependent manner. Deletion of *MTG3* causes a defect in utilization of glycerol as the sole carbon source and aberrant processing of 15S rRNA indicating a role in small subunit biogenesis. Moreover, conditional alleles of MTG3 give an altered subunit ratio, with a reduction in 54S subunit level at the non-permissive temperature.

Keywords: Mitochondria, *Mtg3*, GTPase, *Saccharomyces cerevisiae,* ribosome biogenesis

P 24

Virtual Screening, pharmacophore development and structure based similarity search to identify inhibitors against IdeR, a transcription factor of *Mycobacterium tuberculosis.*

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IdeR, an essential gene of *Mycobacterium tuberculosis,* is an attractive drug target as its conditional knockout displayed attenuated growth phenotype *in vitro* and *in vivo*. To the best of our knowledge, no inhibitors of IdeR are identified till date. We carried out virtual screening of NCI database against the IdeR DNA binding domain followed by inhibition studies using EMSA. 9 compounds exhibited potent inhibition with NSC 281033 (I-20) and NSC 12453 (I-42) exhibiting IC_{50} values of 2 μg/ml and 1 μg/ml, respectively. We then attempted to optimize the leads firstly by structure based similarity search resulting in a class of inhibitors based on I-42 containing benzene sulfonic acid, 4-hydroxy-3-[(2-hydroxy-1-naphthalenyl) azo] scaffold with 4 molecules exhibiting $IC_{50} \leq$ 10 μg/ml. Secondly, optimization included development of energy based pharmacophore and screening of ZINC database followed by docking studies, yielding a molecule with IC_{50} of 60 μg/ml. More importantly, a five-point pharmacophore model provided insight into the features essential for IdeR inhibition. Five molecules with promising IC_{50} values also inhibited *M. tuberculosis* growth in broth culture with MIC_{90} ranging from 20 μg/ml to 100 μg/ml and negligible cytotoxicity in various cell lines. We believe our work opens up avenues for further optimization studies.

P 25

High-level soluble expression of recombinant hTNF-α in *E. coli*

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Tumor Necrosis Factor-α (TNF-α) is a therapeutically important protein involved in the treatment of a wide variety of melanomas and soft tissue sarcomas. The gene for hTNF- is of 474 bases encoding a protein of 17.5 kDa. The soluble expression yield of this commercially important protein is very low due to formation of inclusion bodies in heterologous systems.

In the present study we have utilized the SUMO fusion technology for the high-level soluble expression of recombinant hTNF-α in *E. coli*. SUMO is a highly soluble protein that exerts a chaperone-like effect on its fusion partner thereby promoting its soluble expression with improved stability. The hTNF-α gene was cloned under T7 promoter and N-terminus SUMO fusion tag. The 6X-His tag was also introduced at the N-terminus to aid in its downstream processing. Shake-flask expression studies revealed that terrific broth led to maximum SUMO-TNF-α (35KDa) production with almost 95% solubility at 37°C. The protein was purified to near homogeneity using two-stage Ni-NTA chromatography with an additional SUMO-protease *in vitro* cleavage step. The cleavage of SUMO fusion protein was also done via co-expression of yeast SUMO protease *in vivo*. The native protein obtained after *in vivo* cleavage was recovered using sonication followed by ion exchange chromatography. The native TNF-α protein was found to be biologically active and could successfully cause apoptosis in TF1 cell lines. The bioprocess optimization of SUMO-TNF-α was also carried out where 1.2 g/L of protein was obtained in fed-batch fermentation at a cell biomass of 65 g/L. The scale-up studies are in progress to improve its expression yields to develop a cost effective production strategy.

P 26

Multiple regulatory elements control activity of Toxin-Antitoxin loci in *Mycobacterium tuberculosis*

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Toxin Antitoxin loci are two or three component system that are ubiquitous in bacterial genomes. These loci encode for a stable toxin and an unstable antitoxin. The antitoxin binds to the toxin and neutralizes the killing activity of the cognate toxin. TA loci have been identified in several bacterial genomes and are postulated to play important roles in pathogenesis, persistence and drug tolerance mechanisms.

Mycobacterium tuberculosis, the causative agent of the deadly disease tuberculosis, harbors 79 TA loci in its genome. In contrast, the non-pathogenic relative *Mycobacterium smegmatis* has only two complete TA loci in its genome. This is suggestive of the plausible role of the Ta loci in mycobacterial pathogenesis and persistence.

The HigBA TA locus of Mtb has been shown to be up-regulated in response to chemical and environmental stress in Mtb. This locus encodes Rv1955, the HigB toxin, Rv1956, the HigA antitoxin and Rv1957, a molecular chaperone involved in folding of the HigA antitoxin. Besides, an ORF upstream of Rv1955 has also been reported.

We have identified two promoters upstream of the HigBA locus that direct transcription and expression of the TA genes. These promoters show differential activity and regulation by the downstream toxin and antitoxin gene product. Further, the region also contains an enhancer element that up-regulates the activity of both the promoters. The enhancer element found to be active with the heterologous promoters of varying promoter strength also either upstream or downstream of those promoters. The product of upstream ORF of Rv1955 is not essential for promoter activity. This is the first study demonstrating presence of multiple promoters and diverse regulatory elements for a TA locus.

P 27

Screening of small molecule libraries to identify potential inhibitors against *Plasmodium falciparum* Dihydrofolate reductase and evaluation of their anti-malarial therapeutic efficacy in murine model

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Malaria still remains one of the most devastating infectious disease caused by protozoan parasites of the genus *Plasmodium*. Out of all *Plasmodium* species infecting humans, *Plasmodium falciparum* is considered as the most deadly human malaria parasite. Globally, the disease infects around 214 million people causing around 438000 deaths. Combating malaria is a challenging task due to the emergence of resistance in *Plasmodium falciparum* towards the commonly used antimalarial drugs. Thus, the need of the hour is to either find novel drugs or new combined therapy using the available drugs. *Plasmodium* Dihydrofolate reductase (PF_DHFR), one of the key enzyme in the folate biosynthesis pathway of the malarial parasite is clinically relevant and validated drug. In the present study three-dimensional model of PF_DHFR was used for virtual-screening of small molecule databases from NCI, USA. Identified top hits were then tested *in vitro* against the growth of *Plasmodium falciparum* (3D7) in culture. PF_DHFR was cloned, expressed and purified and top hits were evaluated for their inhibitory action towards the enzymatic activity of PF_DHFR spectrophotometrically. Cyto-and hemo-toxicities of the lead compounds were assessed *ex vivo*. Finally their therapeutic efficacies towards treatment of malaria were evaluated in *Plasmodium berghei* infected murine model of malaria. Top 127 compounds identified through virtual screening of NCI libraries against PF_DHFR were assessed *in vitro* against the growth of *Plasmodium falciparum* (3D7) in culture. 29 compounds out of 127 have been found to inhibit growth of the parasite at a dose lesser than 5μg/ml. The lead inhibitors were further investigated against recombinantly expressed PF_DHFR spectrophotometrically and found to show low μM IC_{50} values. Top 3 lead compounds (BCHM 3, BCHM 9, BCHM 14) having IC_{50} values in nano gram range against *Plasmodium falciparum* were tested for cytotoxicity in liver cancer cell line (HepG2) and showed acceptable cellular tolerance at higher doses (up to 50μg/ml) and insignificant hemo-toxicities against healthy human RBCs. These three lead molecules were examined for their therapeutic efficacy against murine model of malaria and were found to be effective in suppressing the blood parasite load. The present study put forward some of the novel potential inhibitors of malarial parasite which may find effective means in chemotherapy of this deadly infectious disease.

P 28

Host mediated pathogen gene silencing: Developing a strategy for engineering resistance against necrotrophic pathogen Sclerotinia sclerotiorum in Brassica juncea (Indian mustard)

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RNA interference is a new and attractive approach for regulating and modifying gene expression and thus understanding the gene function. This approach has also been used to develop pathogen/pest resistant transgenic plants that conditionally or constitutively express a hairpin RNAi against a vital pathogen or pest gene. I tried to target the fungus Sclerotinia sclerotiorum *by* developing an RNAi construct that contains a fragment of different essential genes: Chitin synthase (CHS), Oxaloacetate acetylhydrolase1 (OAH1), superoxide dismutase1 (SOD1), Sporulation-specific mitogen-activated protein kinase1 (SMK1), PACC-like gene (PAC1), Lanosterol 14 α-demethylase (Cyp51) under 35S constitutive promoter.

CHS is an enzyme which catalyzes the last step of chitin pathway. Chitin is an important compound in all fungal cell wall. OAH1 produces oxalate which it is toxic and a key factor in fungal pathogenesis. SOD1 destroys radicals which are normally produced within the plant cells and which are toxic to biological systems like fungus. SMK1 functions to regulate sclerotial development through interconnections with pH-dependent and cAMP- dependent pathways. PACC genes encode the major transcriptional regulators of several pH-responsive pathways in fungus. Cyp51 is an enzyme which is involved in the ergosterol biosynthesis pathway. The ergosterol biosynthesis pathway is required for generation of a major constituent of the fungal plasma membrane, ergosterol

To have an easy and fast way to check if my constructs produce functional siRNA in planta I cloned an RNAi against a reporter gene (GUS) along with my target genes to achieve this aim. GUS gene is not present in the most higher plants and so by inserting a fragment along with my gene and followed by inoculating with *A. tumefaciens* and then histochemical and fluorometric study of this transgenic plant would be done, thereafter I will know that my construct successfully work in plant or not.

P 29

Concatenated Long Period Gratings separated by Single Mode Fiber as Refractive Index Sensor

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This paper presents the modeling and characterization of proposed sensor of two concatenated Long Period Gratings (LPG) with inter grating spacing of single mode fiber for sensing of refractive index. Optical fiber sensor has attracted a lot of attention in bio sensing and chemical sensing because of their advantages like small size, cost effective and immunity to electromagnetic interference. In last decade, refractive index sensor has been intensively studied and various configurations have been proposed such as LPG, fiber bragg grating, polarization dependent fiber, photonic crystal fiber and Surface Plasmon based sensor [1-3]. However, LPG fabricated in a standard telecommunication fiber by UV exposure exhibits undesirable changes in spectral response and is fragile due to its high bending sensitivity. In this paper, we propose a highly sensitivity refractive index sensor using SMF (Single Mode Fiber) as sensing region between two concatenated LPG without disturbing the LPG section. It is shown that the transmission characteristics of the proposed sensor can be controlled by optimize the physical parameters like length of inter grating spacing, period of LPGs and cladding radius of inter grating spacing. The proposed sensor configuration can be used as wavelength interrogation and single wavelength interrogation (power interrogation). The sensor shows maximum sensitivity at LP08 mode and cladding radius of IGS 58 μm. The refractive index sensitivity of the sensor with an interaction length of 15.27cm is ~ 1000 nm/RIU in the range of 1.330 to 1.350.

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P 30

Study of Asymmetric Dielectric-Metal-Dielectric Waveguide and its Applications

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The dielectric-metal-dielectric plasmonic waveguide structures find applications in integrated optic and fiber polarizers [1] and sensors [2]. Surface plasmon waves guided by thin metal films have been intensively studied over the last two decades [3]. However, most studies have been confined to relatively low index dielectrics. With growing interest in silicon photonics and other semiconductors dielectric of relatively higher dielectric constant we carried out a detailed study of the modes supported by a gold film (ε_m) between dielectrics of relatively higher dielectric constant ($n_1$and n_3). The study clearly shows that two modes, i.e. the "antisymmetric" (a_b) short range and "symmetric" (s_b) long range bound modes can exist only when the contrast between the indices is low with the antisymmetric leaky (a_l) mode and symmetric leaky (s_l) mode. Further, it is only in this region that attenuation and effective indices of the modes can be tuned by change of metal film thickness. Some early studies on such thin metal film plasmonic waveguides have also included "leaky modes" in the bound mode domain as solution of the boundary value problem [3]. For completeness we also include such modes in our study, although they are not important for guided wave structures. Our results show that the long range surface plasmon mode exists only when the condition, $\frac{\varepsilon_h - \varepsilon_l}{\varepsilon_h \varepsilon_l} < \frac{1}{|\varepsilon_m|}$ is satisfied, where ε_h is high dielectric constant, ε_l is low dielectric constant and ε_m is the metal dielectric constant. As this condition is not dependent on the metal thickness it will only state whether the symmetric bound mode can exist or not, but may not define the actual cut-off.

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P 31

Impact of Graded-Channel (GC) Design and Gate Dielectric Engineering on Device Performance of Tri-Gate MOSFET for Low Power/Low Voltage Applications

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The demand for smaller and faster devices with low standby power, low operating power and high performance such as smartphones, laptops etc. has led to the miniaturization of devices over the last few decades and has led to the evolution of Integrated Circuits. However, downscaling of devices leads to various unwanted effects called short channel effects (SCEs) such as threshold voltage lowering, drain Induced Barrier Lowering (DIBL), hot carrier effects (HCEs) etc. To deal with SCEs, Tri gate MOSFETs have been recognized as promising candidates as they offer higher packing density, better short channel immunity and high switching speed. In a Tri gate MOSFET, the channel is surrounded by three gates on three surfaces, thereby providing better electrostatic control over the channel. This leads to effective suppression of "off-state" current and significantly enhanced "on" current.

In order to address the issues listed above, graded channel (GC) design has also been proposed. In the graded channel profile, a high doping concentration near source end improves threshold voltage roll-off and suppresses DIBL while a low doped region near drain end reduces the electric field, thereby, leading to a reduction in impact ionization and reduced HCEs. Furthermore, scaling down of device dimensions also demands an accompanied reduction in oxide thickness. However, continuous scaling of the oxide layer thickness increases the possibility of direct tunneling of carriers and also leads to oxide breakdown. Therefore, to overcome these effects and to improve gate controllability, high-k gate dielectric materials are used along with SiO_2 layer which results in increased physical thickness and reduced effective oxide thickness.

Thus, in order to address the aforementioned critical issues, we have proposed an analytical model for Graded-Channel Gate-Stack Tri-Gate (GCGSTG) in the present work to examine the effectiveness of GC and GS designs in enhancing the device performance of Tri gate MOSFETs. The device characteristics have been critically examined over a wide range of parameters and bias conditions and it has been demonstrated that GCGSTG provides better short channel immunity, hot carrier reliability and enhanced device performance as compared to graded channel (GC) and uniformly doped (UD) devices.

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Study of Ferroelectric based Junctionless devices for Ultra low Voltage/Power Applications

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With the ever increasing demand of cost effective and reliable electronic devices such as laptops, mobile phones, devices used in the field of medicine etc, there is a need for integration of large number of devices on a single chip. This has led to remarkable advancement in microelectronic industry due to continuous miniaturization of CMOS based devices. However, due to scaling of device dimensions the device performance degrades significantly leading to various critical issues such as increased leakage currents, overheating, poor switching time along with fabrication related issues etc. To address these issues, a lot of interest has been put into various emerging technologies such as multiple gate geometries, Junctionless transistors, TFETs, Ferroelectric Field Effect transistors (FeFETs) etc. Various studies have reported Junctionless transistors as a potential candidate for future CMOS industry due to numerous advantages offered such as better fabrication feasibility and bulk conduction mechanism as compared to inversion mode transistors. Also, Ferroelectric FETs have been in the spotlight for both digital logic and memory applications due to their compatibility with current CMOS technology along with their ability to achieve sub-60mV/dec subthreshold swing leading to faster energy efficient transitions.

In present work advantages of both Junctionless transistors and FeFETs have been integrated along with double gate geometry i.e. Double Gate Ferroelectric Junctionless Transistor has been studied extensively. An analytical model has been developed for the device considering Landau's Devonshire theory and parabolic potential approximation. Further, ferroelectric material silicon doped hafnium oxide (Si:HfO_2) has been considered as the gate insulator since, it can be scaled according to the current technology nodes and is found to exhibit good interface properties with silicon. The accuracy of the proposed model has been validated by comparing the analytical results with simulated results obtained from TCAD Silvaco ATLAS simulator. The results obtained show significant improvement in device performance in terms of significant voltage amplification, sub-60mV/dec point subthreshold slope values, reduced subthreshold current leading to improved I_{on}/I_{off} ratio, thereby signifying suitability of this device for ultra low voltage/power, energy efficient digital/analog applications.

P 33

Effect of cadmium content on structural and optical properties of ZnCdO thin films: before and after annealing

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In this work, we have investigated the effect of cadmium content x on structural and optical properties of ZnCdO (CZO) using sol-gel spin coating method. Nanocrystalline CZO films were deposited on glass substrates at room temperature and later thermally annealed at 500 °C in order to study changes in crystallinity of films. High resolution X-ray diffraction (HRXRD) studies were performed to detect and analyze phase separation in films. A gradual transition from wurtzite ZnO phase for $x < 0.05$, to a mixed phase comprising both wurtzite ZnO and cubic CdO phase co-existing simultaneously for higher values of Cd content x, was observed. Optical absorbance curves exhibited red shift with respect to an increase in x, while transmittance measurements revealed steep curves for $x \leq 0.05$, indicating the direct nature of CZO films. Maximum Cd content of x=0.3 in as-deposited films induced lowering of band gap from 3.29 eV to 2.85 eV. Proper band gap engineering of such CZO films can lead to their application in formation of heterostructures with ZnO films to produce efficient thin film solar cells.

P 34

Polarization Compensation in InGaN/GaN MQW Solar Cells: Effect of Polarization-Matched InGaN Interlayers

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Polarization-matched InGaN interlayers are proposed to improve the photovoltaic properties of InGaN/GaN multiple quantum well solar cells (MQWSCs). Properties of four MQWSC structures have been simulated and analysed using APSYS. The phenomenon of polarization compensation using a positively doped polarization matched $In_{0.1}Ga_{0.9}N$ layer at the last quantum well and p-GaN hetero-interface has been employed to improve the photovoltaic properties of the MQWSC.An increase in short circuit current density is observed, which is attributed to the decrease in the effective polarization across the absorber region. The optimized MQWSC with PCI and InGaN barriers shows best results with short circuit current density (J_{sc}) of 0.935 mA/cm^2 and open circuit voltage (V_{oc}) of 2.05 V. The major improvement is reflected in the cell's efficiency with an overall increase of 58 % over conventional MQWSC.

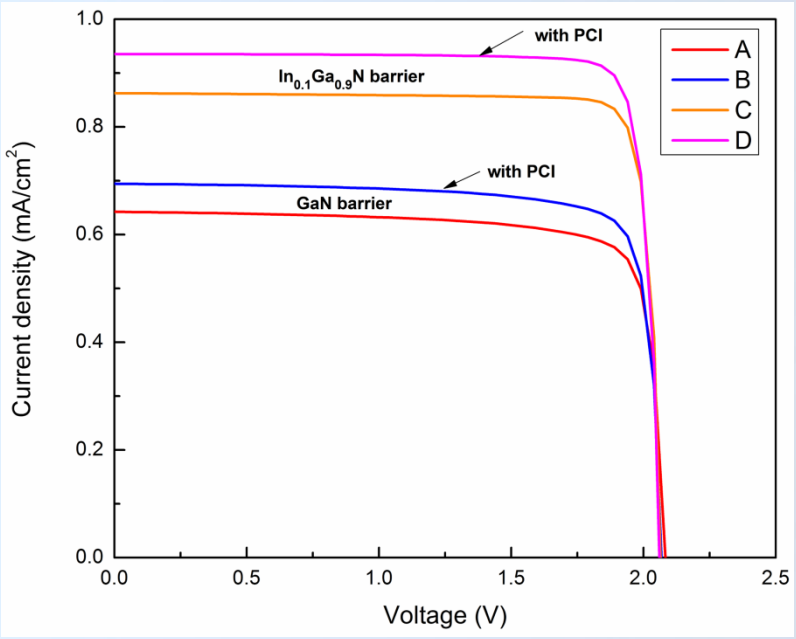

Fig. 1: J-V curves for cell A, B, C and D under 1 sun AM1.5G illumination

P 35

Recognition of facial images using Hopfield neural network

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Hopfield neural network (HNN) [1, 2], a type of the recurrent neural network (RNN) has been used for solving optimization problems and pattern retrieval. This network behaves as a content addressable memory i.e. it can retrieve a stored pattern even if a subset of the stored pattern is given. In this paper, we present an approach to use HNN for machine recognition of human faces. The approach presented here uses Otsu's method [3, 4] to transform grey scale facial images into binary facial images and Hebb rule [5, 6] to store binary faces in the weight matrix of the network. The network is then tested with distorted and occluded facial images; the network is allowed to evolve asynchronously to a stable state. We then calculate the hamming distance between the original facial image (undistorted) and the stable facial image, a hamming distance of zero indicates successful retrieval. Our results show 100% retrieval for grey scale facial images of 60×60 pixel size and 10×10 pixel size for up to 30% and 11% distortion respectively. This suggests that HNN burned on an integrated or neuromorphic chip [7] connected with a camera can be used for face based identification and security applications for visually challenged/ sightless persons. Our future work involves the construction of chip and testing the network for real time applications.

Keywords: Asynchronous retrieval, auto associative memory, face recognition, artificial, Hopfield neural network.

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pH and Bio Sensor using Semiconductor Properties

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Silicon technology is one of the most promising for sensor development. Moreover, device simulation tools, originally introduced to design electronic circuits, can be adapted to design silicon-based chemical-sensor and biosensor. In this order, electrolyte region has been described by modifying properties of intrinsic semiconductor material as the intrinsic semiconductor has similarity with the electrolyte. Ionic solution (electrolyte) contains mobile ions whereas the intrinsic semiconductor material contains thermally generated mobile carriers (holes and electrons). Therefore, these electrons and holes represent the mobile ions of the solution with dielectric constant of the semiconductor material to be 78.5 (which is the dielectric constant of water). The molar concentration of the electrolyte solution was specified by the density of states N_C and N_V according to the following approach. The dissociation of H_2O is $H_2O = H^+ + OH^-$ at the chemical equilibrium, therefore, the mass action law of water i.e., ions product of water is defined by $K_w = [H^+]\,[OH^-]$ [23]. In pure water at 25 ºC:

$[H^+] = [OH^-] = 1.0 \times 10^{-7}$ mol/L

$K_w = (1.0 \times 10^{-7}\ \text{mol/L})(1.0 \times 10^{-7}\ \text{mol/L}) = 1.0 \times 10^{-14}\ \text{mol}^2/\text{L}^2$

The mass action law of water is similar to the mass action law in the intrinsic semiconductor. The mass action law, stating that under thermal equilibrium the product of the free hole concentration p and the free electron n is equal to the square of the intrinsic carrier concentration n_i. If n = p, then

$$np = N_C N_V e^{-\frac{E_G}{kT}} = n_i^2 \qquad \text{where, } N_C = 2\left[\frac{2\pi m_e^* kT}{h^2}\right]^{\frac{3}{2}}, \quad N_V = 2\left[\frac{2\pi m_h^* kT}{h^2}\right]^{\frac{3}{2}}$$

The ionic charge concentration in the electrolyte which is equal to the density of state of intrinsic semiconductor material has been calculated below formula.

$$n_0 = N_V = N_C = N_{avo} i_0 \times 10^{-3}$$

Where, i_0 is the ion molar concentration (1M =1000 mol/m^3) in the bulk of the solution. As per the definition, pH = - log [ion concentration in moles per liter] = -log [i_0]

$$pH = -\log\left(\frac{N_V \times 10^3}{N_{avo}}\right) \text{and } pOH = -\log\left(\frac{N_C \times 10^3}{N_{avo}}\right)$$

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Optical Characterization of P3HT: Graphene Composite photovoltaic Application

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In this study, graphene nanosheets were incorporated in organic polymer P3HT (Poly (3 hexylthiophene-2, 5-diyl) for photovoltaic application. The optical absorbance and photoluminescence were performed using Shimadzu spectrophotometer (UV-2450) and spectroflurophotometer (RF 5301 PC) respectively. P3HT film showed absorption peak at 517 nm. It was observed that after adding graphene, there was little increment in absorbance, while photoluminescence was observed to be quenched. Increase in absorbance help in generation of more number of excitons while the quenching reveals that charge recombination decreases with addition of graphene. Thus the addition of graphene in P3HT increases photovoltaic efficiency.

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Multilayer SOI spot-size converter for coupling between nanowire and fiber

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We have presented a new design for a spot-size converter (SSC) which helps to drastically improve the coupling between an optical fiber and a Silicon nanowire (NW) in optical communication. The design of the SSC consists of evanescently coupled NW and an array of Si waveguides. Due to the expanded transversal dimensions of the array, its optical mode has much higher spot-size than the NW. At the coupling length calculated from the effective indices of the first two supermodes of the SSC, power inputted from the NW gets transferred to the array. When the fiber is butt-coupled to the end of this SSC, a high coupling efficiency is obtained. We have used an in-house algorithm of the Finite Element Method to carry out the modal analysis of the NW, array and SSC. Another FORTRAN code for the Least Squares boundary residual (LSBR) method is used to calculate the power at the junctions. When we couple a NW directly to the fiber we obtain a coupling efficiency of 2% whereas when we butt-couple the fiber to the SSC the efficiency is increased to more than 87%. This new design of SSC is taper-free, can be fabricated using CMOS compatible technology and has short-device length and relaxed alignment tolerances.

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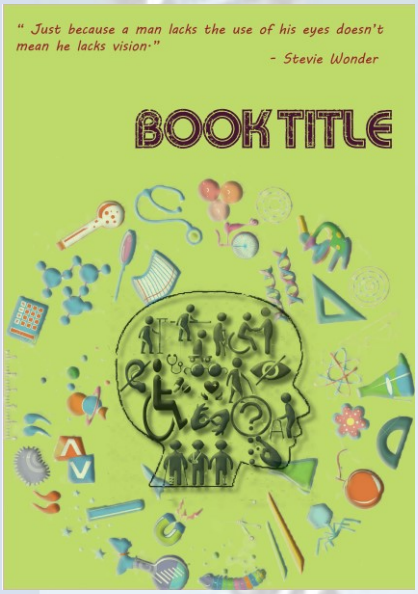

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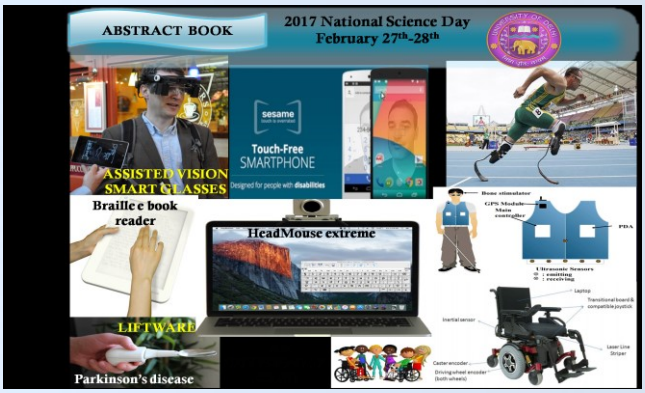

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South Campus
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When the University of Delhi expanded in many directions to keep pace with a rapidly growing city, South Campus was established in 1973 to facilitate access for South Delhi residents. It moved to its present location on Benito Juarez Road, near Dhaula Kuan, in 1984. The Campus is now spread across 69 acres of green, hilly terrain and its buildings blend attractively with the natural surroundings. The various Departments are located in the Arts Faculty, the Faculty of Inter-disciplinary and Applied Sciences and the S.P. Jain Centre for Management Studies. Besides these, the Campus hosts a substantial library, a Health Centre, a bank, a post office, DTC Pass Section and administrative and examination blocks. South Campus also provides some residential quarters for faculty members and the non-teaching staff. Outstation students are offered accommodation in three hostels: the Geetanjali Hostel for Women, the Saramati Hostel for Men and the Aravalli P.G. Men's Hostel.

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